

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

CTCTCCCCC CCCCTCTCTC TCTCTCTCGC ATACTAACTA GGTTTGACTG TATTACTCGT      60
ACCAGATTTA AAATTAGACT AGCCTTGCCA CAACGCCCTA CTGAGAGGTA CTGTGGAAC      120
GTAGACAGCA TGATGTTCTT TGATGGTGAA AGTCTAAATC TGGACCGTGT TCAGAGATAC      180
CAAATGATGA GGCTGAAAAG GGGAAAGGGG GTTCTTCAGT CTCTTCTTCT TCTTCTTTTT      240
ATTTTTTTTT CCATGATGTT TTCTCTATGG CCAAGTCAAA TGGTGTTGTC ACCCTTGCAT      300
GTTGCCAAC                                     309

```

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Met Phe Phe Asp Gly Glu Ser Leu Asn Leu Asp Arg Val Gln Arg
1           5           10           15
Tyr Gln Met Met Arg Leu Lys Arg Gly Lys Gly Val Leu Gln Ser Leu
20           25           30
Leu Leu Leu Leu Phe Ile Phe Phe Ser Met Met Phe Ser Leu Trp Pro
35           40           45
Val Gln Met Val Leu Ser Pro Leu His Val Ala Asn
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

AGGTCTCTCT GGTTCCTTCT ATATCATCAT TTTATTATTA TGCCTAATA TAAAGTACTG      60
GCTCATAGGG CCAGGGTATT ATTATAGAAT ATTATNTTCG CATGTAAACA AAGATATCTT      120
TGCTTTAAGA TGTGAGAAGA AATGAATTTA CTTTGTTTGC ATTAAGTTAN GGAAGAGTTG      180
TAATATATAC TTTAAGAAAG AAGAGAAGAA AACTAGTATC TNTAAGCGGT AAAAAAAAAA      240
AAAAAAAAAA AAAAAAA                                     257

```

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

CACGAGGATT GATTTCATC TTGCCTCTCC ANAAGGCAAA ACCTTAGTTT TTGAACAAAG      60
AAAATCAGAT GGAGTTCACA CTGNTANANA CTGAANTTGG TGATTACATG TTCTGCTTTG      120
ACAATACATT CAGCACCATT TCTGAGAANG TGATTTTCTT TGAATTAATC CTGGATAATA      180
TGGGAGAACA GGCACAAGAA CAAGAAGATT GGAAGAAATA TATTACTGGC ACAGATATAT      240
TGGATNTNAN NCTGGAAGAC ATCCTGGAAT CCATCAACAG CATCAAGTCC AGACTAAGCA      300
AAAGTGGGCA CATACAAACCT CTGCTTAGAG CATTTGAAGC TCGTGATCGA AACATACAAG      360
AAAGCAACTT TGATAGAGTC AATTTCTGGT CTATGGTTAA TTTAGTGGTC ATGGTGGTGG      420
TGTCAGCCAT TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAG                      467

```

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Phe	Thr	Leu	Xaa	Xaa	Thr	Glu	Xaa	Gly	Asp	Tyr	Met	Phe	Cys	
1				5					10					15		
Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Xaa	Val	Ile	Phe	Phe	Glu	
			20					25					30			
Leu	Ile	Leu	Asp	Asn	Met	Gly	Glu	Gln	Ala	Gln	Glu	Gln	Glu	Asp	Trp	
		35					40					45				
Lys	Lys	Tyr	Ile	Thr	Gly	Thr	Asp	Ile	Leu	Asp	Xaa	Xaa	Leu	Glu	Asp	
	50					55					60					
Ile	Leu	Glu	Ser	Ile	Asn	Ser	Ile	Lys	Ser	Arg	Leu	Ser	Lys	Ser	Gly	
65					70					75					80	
His	Ile	Gln	Thr	Leu	Leu	Arg	Ala	Phe	Glu	Ala	Arg	Asp	Arg	Asn	Ile	
				85					90					95		
Gln	Glu	Ser	Asn	Phe	Asp	Arg	Val	Asn	Phe	Trp	Ser	Met	Val	Asn	Leu	
			100					105					110			
Val	Val	Met	Val	Val	Val	Ser	Ala	Ile	Gln	Val	Tyr	Met	Leu	Lys	Ser	
		115					120					125				
Leu	Phe	Glu	Asp	Lys												
				130												

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTTTGAAGA TAAGAGGAAA AGTAGAACTT AAAACTCCAA ACTAGAGNAC GTAACATTGA	60
AAAATGAGGC ATAAAAATGC AATAAACTGT TACAGTCAAG ACCATTAATG GTNTTNTCCA	120
AAATATTTTG AGATATAAAA GTAGGAAACA GGTATAATTT TAATGTGAAA ATTAAGTNTT	180
CACTTTCTGT GCAAGTAATC CTGCTGATCC AGTTGTACTT AAGTGTGTAA CAGGAATATT	240

TTGCAGAATA TAGGTTTAAC TGAATGAAGC CATATTAATA ACTGCATTTT CCTAACTTTG 300  
 AAAAATTTTG CAAATGTCTT AGGTGATTTA AATAAATGAG TATTGGGCCT AATTGCAAAA 360  
 AAAAAAAAAA AAAAAAAAAA AAAAAAA 387

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCTCTT GAAGNTGGGG GGTGCNGGNN GGGGAAANCG NNTCTCCNNT CCANAAGCGG 60  
 GGGCCNTTTT GTCCGTNNNC TTGTGNAAAA AANCCCGGNG NTGGTGAACG CTGNTNTTAN 120  
 TTACTCCAAA CCTCGANTGG NCNNTTNGTG GTNCNNGGCC GAGGNTGANN TGGNTCCCCC 180  
 CCCCCCTGNT NNAATNCCNA AACTNTTCN GAACCCGAAA ANAATTNTCC ATTCTGCCNN 240  
 NANTGGTTTC NTCCNNCNC TCCTNATTAA AGAAGCNNT 279

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCGGGTGAC ATTCAGCCGG CGGTTCGGGG GGACGGANTC TCCATTCCAG AACCATGGCC 60  
 CAATTTGTCC GTAACCTTGT GGAGAAGACC CCGGCGCTGG TGAACGCTGC TGTGACTTAC 120  
 TCGAAGCCTC GATTGGCCAC ATTTTGGTAC TACGCCAAGG TTGAGCTGGT TCCTCCCACC 180  
 CCTGCTGAGA TCCCTAGAGC TATTCAGAGC CTGAAAAAAA TAGTCAATAG TGCTCAGACT 240  
 GG TAGCTTCA AACAGCTCAC AGTTAAGGAA GCTGTGCTGA ATGGTTTGGT GGCCACTGAG 300

GTGTTGATGT GGTTTTATGT CGGAGAGATT ATAGGCA

337

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Gln Phe Val Arg Asn Leu Val Glu Lys Thr Pro Ala Leu Val  
1 5 10 15

Asn Ala Ala Val Thr Tyr Ser Lys Pro Arg Leu Ala Thr Phe Trp Tyr  
20 25 30

Tyr Ala Lys Val Glu Leu Val Pro Pro Thr Pro Ala Glu Ile Pro Arg  
35 40 45

Ala Ile Gln Ser Leu Lys Lys Ile Val Asn Ser Ala Gln Thr Gly Ser  
50 55 60

Phe Lys Gln Leu Thr Val Lys Glu Ala Val Leu Asn Gly Leu Val Ala  
65 70 75 80

Thr Glu Val Leu Met Trp Phe Tyr Val Gly Glu Ile Ile Gly  
85 90

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAATTANAGG AAGANCCTNT TGAAAAAATT TNTGTTTGTN AAAAAGNTAG GGNAATTGTT 60

ATTTTGGAAG TAGCCTNCCC NAGNGNGGAN AGGGGGGNAT TTTAAGNANG NTTTTTTGNA 120

AAATTTTNG NCGNNGGNA GAANCNAAAA AGNGGAATTT GNNTTTTAAG GGGGNTANTT 180

GNTTGTGGTGG GTTTAANACC CTTGCCAAAA NNAAANACCC CCAAGNNANT TNAANNAGGG 240  
 TATAANTTAG NATTTTTCCC TGGANTTAAA NAGNANATTA TATNCTGGAA NAAANGNAAN 300  
 GGTGTGTATN AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 345

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGAGATTCAG GACCTGCAGA GTCGCCAGAA GCATGAAATT GAATCTTTGT ATACTAACT 60  
 GGGCAAGGTT CCCCCTGCTG TCATTATTCC CCCAGCTGCT CCTCTGTCGG GGAGAAGAAG 120  
 GAGACCCACT AAAAGCAAAG GCAGCAAGTC TAGTCGCAGC AGCTCATTGG GCAATAAAAG 180  
 CCCACAGCTT TCAGGCAACC TGTCTGGTCA GAGTGGAAGT TCAGTCTTAC ACCCCCAACA 240  
 GACCCTCCAC CCTCCTGGCA ACATCCCANA NTCCGGGCAG AATCAGCTGT TACAGCCCCT 300  
 TAAGCCATCT CCCTCCAGTG ACAACCTCTA TTCAGCCTTC ACCAGTGATG GTGCCATTTC 360  
 AGTACCAAGC CTTTCTGCTC CAGGTCAAGG AACCAGCAGC ACAAACACTG TTGGGGCAAC 420  
 AGTGAACAGC CAAGCCGCCC AAGCTCAGCC TCCTGC 456

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Lys Leu Asn Leu Cys Ile Leu Asn Trp Ala Arg Phe Pro Leu Leu  
 1 5 10 15

Ser Leu Phe Pro Gln Leu Leu Leu Cys Arg Gly Glu Glu Gly Asp Pro  
 20 25 30  
 Leu Lys Ala Lys Ala Ala Ser Leu Val Ala Ala Ala His Trp Ala Ile  
 35 40 45  
 Lys Ala His Ser Phe Gln Ala Thr Cys Leu Val Arg Val Glu Leu Gln  
 50 55 60  
 Ser Tyr Thr Pro Asn Arg Pro Ser Thr Leu Leu Ala Thr Ser Xaa Xaa  
 65 70 75 80  
 Pro Gly Arg Ile Ser Cys Tyr Ser Pro Leu Ser His Leu Pro Pro Val  
 85 90 95  
 Thr Thr Ser Ile Gln Pro Ser Pro Val Met Val Pro Phe Gln Tyr Gln  
 100 105 110  
 Ala Phe Leu Leu Gln Val Lys Glu Pro Ala Ala Gln Thr Leu Leu Gly  
 115 120 125  
 Gln Gln  
 130

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TACCCTGCCC TCCTCCCTTT TTTNNACCCC TCTCTTTTTT ATTTTTTCTT TGCTCTTTAG 60  
 AACCCAGTGA AAAATACCAG GGTACTGGGG TGCAACTCTT TCTTATGATA GGTCATTAGT 120  
 GCTTTAAGCA AAAGATATTA GCAGCTTTGA CTGCAGCATT AGCAATTAGG NAAAAAAAAA 180  
 AAAAAAAAAA 188

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

CCTTATGGCC TACTTTAAAA AAAAACCAAT ACCAAAGAAG CCTACAATGT TGGCCTTAGC      60
CAAAATTCTG TTGATTTCAA CGTTGTTTTA TTCACTTCTA TCGGGGAGCC ATGGAAGAAGA      120
AAATCAAGAC ATAAACACAA CACAGAACAT NGCAGAAGTT TTAAAAACAA TGGAAAATAA      180
ACCTATTTCT TTGGAAAGTG AAGCAAACCTT AAACCTCAGAT AAAGAAAATA TAACCACCTC      240
AAATCTCAAG GCGAGTCATT CCCCTCCTTT GAATCTACCC AACAACAGCC ACGGAATAAC      300
AGATTTCTCC AGTAACTCAT CAGCAGAGCA TTCTTTGGGC AGTCTAAAAC CCACATCTAC      360
CATTTCCACA AGCCCTCCCT TGATCCATAG CTTTGTCTCT AAAGTGCCTT GGAATGCACC      420
TATAGCAGAT GAAGATCTTT TGCCCATCTC AGCACATCCC AATGSTACAC CTGCTCTGTY      480
TTCARAAAAC TTCACTGGT CTTTGTCAAT GACACCGTGA AAACCTCTGA TAACAGTTCC      540
ATTACAGTTA GCATCCTCTY TTCARAACCA ACTTCTCCAT CTGTGACCCC CTTGATAGTG      600
GAACCAAGTG GATGGNTTAC CACAAACAGT GATAGNTTCA CTGGGTTTAC CCCTTATCAA      660
GNAAAAACAA CTTTACAGCC TACCTTAAAA TTCACCAATA ATTCAAAACT NTTTCCAAAT      720
ANGTCAGATC CCCCAAAAAA AAAAAAAAAA AA                                     752

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser
1           5           10           15
Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn Thr Thr
20           25           30
Gln Asn Xaa Ala Glu Val Phe Lys Thr Met Glu Asn Lys Pro Ile Ser

```

	35		40		45	
Leu	Glu	Ser	Glu	Ala	Asn	Leu
50					55	
						Asn
						Ser
						Asp
						Lys
						Glu
						Asn
						Ile
						Thr
						Thr
Ser	Asn	Leu	Lys	Ala	Ser	His
65					70	
						Ser
						Pro
						Pro
						Leu
						Asn
						Leu
						Pro
						Asn
						Asn
Ser	His	Gly	Ile	Thr	Asp	Phe
			85			Ser
						Ser
						Asn
						Ser
						Ser
						Ala
						Glu
						His
						Ser
Leu	Gly	Ser	Leu	Lys	Pro	Thr
			100			Ser
						Thr
						Ile
						Ser
						Thr
						Ser
						Pro
						Pro
						Leu
Ile	His	Ser	Phe	Val	Ser	Lys
			115			Val
						Pro
						Trp
						Asn
						Ala
						Pro
						Ile
						Ala
						Asp
Glu	Asp	Leu	Leu	Pro	Ile	Ser
						Ala
						His
						Pro
						Asn
						Xaa
						Thr
						Pro
						Ala
						Leu
Xaa	Ser	Xaa	Asn	Phe	Thr	Trp
145						Ser
						Leu
						Ser
						Met
						Thr
						Pro

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGCTTGGCA CGAGGTCTTT AGAAGAACTA CAAACCTGA ATGGAAACT TCGAAGTGAA	60
GGACAAGGNA ATATGGGCTT TACTAGGCAG AATCACAGGG CAGAAGTTGA ATATACCGGC	120
AATTTTGAGA GCACCAAGG AGAGAAAACC AAGTAAAAAA AGAAGGAGGC ACACAAAAGA	180
CATCTACTCT TCCTGCAGTA CTTTATAGTT GTGGGATTG TAAGAAGAAC CATGATCAGC	240
ATCTTCTTTT ATTGTGTGAT ACCTGTAAAC TACATTACCA TTTTGATGT CTGGATCCTC	300
CTCTAACAAG GATGCCAAGA AAGACCCAAA ACAGTTATTG GCAGTGCTCG GAATGTGACC	360
AGGCAGGGAG CAGTGACATG GAAGCAGATA TGGCCATGGA AACCTACCA GATGGAA	417

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Pro Arg Lys Thr Gln Asn Ser Tyr Trp Gln Cys Ser Glu Cys Asp  
1 5 10 15

Gln Ala Gly Ser Ser Asp Met Glu Ala Asp Met Ala Met Glu Thr Leu  
20 25 30

Pro Asp Gly  
35

(2) INFORMATION FOR SEO ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCTGTGTTCA	GTATAATTTT	ATTTTCTCTCA	ACCTTAAATA	TGAACCTAGG	AAATAAGGAG	60
GGAAGTACAA	AGATTATTGA	CTATACAACN	TACCAGCTGA	AAGAAAGATC	TTCATCAACA	120
TCTGTATCTT	TCCAGAGGTA	TACAGAATTA	AAATTNNATN	TTCAAGCTTT	AATGATCCAG	180
TTTTAAGTCA	ACGGCAGAAG	TATGTTGAAT	ATTTTCATCAC	TCAATCTTGA	ACTGATTTAG	240
AAGAGACTCT	TTGCTGAAAT	TGAATTGCAC	TTATACATGT	AAATTGTCAA	CATGTAATTT	300
GGAATTTTCT	GATTAATAAA	TGTGGTTTTG	GACATCTAAA	AAAAAAAAAA	AAAAAAAAAA	359

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

CTCNCAAAATC GGCNCGNGCA ACGAACGGCT TGGGCGCGGA CTGGTATCCG GGGACTGTGA      60
CTTGCAAGGCT CCGCCATGGA GCCAGAGCAG ATGCTGGAGG GACAAACGCA GGTTCAGAA      120
AATCCTCACT CTGAGTACGG TCTCACAGAC AACGTTGAGA GAATAGTAGA AAATGAGAAG      180
ATTAATGCAG AAAAGTCATC AAAGCAGAAG GTAGATCTCC AGTCTTTGCC AACTCGTGCC      240
TACCTGGATC AGACACTTGT GCCTATCTTA TTACAGGGAC TTGCTGTGCT TGCCAAGGAA      300
AGACCACCAC ATCCCATTGA ATTTCTAGCA TCTTATCTTT TAAAAAACA GGCACAGTTT      360
GAAGATYGAA ACTGAMTTAA TGGGRAGAAC AGAAAAATTT AGTTGSTACT GTAGATTTAC      420
ATGATTAAGA RGCAGCTTTA ATTGCCATGA TCATTCCCTT TTTTGGGAAG GATAAGNACC      480
TTNCGGANAA CAGNACCTAT TTTTGGGATT GCAGNAGNTA AAATATTTCC CNTATTTTGA      540
NTTAATNACC ATAAACCNTA CCTATTTAAT GNGNGTATTT TGTGCAATTT TTTTTNAGN      600
TTGTTTTTAA ATTTGTTTTT AAAATGACCT TNAAAATNAA NTGTNNAAAC ACCNTTTAAA      660
AAAAAAAAAA AAAAAA                                                                675

```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr Gln Val Ala Glu Asn
1           5           10           15
Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val Glu Arg Ile Val Glu
          20           25           30
Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys Gln Lys Val Asp Leu
          35           40           45

```

Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln Thr Leu Val Pro Ile  
 50 55 60

Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu Arg Pro Pro His Pro  
 65 70 75 80

Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn Lys Ala Gln Phe Glu  
 85 90 95

Asp Xaa Asn

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CACGAGGGTT TGGTGAGGAA ATTACCAGAG AACTATTAAA GACTTGGATG CTCTTCTCGG 60

CTTTGCTATT AAGTAAGTTG GACAAGTTGT TTGGCTTCTT TGAGCCTCTG TTTTCTCCAT 120

TCTAAAATTC TAAATGGGA GTGTTGAATT AGATCAGTGG CTTTCGAACT TTCTGCTCCT 180

AGTAGTGAGA AATACATTTT ACTCCACTCC CTGGTATGTA CACGCATTCC TGTGTTTTGT 240

GAAAACCTGA CACCATGCTC CTCCCTCACT ACATGTAAAA CACTTTTATT CATTAAAAAG 300

AAACTGACT GGCTTGGACC TACAAATTAG TTTCATTATT TGTTAATGTT TGAAAGCCAT 360

TAAAAGATGA ATATTAAGGT TTCTTTATAC TCAATACTTG TAGTTTGTGTT TGGGGGAATG 420

AGAGGATGCC CTTGGTACCT TTGTGAGGCC TCTCCACTGA GGGTCAATCA TGACTTCTGT 480

TTTAAACCAG CCCATCCCAT CTTCTCCAGC TGCTCTCCTT ATGTCTTGCT TCTCTCCCCT 540

CCAACCTTCT CA 552

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Asn	Ile	Lys	Val	Ser	Leu	Tyr	Ser	Ile	Leu	Val	Val	Leu	Phe	Gly
1				5					10					15	
Gly	Met	Arg	Gly	Cys	Pro	Trp	Tyr	Leu	Cys	Glu	Ala	Ser	Pro	Leu	Arg
			20					25					30		
Val	Asn	His	Asp	Phe	Cys	Phe	Lys	Pro	Ala	His	Pro	Ile	Phe	Ser	Ser
			35				40					45			
Cys	Ser	Pro	Tyr	Val	Leu	Leu	Leu	Ser	Pro	Pro	Thr	Phe	Ser		
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGGCCCCA TCCTTCAGTG CATTGCACAC TTTGCATGNT GGGTCAGGGA AGATTGTGGA	60
GAGAGGACAG TGCACATGGT TTCCCCACN TNGNCTGCGT GGGGGTATGT CCTGCTTCCG	120
CCACTTCCAA CTGTGGCANT TGGGCACGCC CCTNTCAGGG CACCTCCCT TTTGTTTCC	180
GCAAAATGAG GTTGTAATAG TGCCTGCCGC ACTGTNTGGC ACACAGTAAG NTCTCAAGAA	240
ATGTTAGCTG TTGTTGCCGT TAGAACACCA TAGNTAGAAT ACCATACNTG GCATTCACTT	300
AAAAAAAAAA AAAAAAAAAA	318

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

ATTGAGGAAA ACCACAAAAA ACTTCAAAAC AGCTACAACG GGAAAAAGAG AGTTTTGTCC      60
CACAGTCAGC AGGCCACTAG TTTATTAAC TCCAGTCACC TTGATTTTTG CTAAATGAA      120
GACTCTGCAG TCTACACTTC TCCTGTTACT GCTTGTGCCT CTGATAAAGC CAGCACCACC      180
AACCAGCAG GACTCACGCA TTATCTATGA TTATGGAACA GATAATTTTG AAGAATCCAT      240
ATTTAGCCAA GATTATGAGG ATAAATACCT GGATGGAAAA AATATTAAGG AAAAAGAAAC      300
TGTGATAATA                                     310

```

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val Pro Leu
1           5           10           15

Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
          20           25           30

Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
          35           40           45

Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
50           55           60

Ile
65

```

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCCAAGNAAN TTTCAANTTT TTGCCTTTNC TGGCCTTTAN TGGATCCNA AAGCATTTAA	60
GGNANATGTT CCNAAAANTT TGNAAAGNTA AANGTTTCCC ATGATCGCTC ATTTTTTTTTT	120
TATGATTCAN ANGTTATTCC TTATAAAGTA AGNANTTTGT TTTCTCCTA TCAAGGCAGN	180
TATTTTATTA AATTTTTCAN TTAGTTTGAG NAATAGCAGA TAGTTTCATA TTTAGGGAAA	240
NTTTCCAAAT AAAATAAATG TTATTNTTTG ATAAAGAGNT AAAAAAAAAA AAAAAAAAAA	300
AAA	303

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGCTTGNGC ACGNGGCACA AGTAGCTACG NCTGCAAGCA CCTGCCACCA TAAAGGGGNT	60
GCATTTTGCC ACCATAAANG GGNTGCATTT TTTTAAAAAG CCTAGGCNGC TCTAACATCA	120
TCTGATATGG ACACAANGCN AACAGTTTCC NTATNTACAT CCNTACCTCT AAAAGATACT	180
TCAAAGTGAC AAAAACGTGT TCCTTCCCCA CTTAGAGACA ATGATTACA GGGCCCTATA	240
TGTTCTTACC ACATACAGAG GATGCATTTA TTTTGCTCT ATGACACTTG CAAAAATCTC	300
TACTGTAATT AATTTGGGTC TATTATTAAC TCTCTGTTCC ATCATAGAAT GTGGCCAGGC	360
CTTACAATGG AGAGCCAGAG TTAAACTTC AAGTTGCATC TGTTTTTGGG CTGAGTCA	418

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Thr	Leu	Ala	Lys	Ile	Ser	Thr	Val	Ile	Asn	Leu	Gly	Leu	Leu	Leu
1				5				10					15		
Thr	Leu	Cys	Ser	Ile	Ile	Glu	Cys	Gly	Gln	Ala	Leu	Gln	Trp	Arg	Ala
		20					25					30			
Arg	Val	Lys	Thr	Ser	Ser	Cys	Ile	Cys	Phe	Trp	Ala	Glu	Ser		
	35					40						45			

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGTTTGTTCT GTAAATATTT NGAAAAGTGA CAGCTNTCAA CTCAGGGTA ACTATTTCTA	60
AAAATGTAAA TANGTATTAA TCCTTGATC TTTTATGGTA ATTTNGCATA TTGATATGAA	120
TTANATAAAA TTGTTTAAAA TAAAAGGTGT CCTGAATTA CTGACCACCC ATAGATGTNT	180
ACTGTTACCA GGTTTTACAA TGCAAATTTT CACTAATACC TGGGTTTAAT ACAGCTCACA	240
TCACTGAATG TTACACATGA GTTTAAATGG GTTAATATAC AGGTTTTGTT ATAATAAAGT	300
TACTGATTAA ATTAAAAAAA AAAAAAAAAA A	331

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 583 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

CACGNGGGTG AGGCCGACTG CTGAAGACAG CTCGCCACCC TCCTTGCCTC CACTCCAATC      60
CAGGGGCTGG GGCCACATTC TTTGCCTTCA TTTATCCTCA GATCAGGTGA GATCGACAGG      120
AGGTGTTGAT GGCAGTGCCA GCAATTATTG CTAATCCGTT TGCATCCTTA TGCATAGATC      180
TGAATTCAGA CTTTGTGAAT TTCCAGAGGT GTGGGTNATA TAATAGAATT CAGTGAGTGG      240
GCATGGCTGA TCTTGTGCAA ATTAAAAGTT ATGGGGCATA AGAATAGCAA AAGTTGAACT      300
TCTTTTAAAA AGGAAAGTAC CCTGAGAGCC AGTATTGGTT GAGGCTCTTC AGTATGCCCCA      360
GGTTGGCAGC ACTGAGAACC GCAGGAACGG CCTGTTGTTA CAAAAGGAG ATTGACTCAG      420
CTGCCCTTGG TGCATCTGAC TGA CTATGAC TGCTGAGAGA TTCCAAGGAC CCTTAATGCC      480
AGGGCTAACC TCTCCATGTG CAGTGAGACC TCTGGAGGAA GTGTCATCCT CTGGCTTTGT      540
GTGGTACTCA TTATGGTGCA GTGCGGGCAT GAAATGAAGA CAC                          583

```

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Met Cys Ser Glu Thr Ser Gly Gly Ser Val Ile Leu Trp Leu Cys Val
1           5           10           15

Val Leu Ile Met Val Gln Cys Gly His Glu Met Lys Thr
                20                25

```

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCAAATAGG CTTACAGATA CGATATGTTT TAAATGTTTN GTATTTAACA AAAACATACT	60
GAACTGTTT GGAAATGGCA ACAGGAAGAT AGCAAAATGA ATACTAACAT TACGAAAAGA	120
TGAACAGGTA CATGTTCCAA GGCAGGTGGC TGTGAACTTC CTCTGAGTGA AGGCATCCCC	180
TCCAGCACCT TTCAGCCTGC TAGTTAGGAC GACCCGCCGC CACCCTCCAG GACNTCCAGC	240
CCTGCANTGC NTTTCTTTTN TTTTAAATAA TTCTTCATTG AGTTCTAATA TGTAACAAAA	300
AAAAAAAAA A	311

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAGCTTGGCA CGAGGGCGGT TGAGGCCTTC GGTGGTGAAC GAGTCTCCAG CACCATGTCT	60
GGTTTGTCTG GCCCACCAGC CCGGCGCGGC CCTTTTCCGT TAGCGTTGCT GCTTTTGTTC	120
CTGCTCGGCC CCAGATTGGT CCTTGCCATC TCCTTCCATC TGCCCATTA CTCTCGCAAG	180
TGCCTCCGTG AGGAGATTCA CAAGGACCTG CTAGTGACTG GCGCGTACGA GATCTCCGAC	240
CAGTCTGGGG GCGCTGGCGG CCTGCGCAGC CACCTCRAGA TCACAGATTC TGCTGGCCAT	300
ATTCTCTACT CCAAAGAGGA TGCAACCAAG GGGAAATTTG CCTTTACCAC TGAAGATTAT	360
GACATGTTTG AAGTGTGTTT TGAGAGCAAG GGAACAGGGC GGATA	405

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Gly Leu Ser Gly Pro Pro Ala Arg Arg Gly Pro Phe Pro Leu  
 1 5 10 15

Ala Leu Leu Leu Leu Phe Leu Leu Gly Pro Arg Leu Val Leu Ala Ile  
 20 25 30

Ser Phe His Leu Pro Ile Asn Ser Arg Lys Cys Leu Arg Glu Glu Ile  
 35 40 45

His Lys Asp Leu Leu Val Thr Gly Ala Tyr Glu Ile Ser Asp Gln Ser  
 50 55 60

Gly Gly Ala Gly Gly Leu Arg Ser His Leu Xaa Ile Thr Asp Ser Ala  
 65 70 75 80

Gly His Ile Leu Tyr Ser Lys Glu Asp Ala Thr Lys Gly Lys Phe Ala  
 85 90 95

Phe Thr Thr Glu Asp Tyr Asp Met Phe Glu Val Cys Phe Glu Ser Lys  
 100 105 110

Gly Thr Gly Arg Ile  
 115

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTTCAATT TACCTTGTGA AAACACCCTT AACTTTTCT TNACCCTTAG CTGAAATGTT 60

NACATAGCTT NTGGTGATAT CTTTTCATGA TTTTATATNT CTTAAAATGG TGATGGATGT 120

GACACCTCAT AAAAGTGAGC TTTGAACTGT AGATAACTCT TAAAGAAAAT GTCATTTTAG 180

ACAATTAAAA TATTTGTGCT CAAAAAAAAA AAAAAAAAAA AAAAA 225

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

CGAGGGCAGG TCAGTCAGGT TCCTGGGCGC TCTGTTACAC AAGCAAGATA CAGCCAGCCC      60
CACCTAATTT TGTTTCCCTG GCACCCTCCT GCTCAGTGCG ACATTGTCAC ACTTAACCCA      120
TCTGTTTCTCT CTAATGCACG ACAGATTCCT TTCAGACAGG ACAACTGTGA TATTTTCAGTT      180
CCTGATTGTA AATACCTCCT AAGCCTGAAG CTTCTGTTAC TAGCCATTGT GAGCTTCAGT      240
TTCTTCATCT GCAAATGGG CATAATACAA TCTATTCTTG CCACATCAAG GGATTGTTAT      300
TCCTTTAAAA AAAAACCAAT ACCAAAGAAG CCTACAATGT TGGCCTTAGC CAAAATTCTG      360
TTGATTTCAA CGTTGTTTTA TCACTTCTA TCGGGGAGCC ATGGAAGA AAATCAAGAC      420
ATACACACAA CACAGAACAT TGCAGAAGTT TTTAANACAA TGGAAAATAA ACCTATTTCT      480
TTGGAAGTG AAGCAAACCTT AACTCAGAT AAAGNAAATA TAACC                        525

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser
1           5           10           15
Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile His Thr Thr
20           25           30
Gln Asn Ile Ala Glu Val Phe Xaa Thr Met Glu Asn Lys Pro Ile Ser
35           40           45
Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Xaa Asn Ile Thr
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCAAAAGGTN ACACAAAATT ACTGTCACGT GGATTTTGTC AAGGAGAATC ATAAAAGCAG	60
GAGACCAGTA GCAGAAATGT AGACAGGATG TATCATCCAA AGGTTTTCTT TCTTACAATT	120
TTTGGCCATC CTGAGGCATT TACTAAGTAG CCTTAATTTG TATTTTAGTA GTATTTTCTT	180
AGTAGAAAAT ATTTGTGGAA TCAGATAAAA CTAAAAGATT TCACCATTAC AGCCCTGCCT	240
CATAACTAAA TAATAAAAAT TATTCCACCA AAAAATTNTA AAACAAAGNA AAAAAAAAAA	300
AA	302

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACGAGGTTT CAGACCAGCT TGTGTCAATA GGGTCCTACA GAGCAGCTGA TATCAGCAGT	60
TTTACTAGTA TGCAGGACCT GAAAGAATAT CTCAAAGGGA AAACAATGTT TCATAATGTT	120
CAGGAAGTTA TCTATAGAGC AGCTAAGGAG CTATAATCTT GTAACAGAGT CTACGTGATT	180
GTAGGACAAT AGGCACCACA CAAATATGAG GAAGCAGGTC AGAGAGCGGG CTGACTTAAT	240
GATTAATGCT GAATGTGCTA CAAGCTTGTT TCATTTTCAT TTCTCCTCCT CCCTTTTTTC	300
CTGATTAATT TAATAAAGTT CATAGGGGAG GCTTCAAACA CATGAGAAAT TAAAACCTTT	360
ATTACCAGAG TCAGAGCCTG ACTATATTGA TTGAGTGAAG CTTTCCTTTA TAAAATGCAA	420
AGCATGTAAA CAATTCCAAC ACAGTAACAT ATTCATGAGT TTTTAAATTC ATGAGTTTTA	480

GAGAAAATAT TTTACTTAAA ACCAGCACTT GATGATCTCT GACAATGTTA TGTAGCCTGA	540
ACCTGGAGTT TTGGCTGATG GGTGTCTCA GCCTGTGACA GGTTTTAGCT GGCTTTGGTT	600
CATCTTGAT CACACCCCCA CACTCACA	628

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Pro Glu Pro Gly Val Leu Ala Asp Gly Leu Ser Gln Pro Val Thr Gly  
1 5 10 15  
Phe Ser Trp Leu Trp Phe Ile Leu Tyr His Thr Pro Thr Leu Thr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCAGCTAAG GGGAAATAAT CTTGTAACAG GGTCTGGGTG ATTNTGAGGT AATAGGCCCC	60
AAACAACCAT GGGGAAGCAG GTCAGAGGGC AAGCTGGCNT AGTGTTTAAC ATTGAATGGG	120
CTGAAAGTTT GGTTNATTTT TGTTCCTTGT TTCTCCCCCT CCTTCTNAC CTGAATAATT	180
TTATGAAGTT TATAGGGATG GTTTCAGGAC CTCCATTCTA TCTGTTCTCG AAATATTACA	240
AAAAGATTAT TATTGTAGCA CTNATNTAAT TGGGGTTTTA TTTCGTTGTT NGCATGTCTG	300
TTTCTTCCCC AGTGAGTTGT AAATTGCTTA AGGGCAAACA GACGCATCCT ATTTATCTGT	360
CTGTCACTAA CATTAAGCAC AGCATTTGGT ATACAGTCAT CACTCTAATA AAGTTTGAAA	420

AAAAAAAAAA AAAAAA

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 636 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CACGAGGGAA AAAAAGAGTT TTTTTTTTAG ATCATCAGCT ATTGTTAGTG TTTGTGTATG	60
TTATGTGTGG CTCAAGACAA CTTTGCTTCT TTTAATATAG GCAGGGAAGT CAAAAGATTG	120
GATATCCCTG CTTTATACCA AGAAAGACAA CACCCACAT TTGCAGTGCC TGAAAACACT	180
ACCAGCCATC TGAAAAACAT GTGACTTCTA ACTTCTGTTC TTTTTTGTAG CAGTGGAATC	240
CCACGGTGAT ATCTGAGGGA TGTGGTTACC TTTTGAGGA GGTGACGGT TTCTAAGGAT	300
GATTCTTTCT GAGTGAAATA TTGTCAGTGT CATTGACCTT TTCATTATTT CAACTATTAT	360
TATTCCAGGT TATCAATACT CTGGCTGACC ATCATCATCG TGAGACTGAC TTTGGTGTAG	420
GAGTTCGAGA CCACCCTGGC CAACATGGCA AAACCCCATC TCCACAAAAA TTGGATAATT	480
TGATAATTAT CATTATTGGG TTTCTGAGAC GTTACACATT TAACATTNTN TTCTGCACAA	540
GTTGCCTTTG TGTGAGTATA CTAACTTTCT GTAGAGGTAN ACTTGTAATC ACAAATAAGA	600
ATAAATTATA TAAACAAAAA AAAAAAAAAA AAAAAA	636

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Phe Phe Leu Ser Glu Ile Leu Ser Val Ser Leu Thr Phe Ser Leu Phe

1	5	10	15
Gln Leu Leu Leu Phe Gln Val Ile Asn Thr Leu Ala Asp His His His	20	25	30
Arg Glu Thr Asp Phe Gly Val Gly Val Arg Asp His Pro Gly Gln His	35	40	45
Gly Lys Thr Pro Ser Pro Gln Lys Leu Asp Asn Leu Ile Ile Ile Ile	50	55	60
Ile Gly Phe Leu Arg Arg Tyr Thr Phe Asn Ile Xaa Phe Cys Thr Ser	65	70	75
Cys Leu Cys Val Ser Ile Leu Thr Phe Cys Arg Gly Xaa Leu Val Ile	85	90	95
Thr Asn Lys Asn Lys Leu Tyr Lys Thr	100	105	

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCACGAGGA GCGGGAGCTG GTGCCTTCCC GGAAGGGCTC AGAGGCGGGC TCGGGCAAGC	60
ACTTTAACCT TTTAAGCCCA ACCAGATGAG TTGCCTGCAG TTTTGGAGGC CTTACAGACA	120
TTTCACTAGA CCTCTGTCTG TGTCGGTCCA ATGTCTTTAG CCAAGCTTTG ATTAAAGATG	180
ACTTCCTTGT TTGCTCAAGA AATTCGCCTT TCTAAAAGAC ATGAAGAAAT AGTATCACAA	240
AGATTAATGT TACTTCAACA AATGGAGAAT AAATTGGGTG ATCAACACAC AGAAAAGGCA	300
TCTCAACTCC AAAGTGTGA GACTGCTTTT AAAAGGAACC TTAGTCTTTT AAAGGATATA	360
GAAGCAGCAG AAAAGTCACT ACAGACCAGG ATTCACCCAC TTCCACGGCC TGAGGTGGTT	420
TCTCTTGAGA CTCGTTACTG GGCATCAGTA GAAGAATATA TTCCCAAATG GGAACAGTTT	480
CTTTTAGGAA GAGCACCATA TCCTTTTGCT GTTGAAAATC AAAATGAAGC AGAAAA	536

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met Thr Ser Leu Phe Ala Gln Glu Ile Arg Leu Ser Lys Arg His Glu
1           5           10           15

Glu Ile Val Ser Gln Arg Leu Met Leu Leu Gln Gln Met Glu Asn Lys
20           25           30

Leu Gly Asp Gln His Thr Glu Lys Ala Ser Gln Leu Gln Thr Val Glu
35           40           45

Thr Ala Phe Lys Arg Asn Leu Ser Leu Leu Lys Asp Ile Glu Ala Ala
50           55           60

Glu Lys Ser Leu Gln Thr Arg Ile His Pro Leu Pro Arg Pro Glu Val
65           70           75           80

Val Ser Leu Glu Thr Arg Tyr Trp Ala Ser Val Glu Glu Tyr Ile Pro
85           90           95

Lys Trp Glu Gln Phe Leu Leu Gly Arg Ala Pro Tyr Pro Phe Ala Val
100          105          110

Glu Asn Gln Asn Glu Ala Glu
115

```

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

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TTTATTTTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAAA AAAAAAAAAA
79

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What is claimed is:

1. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:
  - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 28 to nucleotide 276;
  - (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AE402\_1i deposited under accession number ATCC 98190;
  - (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AE402\_1i deposited under accession number ATCC 98190;
  - (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AE402\_1i deposited under accession number ATCC 98190;
  - (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AE402\_1i deposited under accession number ATCC 98190;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity;
  - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
  - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.
2. The composition of claim 1, further comprising a pharmaceutically acceptable carrier.
3. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 2.
4. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
  - (b) fragments of the amino acid sequence of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AE402\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

5. The composition of claim 4, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

6. The composition of claim 4, further comprising a pharmaceutically acceptable carrier.

7. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 6.

8. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 61 to nucleotide 513;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 322 to nucleotide 513;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AE610\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AE610\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AE610\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AE610\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity;
  - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.
9. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:5;
  - (b) fragments of the amino acid sequence of SEQ ID NO:5; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AE610\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.
10. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 523;
  - (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AH106\_1i deposited under accession number ATCC 98190;
  - (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AH106\_1i deposited under accession number ATCC 98190;
  - (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AH106\_1i deposited under accession number ATCC 98190;
  - (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AH106\_1i deposited under accession number ATCC 98190;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

11. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
  - (b) fragments of the amino acid sequence of SEQ ID NO:8; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AH106\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

12. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 130 to nucleotide 309;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AH196\_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AH196\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AH196\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AH196\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

13. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) fragments of the amino acid sequence of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

AH196\_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

14. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 69 to nucleotide 467;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AI6\_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AI6\_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AI6\_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AI6\_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

15. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:13;
- (b) the amino acid sequence of SEQ ID NO:13 from amino acid 69 to amino acid 133;
- (c) fragments of the amino acid sequence of SEQ ID NO:13; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AI6\_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

16. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:16;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:16 from nucleotide 55 to nucleotide 337;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ13\_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ13\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ13\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ13\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:17;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:17 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

17. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:17;
  - (b) the amino acid sequence of SEQ ID NO:17 from amino acid 12 to amino acid 94;
  - (c) fragments of the amino acid sequence of SEQ ID NO:17; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone AJ13\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

18. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 33 to nucleotide 422;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 114 to nucleotide 422;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ27\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ27\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ27\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ27\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

19. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
  - (b) fragments of the amino acid sequence of SEQ ID NO:20; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AJ27\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

20. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22 from nucleotide 47 to nucleotide 517;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22 from nucleotide 116 to nucleotide 517;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ142\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ142\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ142\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ142\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:23;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:23 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

21. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:23;
  - (b) fragments of the amino acid sequence of SEQ ID NO:23; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AJ142\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

22. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24 from nucleotide 312 to nucleotide 417;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK604\_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK604\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK604\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK604\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

23. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:25;
- (b) fragments of the amino acid sequence of SEQ ID NO:25; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

AK604\_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

24. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 76 to nucleotide 372;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK620\_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK620\_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK620\_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK620\_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

25. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
  - (b) fragments of the amino acid sequence of SEQ ID NO:28; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AK620\_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

26. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 367 to nucleotide 552;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK650\_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK650\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK650\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK650\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

27. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) fragments of the amino acid sequence of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone AK650\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

28. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 116 to nucleotide 310;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 173 to nucleotide 310;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AM226\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AM226\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AM226\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AM226\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

29. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:33;
- (b) fragments of the amino acid sequence of SEQ ID NO:33; and

(c) the amino acid sequence encoded by the cDNA insert of clone AM226\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

30. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 281 to nucleotide 418;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 353 to nucleotide 418;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AR417\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AR417\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AR417\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AR417\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

31. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) fragments of the amino acid sequence of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone AR417\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

32. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38 from nucleotide 496 to nucleotide 583;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38 from nucleotide 565 to nucleotide 583;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AU43\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AU43\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AU43\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AU43\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:39;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:39 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

33. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:39;
- (b) fragments of the amino acid sequence of SEQ ID NO:39; and

(c) the amino acid sequence encoded by the cDNA insert of clone AU43\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

34. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 55 to nucleotide 405;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 148 to nucleotide 405;

(d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AW60\_1i deposited under accession number ATCC 98190;

(e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AW60\_1i deposited under accession number ATCC 98190;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AW60\_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AW60\_1i deposited under accession number ATCC 98190;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

35. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) fragments of the amino acid sequence of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone AW60\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

36. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 337 to nucleotide 525;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 406 to nucleotide 525;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BA176\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BA176\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BA176\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BA176\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:45;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

37. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:45;
- (b) fragments of the amino acid sequence of SEQ ID NO:45; and

(c) the amino acid sequence encoded by the cDNA insert of clone BA176\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

38. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 536 to nucleotide 628;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BD140\_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BD140\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BD140\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BD140\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

39. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) fragments of the amino acid sequence of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD140\_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

40. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50 from nucleotide 303 to nucleotide 617;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50 from nucleotide 345 to nucleotide 617;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BD407\_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BD407\_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BD407\_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BD407\_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

41. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:51;
- (b) the amino acid sequence of SEQ ID NO:51 from amino acid 1 to amino acid 32;
- (c) fragments of the amino acid sequence of SEQ ID NO:51; and

(d) the amino acid sequence encoded by the cDNA insert of clone BD407\_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

42. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:52;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:52 from nucleotide 178 to nucleotide 534;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BF290\_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BF290\_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BF290\_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BF290\_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:53;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:53 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

43. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

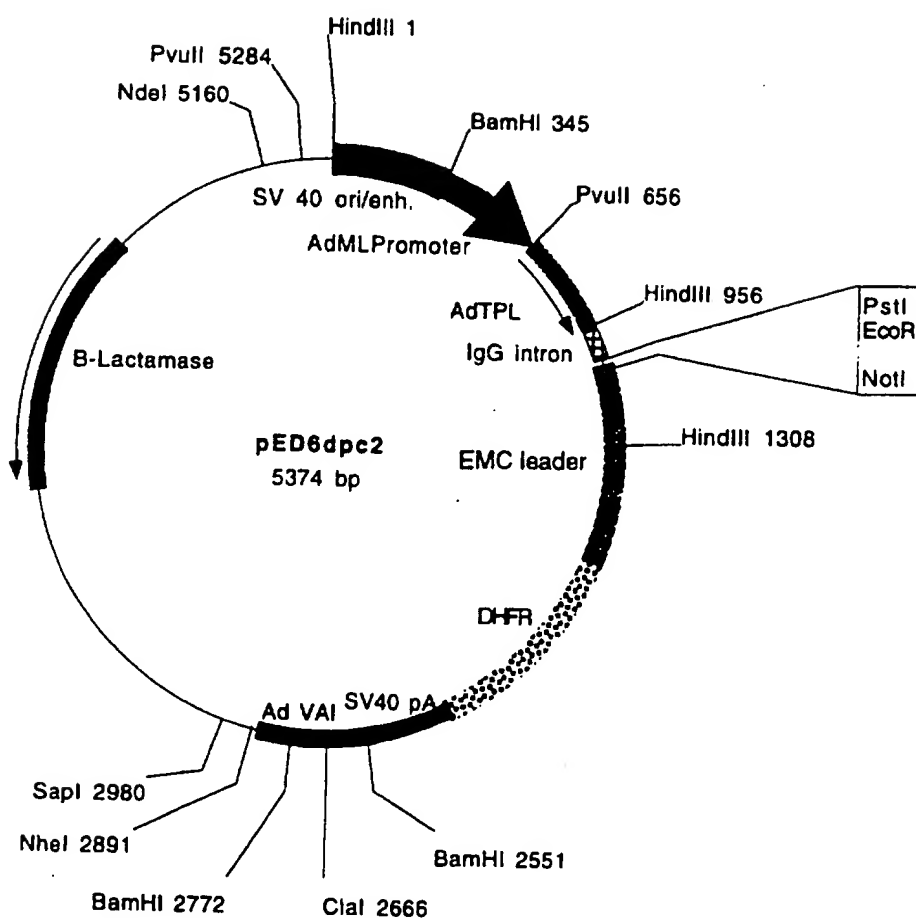
(a) the amino acid sequence of SEQ ID NO:53;

(b) fragments of the amino acid sequence of SEQ ID NO:53; and

(c) the amino acid sequence encoded by the cDNA insert of clone BF290\_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

FIGURE 1A

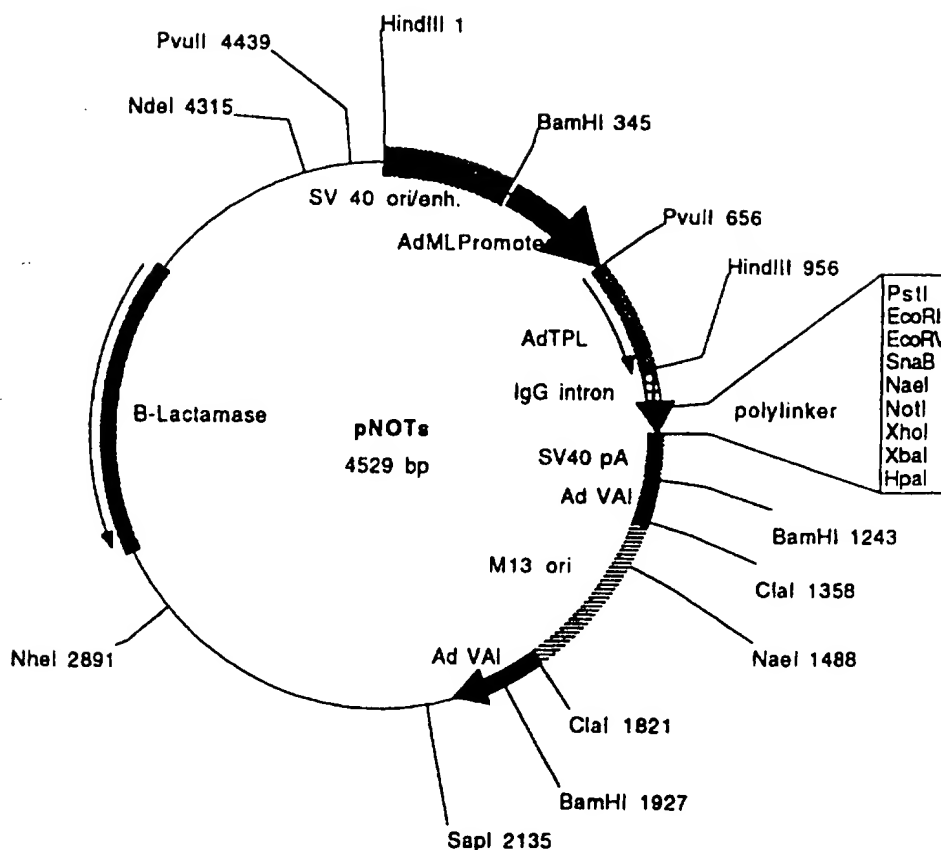


**Plasmid name:** pED6dpc2

**Plasmid size:** 5374 bp

**Comments/References:** pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



**Plasmid name:** pNOTs

**Plasmid size:** 4529 bp

**Comments/References:** pNOTs is a derivative of pMT2 (Kaufman et al, 1989, Mol. Cell. Biol. 9: 1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the ClaI site. SST cDNAs are cloned between EcoRI and NotI

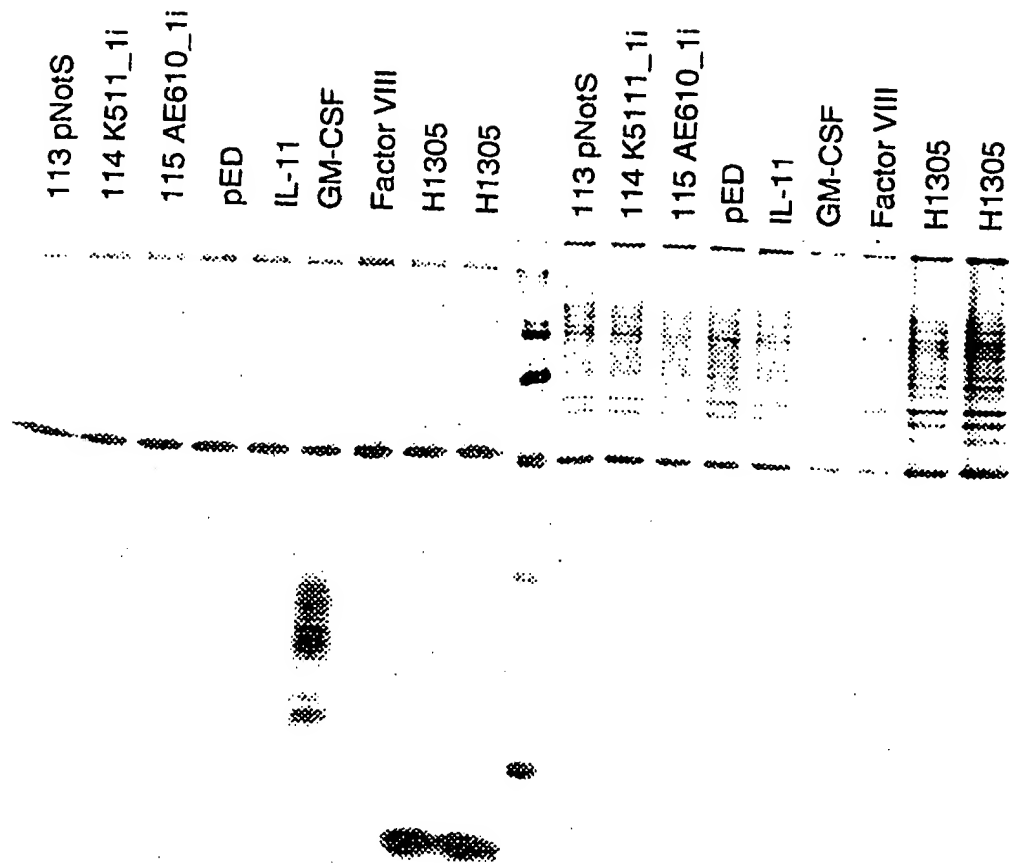


Fig. 2

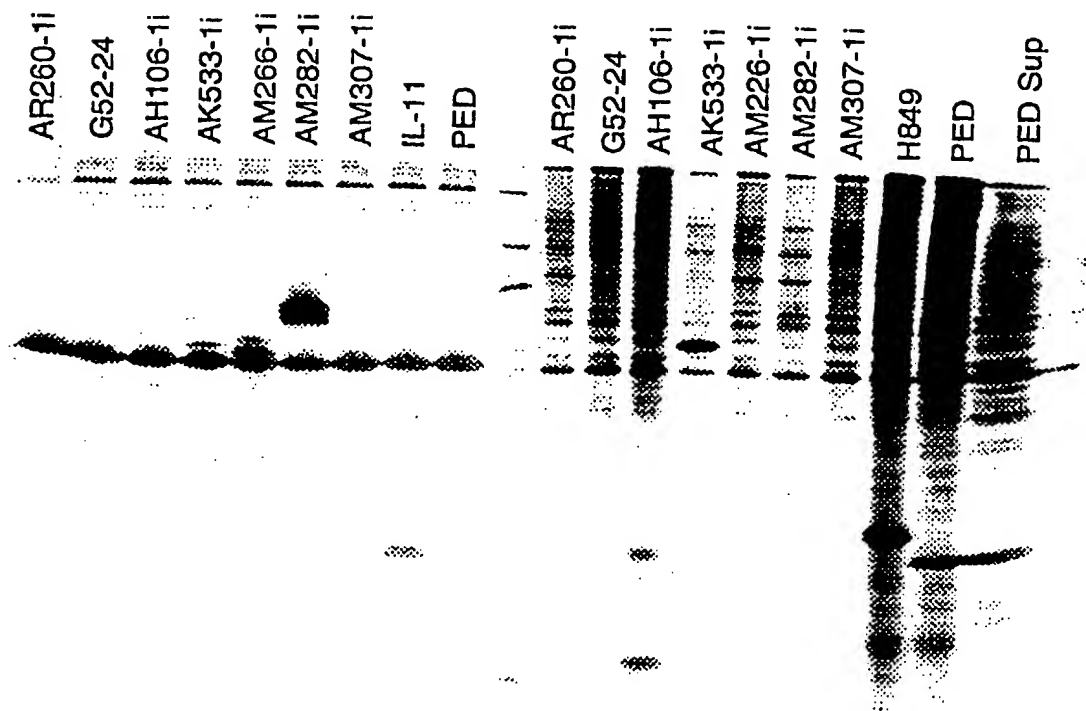


Fig. 3  
4/10

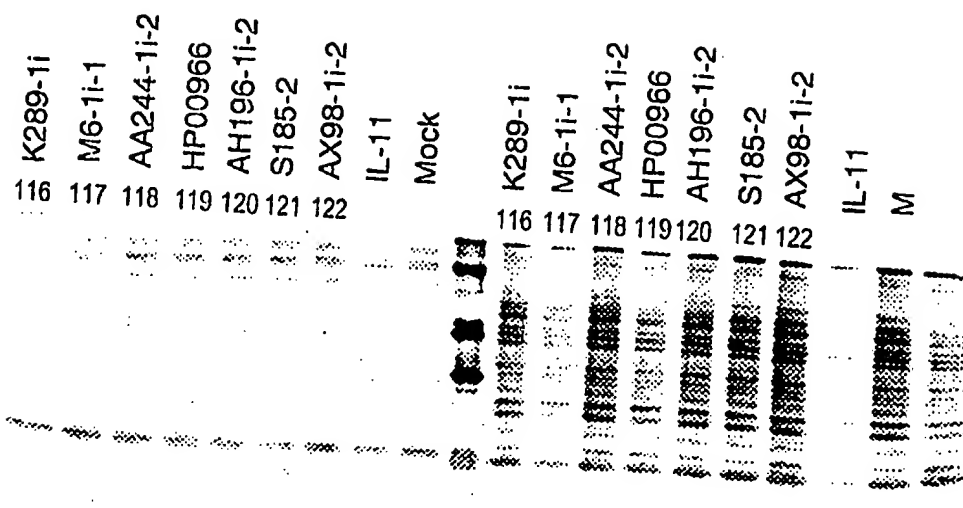


Fig. 4  
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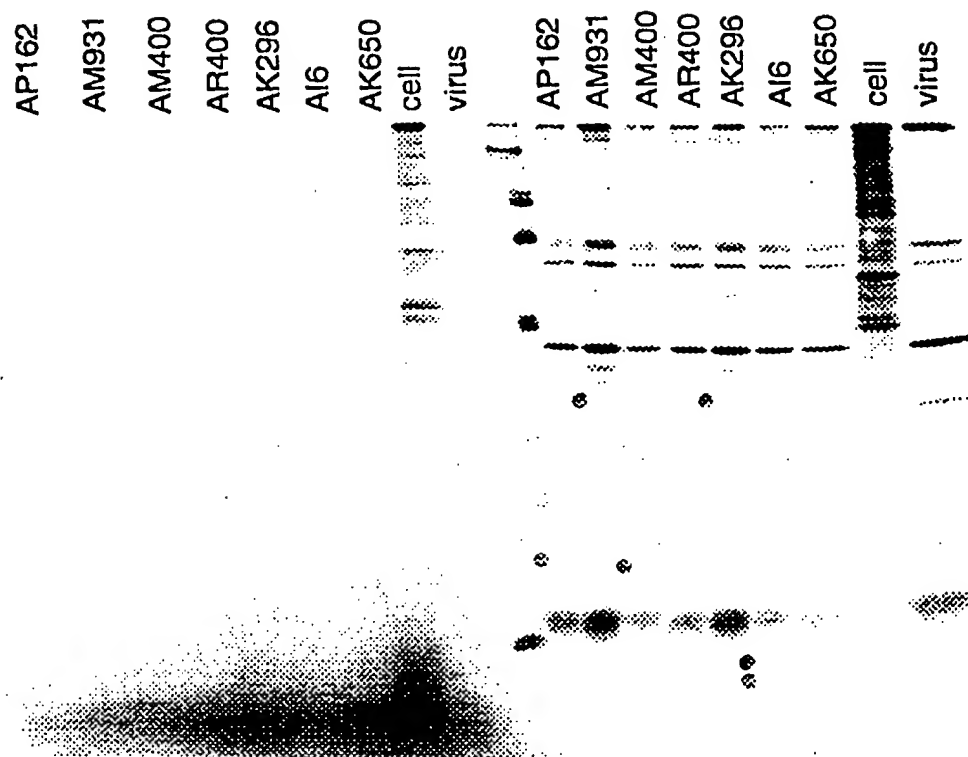


Fig. 5

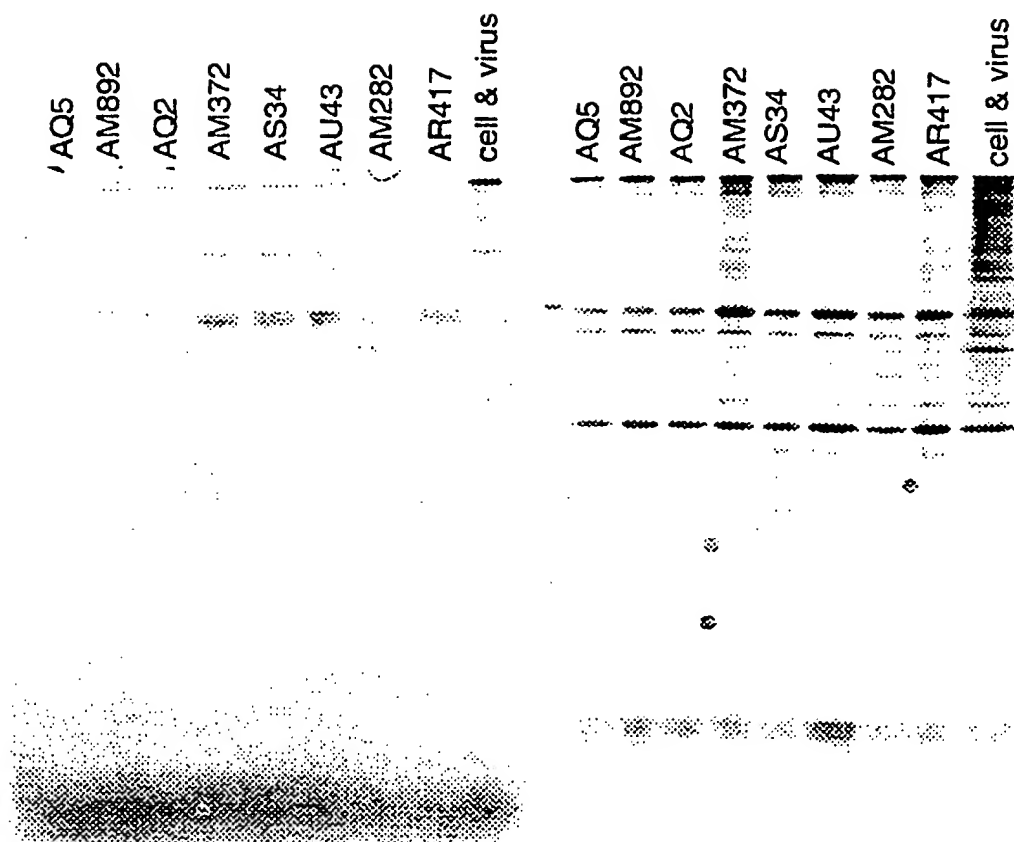


Fig. 6

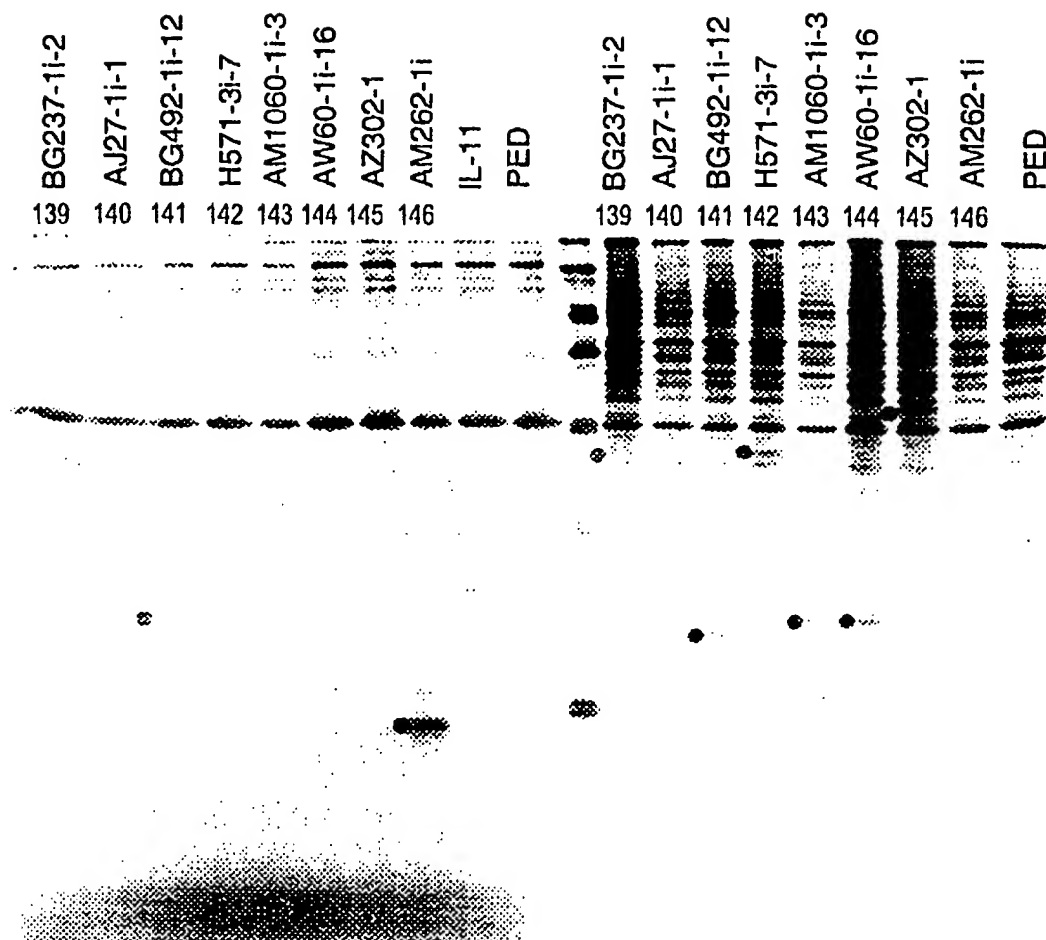


Fig. 7

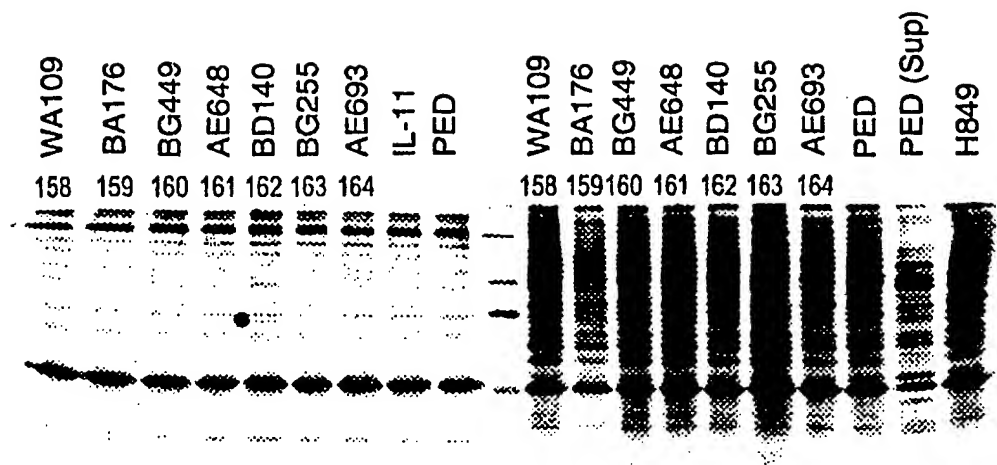


Fig. 8  
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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<p>(21) International Application Number: PCT/US97/20313</p> <p>(22) International Filing Date: 5 November 1997 (05.11.97)</p> <p>(30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US</p> <p>(71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).</p> <p>(74) Agents: GRANAHAH, Patricia et al.; Hamilton, Brook, Smith &amp; Reynolds, Two Militia Drive, Lexington, MA 02173 (US).</p>		<p>(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p><b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a  
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays  
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for  
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to  
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference. (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION  
DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- 10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment
- 15 of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the
- 20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- 25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- 30 As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with - polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15  $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$ .

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25  $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $cum p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of
- 25        polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ), ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$ , to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence. That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by  
5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a  
10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such  
15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a  
20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the  
25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament  
30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTAACTCCACATTGAAGCCAAAGAAAGAACACACACATGACATGAAACACATGCCAGTTGGGAAGGCTCT
						GAAACTCAGTGCATATAGGAACACATTGAGACTAATGAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	---	---	TACTAGACTTTATGCCATGGTGCTTTTC/TAAGTTTAATGCTGTCTCTCTGTCAG
						AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTGAAAT
WI-10744	61	G	C	---	---	AAATGAGGTAAGTTTCAGGCACACA
						GGGCAATTACAGCAAAAAGTCAATTTACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACA
						TTACAGTAACATATGCAATCTTTTGTATATAGTATATCTGCCAATGCCCTAGATA[C/T]AGTG
						GGTCCCTAATAGTATTAGTTCCTTTTCTCCTCTTCTCACTCTGAAATTTATTTTATACTTAA
WI-9975	126	C	T	---	---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATCTTACTGAA
						GCTAGGTTTGTCTTGTGGCTGTCTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT
						GATGTAACCTAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAAGTATGCCACAC
						TCACCCCTCTCTCCAGTTCACTGTATTAATTTCTCCCATATTAATCAAGGGAGTGGACAGGT
WI-8010	247	G	T	---	---	CCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGTGGGG[G/T]CTT
						GCCCGGCTATCTTTAATTTAACTTGATCTTTGGTGTCTCCATCCTAGGATCTGCCCTATAAT
						CTTTGTCTCTGTGTA[G/C]ATTACCTGATTCATCTTTTGATACAAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGTCCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTCTACTTA
WI-5222b	85	G	C	---	---	TCCTGACTCTATAACAACCTCCAAACAGM
						GCCCGGCTATCTTTAATTTAACTTGATCTTTGGTGTCTCCATCCTA[G/C]GATTCGCCCTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATTCATCTTTTGATACAAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGTCCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTCTACTTA
WI-5222	52	G	C	---	---	TCCTGACTCTATAACAACCTCCAAACAGAA
						TATGCACTCCACAAAAGGATATAATTTAAAGTTTTTTCATTAGAAAATAATGATATAAAAATAA
						ATATGTTATTAGGCATTTATTACTAATACTAGTCCCTCTTGGAGGAACACCCCAACCAATAGTT
						ATAAAGTACATGTAATTTATAGTAACATAATTTACTATATACATATGGAATAATCATATTCACACA
WI-8007	242	C	A	---	---	GAAGAGCTGAACAGACATTCCACAGGATACGACTGTGGAC[C/A]AGCTGCTG
						TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTTGTTAG
						TCTATATCACACATATGAGTGAATTT[C/T]GGGGCATGGGAAATACATCTTTTATGAGACATTGA
						ACTGCTACCACACTATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTTAC
WI-9823	97	C	T	---	---	ATGCTTCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	---	TCTACATTCATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTCATGTACAAATTTTCTGCTCGTCTTCAATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAATCCCTGGTGTTGAATGCTCTC
WI-9651	139 T C ---	---	---	TCTACATTCATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTCATGTACAAATTTTCTGCTCGTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCTCTGT CTTAAACCTGTAATGGTATATTAATCCCTGGTGTTGAATGCTCTC
WI-7676b	309 A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGGAGGCTGTGTGAAGGG GCGGCTCTCTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGCACTGCAGCTTCTGCTGTGCTG TCCCGGCTCCTGAGGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGGAGGCTGTGTGAAGGG GCTGCTGCTCTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGCACTGCAGCTTCTGCTGTGCTG GTGCTCCCCCTGCTCCTGGAGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTGTCTTGGTCTGTTCATTCACCTTCTCTCCTCCAAATGAAGGATATTTAAGCATCAIT CATCTGGCCCTTTTGTGAGTTTGAATAATTTTGTGATGACTCCTATGCACATGATAAATTTGTTA TGTCTGCTCTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACTTATAGATATTTAATATCTTT
WI-9986	42 T C ---	---	---	TTGGTGTGAACCTCAGAAATAGGGAAATAGACAAATTTGAAAT/A C]GTACCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGATCCAGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTTGGATTCTTAGAACCTTATTGCAAT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATAGGCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTGCATGCGCTATCCCGCTCTGCTCTC/C]CCACCTTCTTTGGAGCAAGGAGATGC AGCTGATTTGTGTAAACAGCTCAITTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	---	ATAACCCCTTGATGTATCATCCCAACTCACTAATATCAACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAATCCTAAGCATCAAACTTTCATCCATAAAATGTCAGCATTT /CIATTAAGGATGGCTGTGATTATCTTGGGAGGAGAGTGAATCATGCTAG

WI-10826	132	A C ---	---	TCCTATTGCAATTCACAGTAGCCCATGAAGTAGGTAAACACGCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTCCTAATAAGCAAAAGACCTGCAJ/C JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCCGAGCTCTCCATCCCCCAG
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACCTTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAACCTTGCGGTATAGAAATGGAATGGAGAGTTTCAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACCTGCTTAGGCATTGAACCCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T --	---	AAACACACAGAAATCATCAAGAC[G/A]TATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTAIG TAAGAAGTAACCTCGAAATAGTAGGATAGTATATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATCTATGGAACCTCTCGTACTGTAAATTTTCATTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACTTTGAATGGCTTGCC TTTCAATAAAGAGAGTGACATGATTGAACATGTGTTTAGATAAAGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTGTTGGGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACCTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTGTTGGGTGAGCGGATT AT[G/A]CTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACCTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCCCTGAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTACACACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGGCCAGACAGGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGACCAGGGTTCCAAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCCCTGAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGATATAGGACCAGGGTTCCAAACTTT

WI-7330	207 C T	...	...	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGTGGAAATCTCTCTTTAATTTGGCATATAGGTTT GTGACAAAGAAGTCATACTTTGGTGGCTAAGTTTACTAAGGAAAATAACTGAAAGATTAAAG TGAGAG(C/T)TGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211 G A	...	...	TTAAACACAGTTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACIT GCACAATTATCTCTTGGCATCATACAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGCTAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC(G/A)CAGAGACCTTGGACTACAGATGACACACATGCCACIT
WI-7166	59 C T	...	...	TCTCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA(C/T)GGAT CATCAACAAGATTTCCCTGTGCAAAATATTTGACTATTTCTGTATCTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAAACTTGTGCTGTGAACAATTTGCGAAAAGAGTCTTCCAAIT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C	...	...	GCITCTCCCGAGGAGCGGGTCTTGGCTGGAACTTCCAGAGAGGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTCGCAACAGCTGCAAGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGAGCTGAGTCTAOCCTGGCCACAGT(C/T)GGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188 G T	...	...	GCITCTCCCGAGGAGCGGGTCTTGGCTGGAACTTCCAGAGAGGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTCGCAACAGCTGCAAGCTGCTTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGAGCTGAGTCTAOCCTGGCCACAG(C/GC)TTTGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275 A G	...	...	GTACTTTAGGCTGTGGAGGGTGGGCATTTAGTGGTGACCTTGCACAGGGTTTCTAACAGATGAC CCTGTGAATCAATAATTAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCACCCTATATG GCCATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGCTCTGGCTG
WI-7685	46 T C	...	...	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTCT(C/T)TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACAGGCTTGGAGCTGAGCCTCACCCTGACTCTCCGAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCCTCCTCCTGCCGACTC CTGGGTTGAGCTGTTGCCCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87 G A	...	...	TGTGACCAATTGTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTGGCCAGAATTTC CTGGGGGAGGGCTCCCTTGAJCCCTGATCATGTCTACCTAATGCTTACTCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCTATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[AG/TTCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCAC[AG/GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTATGGGTAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/TTACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTATGGGTAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGCACCTACTTAGA[GA/CA]GAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-7719b	281 T C ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAAATGTACAGTTATCC[AG/TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94	C G	---			TCCCTTTATGACCCCAAGAGATATTTATTAAACACCAATTAACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTTGGAACATATGCAGTGTCTCCGGCCACACA TCCTGCTGGGCCCCCTACCTGCCCAATTCATCTCTGCCAATAAATCCTGTCTATTGTTTCATCCTG GAGAATTGAAGGGAGGTCAAGTTGTTTGTCATGATTTGTCAGAGAACCT
WI-7842	57	T C	---			CACAGCATGCCCTTGGAGGCGCGGCCACCAAGATGCTGAATCCCCTATCCCATTCTGTC/GTATGAG TCCCATTGGCTTGCAATTAGCAATCTGTCTCCCCCAAAAAAGAAATGTGCTATGAAGCTTTCTTTCTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145	A C	---			CTGCCTCATACGCCACTGGAGTCCACACTTGAATTTGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCAACCCAGCTGTACCAAGCCCGGGCAGGTGCAGCCCTTCTCTCC TGCTCTGC[A/C]TCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGTCTGCTCATCTCCTCTTACTGGGCGCTGGGCTCTAGCCCAA
WI-4767b	173	C A	---			TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCT CAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AATCATAAGGAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACCT
WI-4767	50	A G	---			TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGTATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGGGGTATG TTTCTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCATAAGGAATTCCTACTAAGAC TCTCTAACCCAGAGATTTTAACCT
WI-7718f	222	C T	---			ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60	T C	---			ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31	G A	---			ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91	C G	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718b	248	A G	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718a	42	A T	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGC[AC, TG]TTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAG TCAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7227d	99	G C	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C	---	---	CCCAATGCCTCTCCACGATGCAAGGACTCCTGCTGCTCCTGGAGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTAATGCTATGTTGTATGCTTTCATCGAACAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAAGTGAAGCAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCAACATGATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTCTCTGGAGTGGGAGACAAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCGTACTGTCTATGTGTGATCCTTCATCGAACAAACTGATCGGAA AACTTGAATCTGTACTGAAATGAGGAGAGAAAGGACATGTCTATTGAACAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCCCTGTACCCCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCTGATATCGCTTTGGCATGATTGCAATGGAGGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/A/GTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTGT CTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCCCTGTACCCCTGGACTCCTATGATGGCTGCTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCTGATAATCGCTTGGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTG TCTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCGACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTACC AGCCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAGATC AGATGTGGCCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGACA AAAGGGCTC/TJGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCGACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCT ACAGCCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCGACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCT ACAGCCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGAGCCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG/GA/GATGTAGATTGTACATTCAATCCTGAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAATAAGGAGACAAATAAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTGTGCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGAGCCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG/GA/GATGTAGATTGTACATTCAATCCTGAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAATAAGGAGACAAATAAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTGTGCC

WI-1795b	130	T C ---	---		GAAGCAACCAAGATCTTTATCCCATCTAGATTATGTCTGGGTCTTCAGACTCCTACGATTAA AATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTTCAGAAAAGAAAGTTC/C GTCTACCAATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-1795a	47	T C ---	---		GAAGCAACCAAGATCTTTATCCCATCTAGATTATGTCTGGGTTC/CCTCCAGACTCCTACGGA TTAAATTTGATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTTCAGAAAAGAAAGTC GTCTACCAATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-10616d	136	G A ---	---		CACACAATTTGCAAAACACTTCAAAAGTGAAGGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCTATCAGATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616c	136	G A ---	---		CACACAATTTGCAAAACACTTCAAAAGTGAAGGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCTATCAGATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616b	141	C T ---	---		CACACAATTTGCAAAACACTTCAAAAGTGAAGGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCTATCAGATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616a	116	G C ---	---		CACACAATTTGCAAAACACTTCAAAAGTGAAGGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCTATCAGATTGCCA CCAGTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-1126c	52	G A ---	---		CTCTATTCTCTGGGCAGTGCCTTCTTTGGGGCAAACTTCCAGTATCAGT[G/A]TACTAATAATAA AAACCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATCCAGATTGTTTTCOCAGCAAGAA AATTTATTCTCAAGATATAAAAATAAATAATTAATTTCAAGTTCTCTCAAAAGGAATATGAAT TGTTAAATGCAATCCAGCTGAACCTTTTGGACTTGCTTTATTCCT
WI-1126b	230	T C ---	---		CTCTATTCTCTGGGCAGTGCCTTCTTTGGGGCAAACTTCCAGTATCAGTATCAGTATATAAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTTCOCAGCAAGAAAT TTATTTCTCAAGATATAAAAATAAATAATTAATTTCAAGTTCTCTCAAAAGGAATATGAATTTGTT AAATGCAATCCAGCTGAACCTTTTTC/GGGACTTGCTTTATTCCT

WI-1126a	97 T C ---	---	CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATCACTAATAATAAA CCCTGTAAAGTCTGCTGCAATTTCAAGATTC/CJCAATATATATCCAGATTTGTTTTCCACGCAAGAAA ATTTTATTTCTCAAGATATAAAAATAAATATTTAAATTTTCAGTTTCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACITTTTGGACTTGICITTTATTTCTT
WI-11183c	124 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/CJACTAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAAT/CJATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAAGATAGGTATTAATTCAGATGATTTTGGC/CJCTGTGCTACATAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGGCTTTAGTCTATTGCTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTTGTATTCA CCCATACCTCTATGCCGTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTTCTCTGTACTTTCTCTG TTCCACCAACCTTTCTTTTATCTTCAGGACACTCA/GAJTTACATGGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTTTCC
WI-10770a	49 G T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA/C/JAGCCACCTCCCGAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGCGCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGI G/CJTATCACTGGACACAGCCACCTCCCGAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGCGCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68 G C ---	---	GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACIGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCCACCCAAATAACGTAAGTACCTATGTG G TGCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCCACCCAA C JAAATAACGTAAGTACCTATGTCAIGCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCCACCCAA G JAAATAACGTAAGTACCTATGTCAIGCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTAAT C TGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATCTA ATTTTCTTCCCTTACCTTACTCTCCCCACCCAAATAACGTAAGTACCTATGTCAIGCCATGT AGTTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ...			AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAGGAGGGTAAATGCAAGGGGAGCCC CACCTCTCACCA C T TTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATACTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAAGGTATGGACCAAAAGTCCCGAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ...			AAAGGGCTACAACTAAGGCCAAAAACCATGA C TGGTATAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTACCACTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATACTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAAGGTATGGACCAAAAGTCCCGAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ...			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ...			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA C G ACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTCTGA

WI-7038a	31	G A ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGC[G/A]CTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTAGATGCTGGGCTGCTCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAGACTGTGAGGAGGTCGGAGTCTGTAAACCAGATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAITTTATGGTGTAGTCTGA
WI-3429b	64	G T ---	---	ATACGCTTCTGTCTGCCACAGTGAACCAAGCACCAGGTCGGCAGGTCGGCTCCACACA[G/T] CCCTCAGCCCTCAGCTTGCATGTGCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGCGGTCTAGAA TCCTGACTGTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	ATACGCTTCTGTCTGCCACAGTGMCCAGCACCCAGGTCGGCAGGTCGGCTCCACA[C/T]AG CCCTCAGCCCTCAGCTTGCATGTGCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGCGGTCTAGAA TCCTGACTGTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAAATAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTACGGTGACCT GTGAGCCCCATTCTG[A/T]GGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAAATAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATTAAGAGTGAAGTACGGTGGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAAATAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATTAAGAGTGAAGTACGGTGGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T ---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTTGGGGAAGATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACAAAAGCCCTTAACTTCACTTCCAACTCACTGAAT TTCATATACCTCCATTATTAATTAATCAATCATCATTCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCACTAAGTGAATCTCTAAA
WI-6711a	361	T C ---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTCAGTAAAGTATTTGGGGAAGATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACAAAAGCCCTTAACTTCACTTCCAACTCACTGT GAATTCATATACCTCCATTATTAATTAATCAATCATCATTCAGAGAAAAGACACGGTGCCAACTG GGTTTGGTGGTGCCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA

WI-10613b	172	A C ...	...	...	ATTGATGCCAAATCATAATACCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTATTTGAC/GC/CCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTCCACTCTATAATTTTAAGTCICGGACTTAGGATGTAG
WI-10613a	44	G A ...	...	...	ATTGATGCCAAATCATAATACCTGCATTCTAGAAACATACA/GATGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTTGTCAACTTTTGACAGGCCAGGCAATTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTCCACTCTATAATTTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ...	...	...	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAAJ/ TJGGAATGAACCACTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81	G A ...	...	...	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28	C T ...	...	...	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGA AGCATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103	T A ...	...	...	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAAACTCAATCAGCAACC ACAGMAAGCTAAAGACATCTTTTAAAAAAGCCCTTAAAGACAGCCATTTTAACTTAATTCG TAGTTATGATTTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGTTAGGTTCTTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-10681a	41	A T ...	...	...	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGAT/CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCTTTTAAAAAAGCCCTAAAGACAGCCATTTTAACTTAATTCG TAGTTATGATTTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGTTAGGTTCTTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-7222c	126	G T ...	...	...	GCCTCTCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGTGAGATGACTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG/GTAAATA AGGAGGGGGAATCCCTTGAACAAGAAAGAACTGGGGATAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGTTATTTCAAGACTCGAATTCATTTT

WI-7222b	255	GA	---	---	GCCTCTCCTCAACTGCTCTGGACCAAGGCTAGGAAAGGGGCTGTGAGATGACTGTGGTCCGCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	GT	---	---	GCCTCCTCAACTGCTCTGGACCAAGGCTAGGAAAGGGGCTGTGAGATGACTGTGGTCCGCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG/G/TAATAA AGGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	CA	---	---	AAAGATGACACTTAGAACTGGATGACTTGGCCCTTCTCTTCAATCTCCTCCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCAATCTCTTAGATCTGCAGTTGGCTCAACGCACCTAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054c	237	GT	---	---	AAAGATGACACTTAGAACTGGATGACTTGGCCCTTCTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCAATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGCAAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTATAACGCCGCTTCCCTGGGCGTACAGA/G/T/TAATCCTTGGCCCTT
WI-8054b	148	TC	---	---	AAAGATGACACTTAGAACTGGATGACTTGGCCCTTCTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCAATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGCAAA TCTCTTTGTAGT/G/T/TTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054a	131	CG	---	---	AAAGATGACACTTAGAACTGGATGACTTGGCCCTTCTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCAATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGC/G/A CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-10854b	152	GT	---	---	TTCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAACACGAAACGACGATAGTTAACGCTCTGGTAAGTTAT ACGGTGTGCGAGGCAACA/G/T/GGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	CT	---	---	TTCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAACACGAAACGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A ...	...	...	AATTTATATGTAAGGGTAGCAAACTATGGCCACAGGCCCAATCTAGCCATGCCATTTTGTG TGCTGATGGCTGTTGGTGTGCTGAGCGAGTTGAGCCATTGACAGAGGCTGTTATGAGCCTT CAAAGCAAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 A T ...	...	...	AATTTATATGTAAGGGTAGCAAACTATGGCCACAGGCCCAATCTAGCCATGCCATTTTGTG TGCTGATGGCTGTTGGTGTGCTGAGCGAGTTGAGCCATTGACAGAGGCTGTTATGAGCCTT AAAGCAAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATCTAGATATTTAAA GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGGTTTT	TTGTTTGTGT GAAATGT	TGACATTATAT AAACGTAAAA	CGGACACGTGATATACAAATACAGATCGTGGTTTGTGTTGGTGTGTTTGTGTTTGTGTTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TDOC	TTCAAGTAACGTGCAAAATAGGAACACAGAG[AV]GGGAGCCCGAGGTGGGACAAATCATGGCTACCC TCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTTAT
WI-8170b	259 G A ...	...	...	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAAGTTAG CATTTGGTGGAGAGATTTACAAGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATAAGGTAAAAGGGCCCTCAATGAATCTACGGAAAAACATAACACAAG
WI-8170a	204 T A ...	CCTTTATTAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAAGTTAG CATTTGGTGGAGAGATTTACAMGGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATTAAAGGTAAAAGGGCCCTCAATGAATCTACGGAAAAACATAACAC
WI-8172	136 C G GACA	TGAATAAAA ACAATTTCTGT	AAAGGTAC	CAGGATTCCTTAAGTCACTTCCAACTACCTCAGGTACATGTTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAAGCTTTTAAATCCTTCGGTAACCTCCCTTTTAAATGTTTCTTGACAT ATC/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56 G A TGC	...	...	AGCAGGGTTTGAATGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGG[G]AGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGTCTGTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 C T ...	...	...	GCCTTATTGGGATTGCAAGGTTACAAAGTTAAAGACAAAAACCAAGCATGGGATTTTGCCTGAAAT ATTAGCGTTAAAGGAG[C]TTGAGTTGAGTCAAAACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G]AGATGGTCAGGCTTCTCTG TTCTTAAACAGCAGAGCCCGCAACCTAGAGGCGCTCACCTAGCCTCTTAAT

WI-8827	22 C T A C T A T G G	T C C C T G G G A G	G C G A T T A G G A T	GGTGTCCCTGGGAGACTATGG[C]TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTTAGTTCCTTTATCCACCCAGTCTCT
WI-8833	51 A T A T T C T C T G	T C T C C A T G C C	C C T C A C A C A T T	CTCCGGCCTCTAAAGCTCTCTGTAGACTGTCTCTCCATGCCATTCCTG[A/T]JGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G ---	---	---	ATTTTTAGCCATGTGGTAAAGTTCAATTTTCAGTACATGGGTAAACCCAGGCCCTTTCCCA[G/T] TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTACTGTTCCTTAGAGAG GCTACAGGCTAAATTCACITTAGTTGGTTGTCTAATGTCTCATTTATTCCTGAAGCTCGTG
WI-8850	21 A G C T T T G G C C T	G G G A C T T A A C	C A A A C A G C C A	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCCTGGCTTTGGCTCTGGCTTGGCTTTTGGTTTCTT TCTCTTACTGGTCTTCTCTTCTTCTTGGCAGCCACCTAIGCTGT
WI-8853	79 C T A G G A T A	C C C G G G C A T T G	A G T C T T C C T G A	ACTTTCTTGAGCTGAGCAAGCTCATCTCTTAGCTTCTGGTTGATAAOGCTGGTTAATCCCCGGG CAITGAGGATA[C/T]ATGGAAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G ---	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCTATGGTGAACA[A/G]JACAACATGCT TCGGACTTACCAAGGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C C A	C A C A G A C T G A	G G T A A G T C C G A	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]JGGTGAACAACAACATGCT TCGGACTTACCAAGGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C ---	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGGTAATTATACCAAGGATGCTCCATCGCTCTTTG
WI-8456	93 G C ---	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATTTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAATAACATTTCTAAGTGTCACTC TCAACTTCTGTATTCTTGCCATGGTCCAGTAAACAGTTACACGGGAGACCACAAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGGCTCTCAGTCAACCAC
WI-8496b	157 A G ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGATGGTAA[T/G]ATTGTATCAGTGCATATTTATGAAA ATTATATCTCAAGTAAGTACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCGAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGATGGTAA[T/G]ATTGTATCAGTGCATATTTATGAGG AAATTCATATCTCAAGTAAGTACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCGAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G C C A G C	G T G A G G A A G	A A C G G C A G G A	CTGCAGGCTCTATGTGAGGAAGGCCAGC[A/G]TCCCTCTCTGCCCTGTGTCAACCCACATCCACAGACA GCCCTAGTGCAGGTGAGCCACTGCCACCCACGCCACACGGGAACAGGACCCCATGCTGC

WI-12108	40	CTATA	TGAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAACTCAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29	GACACAGGCA	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCCTATGTA G3	CAGGCAACGCTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAGACATTTCTCTTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT CTGTGTTAACTGCCTCCATCTTTCTTGGTGAGGACACG
WI-12201	61	CTCCTGATG	CCCACTGATCA CCTGCTGATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTCGAGGTGTTATGTCCCAAGCCCACTGATCACTGCATG[CT]GCCA GGTATGGTCGGGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	ATCTGACTT	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATAGAGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	AGCCTC	TGGCTCGCTG AGCCTC	AGGATCAAA GAGAAAAGGC	TTTTCGTTTGTAAATGATCCGAATGCTTGAGAGAAACCCCTGGCTCGCTGCCT[CA/G]GCCTTTT CTCTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	AGTT	CATGCCCTTTA AGGATTAAGT	TCCTTTCTCTTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTATTTGATGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[G]CCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	TCAATT	GTTGAGTATT GTTCTGCTCAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAATAATTATCTGATACACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCAATTAGTTGAGTATTGTTCTGCTCATAATTT[CT]CCCAATATGTACCAGACCTTCCC
WI-12326	25	GACA	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCACTG[CA/G]CTTCCAGAATACAAAGTACTTTAATACATATTTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	CT---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTCAGCATATGTTAT[CT/TT] TGAACATAATTTACAAAAGTGAACAGTTGGAAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	CTATCACACCA	CAGACACAGC ATCACACCA	GACCTCCCGT G33C	ATACTGGTTTAACTCATGTCACACCA[CT]AGGGCCCCACGGGAGGGTCTGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	AGTTTT	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAAGCAGGAGGAAAAATCCAATAAATTTTTTAA[ A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAAATTGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	CTGTGCCCCA	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATCTGCATCTCCTTTATGGATAAATCATGTGCCCCA[CT]GAGAGCCCCAAAGCTTGTGATGACAT TCTGTAAAGTTACAAAATGTATCTGAAGAAGTTATCTGTTCTGICC

WI-11352a	69	T C G	AGCACAGCAG ATAGTGGAAA	GACCTCTGGTA GGACACTTAGC	TGACACATGGTTCTGTCTTCCAGAAAGGAGAGAGAGATCATCTACATAAGCACAGCACATAGTGGAA AGTCGCTAGTCTACGAGAGGTACATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GGCCGGCTGA GCAC	TTAGCCCATGCTGTCAATTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAGTCGCTGCTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGGGT GATTTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCTGATGGTGACACAGAGACTTTCATATCTTGTCTTTTAAAGTC TCTTCAGTCGAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A A G T T C	TGTTTGAATTT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGTCTCAGTTGGTTAGAGTGTGGAGCTCAAAAAATTAAGAAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C/A]TATATTTTAACTGGATACAGGCAATGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGACTTTA	GTACATTCAG TGTTTGTAA	TTCTATCATTCCTTAAATGGGAGGTTATGTGTTCTTGAACCTTAAATAAATACTCGCTTTTACA AAACACGTAATGATCTTTCTTGTGAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTG AAATGGTGT	AGCTTATTTT ATATTCACCCA	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTCTTGAATGGTGTCTTATGATGGGTGAATA TGAAAAATAAGCTTACCTCATCCACTCTAAAGGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC CAGC	TGCCAGGGCT TATTTG	CTGTGCTCTTCCCACCTAAACCGTGAGTTCAGTATGTCTGGCAGCACGCTGTCTTGTCTTGGTG TATCCCACTACTGAATCCCCCAACCCAGC[C/A]CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGC	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAGTCGCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTCTATTTATCTATTTATCTCTCACATACATTT CATGTATCCCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTCTTTTGTAGTAGAGC[A/G]GGAAACAGTTGTCAATACTACCTTCTGTGG TCCCCTGTAGACAACATACCTTTCTTTTGAATGTAAATGTCA
WI-11276	41	A G A G A C	GGCAGCAGG AGCAGAC	TGTACTGAGGA GGCGGTG	AGGCAACACTGCTTTATAGGCGGGCAGCCAGGAGCAGAC[A/G]CACCGGCTCCTCAGTACACATT CCCCAACCCCTGGCTGGTCTGCCACTCAGGGCTGGGCTGGGAGGGGCGAGCGGTAGGCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTC ATATGTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACA CTATTGCAT[A/G]GGGAAAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGGTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTTAGTTTATTACATG[A/G]TACAAATCATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAGACAC	AACTAAACCA CCTGTAATTT GTACC	AATGGTCGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACATAC[CT]GGTACAAAAT ACAGGTGGTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGAAGAGAACACACTTGTGGGCTT[A] GTTCAACATGGACTGATAGGTCCACCCACAGATTCTAAGTGGTAGTCTGGGGTG
WI-12345	37 C A	GTGGAGGAA AAAGAGGAA	TTGCAGAGGG TTGAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71 C A A A A	AAATTTTGG AAGTTTTTCAG	AGTITTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTATTTCAAATTTTGGAGTTTTCAGAAAAAATAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACATATAACACTTAGCAGAGGAGGACTTTTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCT AAA	TTTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTACACATACAGAAATTCAGTTTACAAATATCCAGAAAGGCAATTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAAACCTTG GATTT[C/T]CCAAGACCCGAAGACTCCTCCAAAGTTCTCACTGTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCGCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCTC
WI-11585	79 T C A A C A A A A	TGGGTTTGCA TCAACAAA	CCATGCTTCAC TGATACTCC	TTAGAAGGAAAGAAATAAACAACCGGTAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGTT TGCAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAGAGCAGGGGTAGAGT TT
WI-11604	68 G C		---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTCAGCGCTCACCATTTC TTTGTACTCTGCAGTT
WI-11614c	108 C A		---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCAA[C/A]ATATAAGTATTCGTCAGCTAG GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAATCCAGAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATAAAGTATTTCGTCAGCTAG GGACTTCGT
WI-11626b	83 T C		---	TTGATTTTACTAAGGTTCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATGTTCCATTGCTAC AAGAACAAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCCCACTGGAACATGAAGGTA[G/A]GATAAGTGTACAGGATAATATACT CAGATAATTTTAAATAAATTACTTAATAATAAGMAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTCTCC ATTGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTGCGCATGTCAAGTCCATCCATG
WI-11638	61	A G	GGACTTAAAA AGATCTGCTTA GCTCT	AGAACTTGGT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCCT[AG]TA TATCCACATAACTCTAGTGTACATAAAATAATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTTACAG TATACAAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCACT[C/G]ATAATCATCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGGCCAAAAGACTATTACGCAACTG[C/A]AACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTGGGT
WI-11656	28	G A A	ATTGATTTAG AAGGAAGTGC AA	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTGAAGGAACTGCA[G/A]CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAATGTCTCTGAACAATCAGATTCCTCCAGCCTGGAT
WI-11680	55	T C	...	...	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC CAGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACCTTTGACATCTTTATCACAGCAGGGGACAGT[C/A]AGGTTGGCTTCTCTA ATGCCCAACCATCTTGTTTTCAGAAATCTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAAATTAT ACTGAA	TTACATGTGGTCAATGGTGACATACITTTCAATAATTAAAAATCGAATAATACTAGAAATAACACAGC AG[C/T]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTTGTAACAATTTATTGGC[T]GGCTG GAATTTGTTCTTTGGTGATTGTCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGCTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GGAOCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCAAGCTTTCCAGCACACAGCCAGCCCACTCTAGACACGCCCTTCAC TCCAGTCCATTCTGGCAOCTAGCCCTCAGTCTTCACT[C/A]CTCTCCCTCTCCACACACTCTCTC

WI-11715b	123 C T	AGCTGGCTGC AGCTT	TCCCACCTCG TGGCT	AGATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C	GGACACAATG TAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGAGAAAGAGGCTGGCTGCAGCTTCAAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C	AACAATCCTT AAAACAATA TCAACA	CTGTGGTTTG TGTTGCAG	CTGGATTTCCCTATACCTAACCAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAAACCACAGGC AAATGAAAACAGATGCCCCAGACAGACGCCACCCACCATGGCACACAC
WI-11728	16 C G	ATCTGTGGTTT TCGGCTG	---	TTTATTATCAAACT[G/C]CAATTCCATTTTCAAAATGTAAATGTAAATCATCAGCTCCCCCATCCACTTT CTCCCATCTTATCTCTTTCCCAACCCTACACTTCTCTCCCTACAAACCGGGTCCAAA
WI-11758	61 A G	GCCTCACAAA GTAATTTCTAA AATAAA	TGATTGGCCCT GTGGTCTA	TTTTCCCTCTTTTATTAAAGTCCGCTATACTAACTAGAGGAGAAATCTGTGGTTTTCGCCTG[G/G]TAG ACCACAGGGCCAATCAACACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G	GGCTCACAAA GTAATTTCTAA AATAAA	AAAAGTGCTCA TCTGTGAATC T	CCGGCTCACAAAAGTATTTCTAAATATAATTTGCT[G/G]TAGAGTTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACATTTT
WI-11773	93 T C	GGCTCAGAGA GCAAGGGAA	---	AGCATATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAAAACAGCAGATCAGAGATTAAAGAAAT ATTATTGCCTCCTTTTTCCTCCCT[G/C]GTGATTGTAAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G	CCCAACTTACC AAACCTCTG	AAACTCAGA CTGTAAATTTT GTG	CATGACAACTCTTTTATTAAATGGCTCAGAGAGCAAGGAA[G/C]CAGACACAAAATTTACAGTCTGA GTTTTGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G	TCATCTAATCT GTGAGGTATTT AGTATACA	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTG[G/G]GCTTAGCCTCGCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A	GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T	GTGAGGTATTT GGTATTAGAA AAGTTTAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCCAATTCCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTTGTCTATAGACAATCTGA AAATTGGGTTCTGAAC
WI-11906	52 A G	TGTTATAACAT CAAAGAAAGA GATCTGAA	TTAATTTCTGC AGTTCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAAGAAATCTGAAT[G/G]TGAGGGAACCTG CAGAAATTAACTTCAGICTAATCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTG GGTGGTCAAGTACGCTATTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAGAGATC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCAATTG/GTT TTATTAGTATATAAAATGGCTTTACAGGAAGCAATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTTGTCTGGAGACIACAGCTAGTCTAAGAAAACCTTCTTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATCACAAGTACAACACTGCTTATTTTCTTGTGTTGAAGATCAGATCTCTGGTTATTTAAAT/ GIATCAACATTCAACACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA TTTATT	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACACTGCAGAAAGGCGAGACAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAATTAATAAAAAATCTGTAAACACATTTCTCTCATTTCTGTTACGA ATACTTCTTTTGGATATGCAAAATCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGGTTCAAAAATAATTAAGGATCTTGTACCTT/ GTGTTTATTTCTGTTTCAACTAAGGAC/TJAGACTTCAGAGGCGATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T A C	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA AC/TGTTACAGAAATGAATAAGATGGAAAATTTTAACAAATTG
WI-13654	49 A G G T	AACAGTTAAT GAAACACATC G	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA/GGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTTACAGACAAAACAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAAGTA C/TGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTCTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGGGGGTGATGTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATGAATACATGACCATTTTCTCTCTTTTAGC ACGTTCTTGTCTCTC



WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACCTCT TAGCCCACTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCCACTGGGCTAA GAGAGTATTGTACAGAATATGCACATCTCACTGACTTAACAGAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[A/G]TTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGATTCCTGAT[G/C]TTTTCCTTTGCCAACTATTCATTATTGACCAATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAGAAAGGCCCGGAAATATAGTGAGACTCA
WI-14284	55 C T	---	---	ATTCAAACAATCCAGAACAGGTTCTCACACITTTAGCCCTTTAGTGCACAAACAC[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTCC ACCAAATCTT	ATGACCAGACCAGAAAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATCTTTGGTGGAGGGGATA CCGCTGCTATTCAGAT[G/C]AAGATTGGTGGAGAGACCATGACAGATGACAAACGG
WI-13522	33 C T A C A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAAC[C/T]GAGAACCACTGACTTCAAAATATTATGAGAG AAATTAATCTCCAGGGAAATTTTGCAGAGAAGATAATA
WI-13529	42 T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATTCCACAACACATTATTGAACAGTTACCA[C/T]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCCTCGAGGGGTTTATAGCTAACAGGGGAAACAACTCTC A
WI-13859	84 G A	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C	---	---	TGAAAGGATACAGAAAAAATCAACGAAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAAGCTTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52 G A	---	---	TTTATTGTTTGGTAGAAAAACAGGGCTTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAAGAGCT
WI-13477b	61 A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAGGACATTGTTTTTTCATTAGCTGTCTTCAA[A/G]GAC AGAGAAATAAGATAAATAACCTTAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32 A G A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAGG[A/G]CATTTGTTTTTCATTAGCTGTCTTCAAAGAC AGAGAAATAAGATAAATAACCTTAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAATAATATATGTGCAGTTATAAAAAT GTTGGGTACTTTTTTCCAAAG[AT]AAAAATGTTTCTGAAATGTGCACACTAGAAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTACCATTAAGAAATCAACA TGTGCACAAAAGAGTAAAAATTTGACCACAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGGCGAGTT AGATTCCA	AAGGTCGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]TGGAAATCTAAGTGCAGAGAG AATCAAGACCGATGGTGTGAAATCTGGGCGAGCTTCAAAAATTTCTGCCTCCTTAAAAACATTTTAC CCAATTTTTCATTATTGCC
WI-13857	28 A G ...		...	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCAATTTTGTGTAGCTTTTATACAGTACAGATTTTCAATGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[GT]GTTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ...		...	TTAATCAGTCTGTGTCAAGAAAGAACAGGACTTGATCAAGTTCAGCCCTCACCACCTATATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTTGTCTAAACCAAGAGAGAA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATCCAAAGATGGGAAGCGGATTTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAACTATG/GCATCCCATCCACTCTTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A	TTTATCCAAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCTTTTATCCAAAGATGGGAAGC[GA]CATTTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAACTATGATCCCATCCACTCTTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCACACTGGGCTGGACACTGCAGTGATTCTAGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA TTTTTTTTTGGTGAGTTGTCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTACCACCAACATTTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTCCAGAAACCTC
WI-13578	48 T A ACC		GTC	TCCAAGGAAAAGAAAGAAAACCAATCAGTGAGAAAACCTCAAGAAATTTGGATGGCTGAGGGAG[GA] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCACTCTCTT GAGTDOCT
WI-13789	62 G A	TTGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCCTTGGGCA GTACTTTTT	AATAACAAGTTTAAGTTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGC GA/TGCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	...	CCACACTGAA GACTCACCAG	GTCTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAA[GT]GTGCCCATACTAATTTTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTACTAGAGAGGTTTCTTTTGGCTACAGTAACA
WI-13367	84 C G A	...	TTAATGAGCC TAAATGAGCC	GTCTCAGTTCTTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAAGACTCACCAGAA[CG]AGGGTGGGTGGGGAATACTTAATCAATATTGTGGAATTTACCCGAT GAAATCCAGTTATTCTCT
WI-13600	26 G T	...	TTAATGAGCC TAAATGAGCC	CTCAGTTTAAATGAGCCAGCATCCAT[GT]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATAGTGGAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATTCCCTTCTCTACCC
WI-13602	89 G T	...	TCCATTCTGGA TCCATTCTGGA	GATAGGAAAAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCTCATTCTGGAGACAAACACA[GT]AAATCTATTAAATATTGTCATGAGGIATGCACCT GCCCC
WI-13650	76 A T	...	AAAGATTTCAC AATATTTTCACT	GCATTAACTTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTTCACAATATTTTCAC TTTTAAAC[A/T]AAAAACTACTCTTCATATCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	...	CAATTCAGG CACAAAGCTA	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAAA	...	CAATACATT GCATTTTCTCTA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAAATCAATACATTTCATTTCTCTAAAA AAAGAAGACATTT[A/G]TTACAGAAAAACTGGGTATCATGCAGGAAAAAGCAGAAAAAAATTT
WI-13909c	93 A T	...	TTCTCACACT CTCTTCAAAC	ACTTAAACTGGCTTATCTTACGGTAACTATCTCTGTATTTCCAGTGAAGTTTCATCTCTCTCACACT CTCTTCAAACCTGAAATATCTTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	...	TTCTCACACT CTCTTCAAAC	ACTTAAACTGGCTTATCTTACGGTAACTATCTCTGTATTTCCAGTGAAGTTTCATCTCTCTCACACT CTCTTCAAACCTG[A/A]AATATCTTTTTCAGAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	...	TTCTCACACT CTCTTCAAAC	TTTTTATTGAATTTCCAAATGTAGCAAAATCATTAAAACAAAATTAATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[C/A]ATGGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C A C A T C A	...	ACAGAAAAAT TAAGAATCAA	TTTTTATTGAATTTCCAAATGTAGCAAAATCATTAAAACAAAATTAATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGACATGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15399b	104 G A AAA	...	AGATAATGAA ACATCTGCGA	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAAAGACTACCATTAATTCAAAATTTATATGT AATACACTCATCCAGATAATGAACATCTCGGAAAAG[A/A]AAGTGGGAAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGTCG[A]TTTGGAAAGTACCATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTCGGAAAGAAAGTGTGGGAATCACCTCATCTGTGC TGTAATCTGCTTACAGTCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATGGCTTCAT TTTAAACTAATTTAGTGT[T]C[T]TTAAATTATGAACCTTTTGGTGAATTATGAAGTGTACCAAAC
WI-15747	88	T C A G I G I T	TGCTTCATTTT AACTAATTT CAGIGIT	CATAATTCCAG AAAAGTTGATA TAATTT	C AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACCTGGCTTGCAC[C]TGGACACCTTTTACG GAGGATTCCGGACAAC
WI-13752b	117	C T ...		...	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACCTGGCTTGCAC[C]TGGCTTGCACCGGACACCTTTTACG GAGGATTCCGGACAAC
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTGC	CCCTCCGTAAA AGGTGTCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACCTGGCTTGCAC[C]TGGCTTGCACCGGACACCTTTTACG GAGGATTCCGGACAAC
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTAC[T]GCGGTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTGTGAAC GATAAGCACA GC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAACACACGTAATGGAATTCATGCAGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGCTGAACAAACTGA[C]TGTGTGTATCTTTC CTGATCT
WI-14061	68	C T ...		...	CCCTTGACTATATTGTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C]TAAACCATTTCATCCACCATTTGTAAAAATCTCATCTTCTGGGTCTGGATACCTCAAAAACAGAT
WI-15719	69	A C A T T C A G C	ACCTTTTCATC CATTACG	TGATACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACCACACTGAATATATACTGAATTAACCTTTCAACCCCTTTCATCCATTGCA G[A]C[A]AATTTAAACTCTTGCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAAGTGTGCT TGCTGCTAAT	TAATCCATCAATCTAAATCACACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACTT[C]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAAACTTG	GTTCCTTGATA TGTCGCTTAGT TTT	GGATTTTATTCACATTAACCTTGACA[G]TTAGCAAAAAAATCAAAACATAAAACATAAGCCACA TATCAAGACAATAATACATAGAGATTGGAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTCTTTAAATGCGAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC[G]A]TAGTGACACATAGCTGTCAACACAGTG
WI-13785d	72	G A ...		...	TCAAACTGCACACTATAAAAGTCTTTAAATGCGAGCAGGAGATGTGAAGAC[A]C]CAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13785c	56	A C I ...		...	

WI-13785b	40 C G ...	...	...	TGTTGTGACAG	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGCTT	AAACTGCAC ACTATAAAAG	CTATGTGTAC T	GGCAGGAGGA TTTGTACT	TCAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACACAAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT	TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTACCCCATTTGATACAACATAAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAATACTCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTCTC	TTCTCAGCCT	TTCTCAGCCT	AGAATGGGCTC TTAACCTTGTA	TAGTCTCTACAAATCTTCAATCCATTTTCTCTCCTCACCCCTTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATCTTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT	CTCAGCTTCTT	CTCAGCTTCTT	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/G]GGCAGCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTTGAACCTTCCAAAGGAAGGTAAGTCCCTGTTTGAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 A C	TGAGGTTTTTC	ACCTTATCTT	TTTTCTCCCC AGGGTCTA	GTCTTTGCACAAAGTCTCCCACTGGTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTTCTT[C/G/A] TTAGACCTGGGAGAAAAACAACATGTGTAAGTGGCTCAGGACATGAGGCAGGCCGTTTCACAAGAT GCTGGCTAAGGGCTTC
WI-14065	29 T C AATT	TCATTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/J]GAGATCCCAGATTGCTGCTCATATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCTGAACATTTTGAAGCAGCAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT	AAATCAGAAG G	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/G]CCTTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTTTCTTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGCC	TGAGCACATA	CCTGCTGTCTC GGGC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGAGTTAGAACCAAGGCATGGTTCAAGGATG
WI-15702d	107 T C ...	...	...	...	CAATGTTTTATGAAGAGACTCCGAACAATAAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C/J]GGGTTCTTTGAACAATAAGTTT TGA
WI-15702c	101 T C ...	...	...	...	CAATGTTTTATGAAGAGACTCCGAACAATAAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C/J]GGGTTCTTTGAACAATAAGTTT TGA
WI-15702b	90 C T ...	...	...	...	CAATGTTTTATGAAGAGACTCCGAACAATAAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C/J]GGGTTCTTTGAACAATAAGTTT TGA

48	G C A A G	A A C A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C C G A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A A T A G T T T T T G A
113	T C			T T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G A T C C T C G G G T A A G T T T C C T T C T C T G T A G A T [G/C] G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
56	G C			T T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
3	62	G A		T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
2	86	A G		C A C A T T T T C A G C A A A C A A T C G A G G T G C A A C A G G G T T A T T T C A C A T T A A T A T A T T A A C T G G A T T T T T T G T C A A A T A A T A G G G A [G/G] T C T C T T T A A T A A C C A T C T C C T A C T T C A T G G C C A G T
3	95	A G		A G G C T G T T T T T G A G G C C T G A G G A C C C C A C A C A T G A C A A C G T A A G A C T G T A A C C A T G T G T A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A T C A T C T C C C A C C T C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
8	61	C T	A A G A A G T A A A T T A G G A A G A G C A A G A	A G A A C C G A G A A C T C A A A G A C C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
3	47	C T	A G A C T T G A G A G C T T A A A A C A A C A C T	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T T G C T T A A G G T C T T A C A A G G C C A A
5	31	A G	A A T A A A A C T T C C T A T T T C T T T T G C T T	T G C A T T T A T T T T C A T G T A A G A A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G T A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A C A G A A C A G G A G G C C T T
3	121	G C	A A T A A A A C T T C C T A T T T C T T T T G C T T	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T T C C T A T T T C T T T G C T T [G/C] T T T T T T C T T T C A C C T C A G A A C C C C C T T A
5	50	A G A T C	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T T G G G A G A A T G A A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T T G A C G A C T A C A G C T C C T C T C T T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G

79	102	C T	CACC	TCATTAAACA GGGTATGTCA	ATCATCTGTT TGAGGTTGACA	TTTATGCTGTTGTTGTTTCTACTGGTGGTGGCTCAGTAAATATCCAAATCCTAGTATGATTTCTTT TACTTGCTCTATTAAACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[A/C]CCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGCCGCGAGGCTGGCGAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
02	22	C A	...	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGATCTCTGCAGGGGCTGGACCAGCTGC AGTGGGGCTCCGGCAGCTGCTCTCCAGGACTCTTCCCACACCCC
37	24	A G A	AACTGAAAC GTATTCCTCC	AACTGAAAC GTATTCCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCCA[A/C]ACACCGTAGAACTTTAAAGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAAGGAAGTTTCAGGTGATACAAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
144	24	A C A				ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
24	92	A G	...		...	GACAAAGAGGCGAGTTTCTGTAGTCCAGCAGGGCCAGAGAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGTGACGACTA[C/T]GTGGCCATGCCATTCTCTGAAGTGAATTAATGAACA
25	88	C T	CATAGATTTT	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GTTATTTCTCAGAGTCTGGAGTTAGAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGCTCTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
36	120	G A	ATGCTTTCACA	GCTTCTCACC ATGCTTTCACA	CTTGTTCTGTC TCITTGGGC	TTGTTGTTGGCACCAGAAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATCTGTAAACAAGACT GCATTAAATTTGTTTCTTATGATTTGTTTCAATG
138	23	C T	GAAAAGCT	TGTTGGCAOCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTCAAACTTGGAGCAACCAAGATGCTCTCAGTAGTATATTCA GACAATC[G/A]AATAATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATAATTACT
351	74	G A	GACAATC	TCCTCAGTAG TAGTATATTCA GACAATC	GCATCTTCTT TTAGTGCTAAG TAATATT	TTTTTAAGAGTGCTTCCATCATTTATATTGATTGACACAAAACTTTTTTAACCTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCC
b	59	C T	...		...	TTTTTAAGAGTGCTTCCATCATTTATATTGATTGACACAAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCC
a	26	T G A T	A	TTTAAAGAGTG TCCCTCACATC	TCATCTGTTCT TGTTGTTTTTG	TTTTTAAGAGTGCTTCCATCATTTATATTGATTGACACAAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCC

31	82	G A	---	---	---	TGAATCAATGGACAGTTTGGCTCTGTTTGTAGTGAACCCCTCACAAGCACTCTGCATAGTCCGCTTTCTGCTCTTTAAAC[G/A]TGCCTGGTTCCCTCTGCCAAACITTTAGGATTGGGCTCCTCAGGGGCTTGTCTGA
34	24	A G	---	---	---	ATCACCAACCGTGTCTAAGAACAAAC[A/G]TCTTCATGTCTCAACTCATATCCCGGGACTTTTGCAACTGCAGTACACTTCTGCTGCAATGAACCTGGCTTCTTGAGGGGAAGCCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGGGGGTATATCTGGCTGGCCAGTTGGAACACAGGAG
34	99	T A	CTGGAGGTA	GACTTCTCCAC	CCTCTTGC	CAGAAACCTCTTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCGAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAAGICTTGGCAAG
75	103	G A	GGCAC	AGCAGCTGGG	CCCTTCTTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
79	96	G A	TGGAGGTCA	TCGAATGACCC	TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTGGGAGGCACTGCACATTTTCTTAGAAGGACATGAATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCACTCGAGGAGGAACAG
31	49	C G	ATTGT	CTTATT	---	CACAAATAGTGAATTTATCTGAGCAAGAAATCATTCTCATTAAAAATTG[C/G]AAATAAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
36	105	T A	---	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATAACAATCTTACAACACATTCAGAGCATATAACAAGAATTATTTACAGGCAGCTAATGTTAAAT[A/A]ACCATGAAAAAGAAAAAATTG
37	31	CT	---	---	---	ATCTAGATGTCAGCAAAATGGGCTGAGACTG[C/T]TGTCTGTAGATGCAGTGTGTATGTTCTACCTCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATACAGTC
37	103	A C	AAATAAAAA	TG	---	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCATTACAGAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA[A/C]ACITTTAGGAGATGAAAAACACAAA
38	60	T A	G	AACTCATTTG	TTACTTT	TTAATAATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAAACAATGAGTTTACACAATTAATAATATTAAACACATACTTATGGGATTTGTTGAATGA
33	47	C G	---	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAATTTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
	63	CT	CGTCT	CAC	---	TTAGAAAACTGATAAAAGCAACAACAACCTTTTGGGAAAGCACCATTGGCAGCTCCTTTGTGCTA[C/T]GTGATAAGTGTCTTATCTCAATGAAGCAACCCCA
					---	ACATGGCAGATACAGCTGTC[G/A]TCTTTGAAGACCACCCTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCCCTGACCGTCTGGAGCGTTGAAGGGTGACCAGCACATTTGCACATGCAAAA
15	22	G A	---	---	---	

102	59 T C	GATAACATAA ATGATCATG CAGAATTC	GOCATCTCTC TTTGACTTTT	CCAAACATTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA/T/CIGTTA AAAGTCAAGAGGAGATGGCTAATGCATGCTGGGCT
3	101 A G A	CCACITGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAAATTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCACTTTGAACCTCAAGTCATCA/G/JTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTTAACCA
159	73 T C	CGTTTGACTT GTGCGG	TCCACACTGC OOC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGTTTTATTCAAACTCCTAGCGTTGACTT GTGCGG/T/CJGTACTCAAAATGGGGGCAGTGTGGACGGGAGGGATTGCAACCAAGATTCATACTG CAA
135	50 A T T A T	CTAGGAGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTACTAGGAGGTTGAGGTGTAGATAT/J/TCTTCCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCC
a	112 G A	AAAGGCACAC GGGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATTATGCTTGGCTTTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGTTCAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
340	18 T C	---	---	ACACATATAATTCACATTT/J/CJGAGTGATTAAACCTATTGTTGTTTGAACCAACAAAACTAC AAGAAAAACATTTTCAAACTTTTTTTTCAGGCTGA
308	52 T A	ACCACCACA CTACCCGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACCTTAAGCAACAGTTAAAAAGTACCCACACACTACCCCTGTT/J/AAAACTTTAAC ATTGTGATGCCTCTGTCATCAATTTTAGAAAAACAAGAAAAACACAACACTGAAGGCCCATGTA
816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTATT/J/AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
'c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TJTAGGTGATTGATACAAATACGATCCATAA
'b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TJTAGGTGATTGATACAAATACGATCCATAA
a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTC/JATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
173	57 C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAACTGGGATACAGCAGTAAAGAATACAAAAAATCCTGC/J/TCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

836	28 T C ---			TCCTTGGAGGGATAGAGACAGAGTGTTCGTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATTTGGTTTTGTTTGGCTAATTTGCCCCACCCTATAAAAGCAGTGCACCCAGAGGCAG
856	60 A T A A	TTTGTTGCTA CTTTTACAAA CTTT		ACATTTCCCTTATGATAGCAACAACCTAAATATGATGGATGGTGACACGGAAATACTTTAATTTATTAAGTTGTAAAGTAGCAACAATAATTGAGTATATACTATATAAGTGATAGAGGATGTATATGAAGAAA GGCTATAAAAAGCTCCAAA
863	61 G A ---			ATGGCAATTTACTTTATAGCAATGAACAATATTTGTCAAAGGGCAATATTTTGTCTG(G/A)AGTTAATAAAGTTAATAATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACTACCTGGC
867	46 T C A	GACATCCAA GGCTCTTAAC ACACTC	TGGGGCTGCAG	TTTTAATTAACGTAAAAAGGAGGACATTCOAAGGCTCTCTAACATTCGAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTAATGTGTTAACCCAGGGTGA
733	98 G A A	CCAAATTGAC AGATAATTCTGC	GATGAGGTGAG GCCATTATTT	ACGGAGTCGCTCTGATGTATTTCTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAGAACAATTTAGAAAAATCCAAATTGACAGATATTCGCA(G/A)AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAACAAACACAAAA
ib	79 A C ---			TTTTGACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT(C)JAGGTGCCACTAAGGAACTCTTCCAT(C)JAAGCTGCTGTGACACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGATCTGCCTGTGTTCTGTCTT
a	50 A C C A	CATGTACAGG AAGAGTTGTCT AGTGGCACCT	AAGTTTTCCTT	TTTTGACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT(C)JAGGTGCCACTAAGGAACTTTCTCCAT(C)JAAGCTGCTGTGACACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGATCTGCCTGTGTTCTGTCTT
907	48 G A G G A C T C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC(G/A)ATTCCCCTTGGAGCAGACATTTGTGAAGCTGCTGTGCGGCACACCCATCAATCAGTACTCTGCACTGCAGAGGGGCCACATGCACGATGCTCACGTGTG
911	52 G A C	CCAATACATT CAGTTCCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTCAGTTCCCTGGT(G/A)AAGGTCCCTTTTCCTGGTTGCAGACAGATACCTTGCTGTATCCCTCACATGGCAGAGAAGAGAGGAAGTAATCT
913	88 C A ---			CTGATGCTTTGACATCTGGGGCATTTGCTGTCTTAGAGAGACTACTTCTCCTGGGACCAGCCAAATTCCTAGTAGTAGAGGACTCA(C)CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAACCTACACCTCCAACCACT
914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGCTGAAGCCCTGTGAAGTCATGCACATCTGGACAGATTTTCTCTAGCA(G/C)GAATTTATTGCTGGGCTTGATGGCTTTCACAGC
926	49 T C ---			GTTTATTTTCAAAATGACACATCCCGAGTTGAAATGGGCACCTTAGCGAATTCJACTTGTGGACCACAGAGACTGTCTGAGAACATGTTCAAGACAGTTTTCAAATAAAAAATTTCCCTTAATCAGGTCCA

33	89	C T	AAGGAT	ATGTTTAAACA CAACATATC	TGGAAGAAGATT CCAGGOC	GCATCTTTATTACACAGAACTCATTTATGTCTTAATCATTTAATATATAATATAAGCATGTT TAACACAAACATATCAAGGATC/TJGGGCTGGAATCTTTTCCATCTATAGAAAGCACTAACCATC CATTAAGCAG
30	55	C T	CTCATGGAT	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATC/TJGCGGTATTG GTTGGTTGGTGATTTGGGAGCAACAGGGAGAGCAAA
16	47	T C	---	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA/TJCCTCTAAATCATCTCTA GATCAGGGAGTCTAAGGACCATTAAGGCTCATTAACACAGTACTTTATGGAAGGATT
1	80	A G	---	---	---	ACATTAACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCTTCCACTATGTGAGACAC TAAGAATGGTCTAAGTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
1	32	C T	GGGGTCCCAA	CACAATTAAA GGGGTCCCAA	GGAAGGCACATA CCAACCTC	ACATTAACAGCACAAATTAAGGGTCCCAA/C/TJGAGGTTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
48	56	T C	G	AGGGAACCTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCTTCCAGGGAACAGGGAACAGTCTAAGTTGTAGT/CJTCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
00	52	A G	TGA	CAAAAAGCTA TTTTCTACAC	ACAGGAATGTC AGAAAACAGT ATAATAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGAC/C/GGTAAATATACTG TTTTCTGACATCTCTGTTATCAACTCTCTGAAAATC
58	83	A G	CAAGGG	AATAATTTAT CTCTTCTTTT	AATGCATTAT TTGGGTTTT	GTGATTGATCTGTAATTTGGGATTTATTTATCAACTCTAAAATTCAGATGAAAATAATTTATCT CTTCTTTCAAGGG/CJAGGAAAGCTAGGACATAGCACCACCAAGATGCAATTTTCCAGGCTTTGAAGTGC AGCAGAAAATTCAGGA
176	35	C T	TCGTTCAAAG	GTTGATTTGCT TCGTTCAAAG	TCAAACATAAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTTGCTTCGTTCAAAG/C/TJGCTTAGAATGGAAGATTTAGTTGAGGAG GGGAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
181	31	G T	T	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACCTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT/GTJTTATGCTAAGTATATGTCAGAGGTGGAGAAT AAAGAGGAAAAGAAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGCTCACAAA
192	80	C T	GAAGCTGCAG	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCT	TGATTACATTTTTTAAATATGCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG/CJAGGAAAGCTAGGACATAGCACCACCACTGATCGGAAAGAAACGTA
102	72	T A	---	---	---	AAATCTCTCTTTTACACACAGATGAACCTTTAATAAATACAAATGCACCTGAAAATGCTCTTTGA TTTCC/TJATTCAGTTTAGGCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAAGGCCAGTT
100	90	G A	GTCTAA	GACAGAAAAA GACTCAGACT	GTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGT/CJAGTGAAGTTTGTGCAGAACTAGAAAACAAAATCCACCT

23	68	G A	C A C A A T A C T T C A T G T A C C T A T T T C C T A C C T G	C A C T G G A C A T A T T C C T A C C T G	A T T T G T G A T G T T G G T T A A T C T T A T C T C T T T T T A T A C A C A A T A C T T C A T G T A C C T A T G A A A T A A G A J A C A G G T A G G G A A T A T G T C C A G T G C A A A C A G A G G A C T C A C A C C T G T G C A T A G A C A G C A C C
33	91	A T	A A G G G A C G A T T T A G T A T C T A A G T G T T T T	G G C A T G T C C A G T G T T T T	C A T A A G T T G C A T T A T T C A C G T C C A C G C A T C T A A G C T A C T A A G C T A C T G T G T A C A G T A T C A G G A C T G G A G A A G G G A C G A T T A G T A T C T A A A A C A A J A T C A A A A A A A C A C T G G A C A T G C C C C C T G A A T T G C A A G T T G G A G T T C G T A A G A A T C T A C
70	100	C A T	C C T G C C T T T A T A T T G G A A T T T C G G T C T C T	G G G A G A C C A T G G G T C T C T	A T T T G T G T T T A T T A G C A C C T G A A T T A G G C A A G A G A A C A A T T C T A C C T G A A G A C T C C A T G C A G T C A A A T T C C C T G C C T T A T A T G G A A T T C T A C J A G A G A C C C A T G T C T C C C C A A G T G A G G A A G C C A G G C A C T C A G C C C T T C
2	38	T A C A	T G A A T G C T T C C A A G T A C A A A T T T G T G A	T G A A G T A T G T T G T A T A T G G T A T T G T G A	T T T G G T G C T A C T T T G T G A A T G C T T C C A A G T A C A A A T C A J A C T C A C A A T A C C A T A T A C A A A T C A C A T T G C T T C A A T C A C A A C T C A A A T A T A A A A T A A C C T A C A A A A T C A C A T T G C
2	40	A C T C T A T T G	T T T A C T T T G T T G T C A T T T T T A T T A T	C C A T A A G G T C T C A C A C T T T T C T T A T	T G G G A T A C C C T T T A C T T T G T G C A T T T T T A T T C T A T T G J A C J A T T A T A A G A A A A G T G T G A G A C C T T A T G G C T T C T G C T T A T G G G C A A T A T G C A A T A T A T T G T G T T G T T A A A A T T A T A G C A T
33	35	C T A A	T C T G T G A T G C A A T T G A A A T A A A	G C T G C C A A T T A C A T T A A C T T A C A A	T C T A A G A T T T A C T C T G T G A T G C A A T T G A A A T A A I C J A T T G T A A G T T A A T G T A A T T G G C A G C A T T G C C C A A A G T T A A G A G G A C T A T T C T T T A A C A A A G A C A G T G C T G A C A T T A T T T C A G G T
33	88	T A T C	A A T G C A C A A A A T C T T G T C T C T A G C A	T C A G A T T T T T A C A T C T C T T C T A G C A	T T T T T T A T T T G C A T T T G A G T G C T T A T T A T A T T G G G A A T T G C A G T G A T A T T A C A T T T G T A C A A A T G C A C A A A A T C T T G T C T C T C T C J A J T G C T A G A A G A G A T G T A A A A A T C T G A C C T A G T T G A A C A G C T T A A T G A A C T C A T T G T C C A T
7	58	T C G A T T T T	C G C A C T C T A A A T T A G A G A T A A A T A A G A T G	T G C T G T G G T G A A T A A G A T G	C G G A T A T A A T T A T G T A C C G C A C T C T A A A T T A G A G A T A G A T T T T T T C T G A T A T A C A T T J C J C A T C T T A T T C A C C A C G A C A C A C C A C A C G C A C A G T A G A A C A G T T C C A C A C T G A T A A A T T G C A C A A G A T G G C A G A A C C A A T T A A T A A G J A A T C T G C A A G T T T C C C C A A G A A A C T C T G G A A C C A T A G T G C C T A A T G C C C T T T A A A A T C G A T A C T A A A G G A G A G A G A A T A A A G G A C T G C T T G A T G T G A C A G C A C T G G T T G T A G T C T C A A A A G A C A T G T T G G C A G A T A G C C A G G C C A C T A C T A T G T G T A T T C C C A G T A T C A T G T A C G C A C T A A A A A A A J C J G T G T G C T T G C T G C T G T G A G T G A A C C A T T G C T T A A G A T A A A
6	97	A C C C A G A T C G C	T G A A G A T T A A C C C A G A G T C G C G C A G C A A G A T	A A T T G T G T G C A T T T T G A A G A G A C T C C A A A T A G C	A T C T G G T A T T T G T G T A T C C C A C A A G T A T A C A G A A T A C T C T A T A A A C C A A A C C C A C C C T T C A A T A T T A C A C T A A T G A A G A T T A A C C C A G A T C G C J A C J T C T C T T C A A A A T G C A C A C A A T T A A G A C G
2	59	G T A T G T	T A C A T C A G T A T A A G G T	C T A G A G T A T A G T A A G G T	C A T G G C A G C A A G A T T A C A T C A G T A A T G T A A T A T A T A T A C A G C T T T T T C A T T G A A G C T T T J G J T A C C T T A C T A T A C T A G G C T A T T G G A G T T C C C C A C

100	74	G A ---			TCATTACAGCCAAAGAAAAATACCCAAATTAATTCCTAAATAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
192	92	A T A A T T A C T	C C T T A T T T C C C A A A T A T A A T A A T T A C T	GTCAACATGTT ATAATTTCTTT TAAGAC	TGGTACAGAATGTTTAATTACAGCAGGGCAGTGAITCCAGTTAAATAAAAAATTAATAAACCTTTATTTT CCCAAAATATAAAATTAATAATTAAT[AT]GTCTTAAAAAATAATAACATGGTGACAGCTTT TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCACATGGAGACAGAAG ACGAGACACAACCTCCTCCCCAC[AT]GCGCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
199	89	T C ---			TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCACATGGAGACAGAAG AC[G/A]AGACACAACCTCCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
206	68	G A ---			TCTTTAATTTTATCGGAATCCAGGACACAAC[G/A]AGAAAAACACCCAAAAACCACATGGAGACAG AAGACGAGACACAACCTCCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
213	30	C G G G A C A C A A	T C G G A A T C C A G G G A G C C C T A G G G A G C A A A	TGGTTTTGGG TGTTTTCTT CCTGAATATGC AAATTAATTTAT ATGACA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTCAGTAACAACCTTACATATAGAAATTAACACTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTA[AT]GTGTCTATAATAATAATTCATATTCAGGATTTTG TGAATAGGTGATGGGA
216	96	C T G T G C A G T A A	G G G A G C C C T A G G G A G C C C T A G G G A G C C C T A		GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGAA[C/T]GTGTGGTGGTCGCTGATACTTGGT GCTTGTGTGATGGAGCAGAGTCTCCTGCTGCATGCAGGGGCGTCACATAATTTTAACCTGCACTAAT TTGGCAAACTGTCATTC
258	37	C T A A T G G G A A	G G C C T A A A G G A A T G G G A A A A C C T C A G A T A A G T G C A G T G C T	TCAAGCGACCA CCAACAC AACTCAGATA AGTGCAGTGC T	ATTTACAGTTGGCCAAGATCTCCCTTATGTTGGCATTCGA[G/A]GAGACACTGCACCTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTCACATTCCTAA
265	40	A G G C A T T G C A	C C C T A T G T T G G C C A T T G C A T G G C T T A G A A		CCTTTGCTCTCTGAACCTGGGACAGGATGGAATAATTTTGAATCTGTATGAGGTCGAGGTATGGC TTTAGAATCAAAATGGG[G/C]TGACTTTTCCCCTGTGGTGGAACCTCTGTGAGGGTTGGCA
272	84	G C T C A A A T G G G	C T T G A G A C C T A G A A A G C A A A T A A T C A C T C C	CCAACAGGGGA AAAATCA TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAGGGCATCATTGGATGGAATGATTATGTGTACGAGCACTTGAGGAC CTAGAAAGCAAAAC[AT]GGAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATAIGCTAAAA
279	80	C T C			AAATTTGCTAGTGCAAAATGGACCAGAAATTTGGAAGGGCTATGTAACCTACACA[G/A]TATGCACACCAC AGCCATGTCAGTGTACAGATCCTCTGTGCAITTCAGCTTCTTAAAAACACATCAAAAGGCTGCA
286	51	G A ---			
293	55	C T T A G G A T G	T G T A G T G A C A G A C A G A T A A A C A A A C A G A C	TGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT

92	49	C	A	GCACACCAG	GCATGGGTTAA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAAACCAGGGGCAAAATACATGCTGGATTAAACCC
				GGCAAAATA	TCCAGCA	ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
38	38	T	C	GGGCGCTTGGC	ACTTATCCGTC	GTGGACCTCTACAAAGTACCATGGGCCCTTGGCACTATGTCCTACTCTGCTGACGGATAAGTTGGC
				ACTATG	AGGCAGAGTAG	ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
21	42	T	C	CATTATTGAG	GTGTAGTCTT	TCAAAGTGTAATAGCCATTTATTGAGTATCTTGTCTTGTATTCCTGCTACGTAAAGCATGTAAGACT
				TATCTTGTCTT	ACATGCTTACG	ACAACATTACGACCCCATCTCTCAAGAGGAAGCTGGTATTATGGAAAAACATTTTGTGCAATCAGAT
				CTGAT	TAGAC	T
10	104	A	T	TGGCAAAATA	TTGAAAATGGT	ATGTTGAGAGTAATATGCCCTACATATTTAGTGTAAGTACACCCACAGATATTTTGGGGAGAGAG
				TGCATAACAA	TAAACTGGCA	TTGTTTGCCTTTTGGCAAAATATGCATAACAAAATATTTGGCCAGTTTAAACCAITTTCAAGAGT
				TAA		
				CATTTGCAAT		CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTCCTGAG
				AAACACCATC	GGACCTTATCT	TCCACAGATAAGGTCCCGGAGGAGGGCTTCCCTCTTCTGCTGGGTGACGTTCCGAGCGAGT
39	57	T	C	GTGACTCAGG	GTGACTCAGG	GAAGCCCTTCTGGAATG
				GCATCATATG	GGACAAATTTGT	
34	52	T	C	AACTGTCTAGC	AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGGCATCATATGAACCTGTCTAGCAGTATTATTCCTATTAGCTA
				AGT	AATAGC	TGTTTACAATTTGCTCTGAAGGGTCTAGATGTACACCCCGAGAAAGTGGTGAATCTCTGA
				GGGCTTGACAC	AGATTTTAAAC	TTTGTCTGAAGGGCTTGACACAAAGTTCTAACTTTTCCTGTTTAAATCTCTGGCTTCTGCTGGTGG
19	34	T	C	AAAGTTCTAA	AA	TGAGGAGGCACAGCGCTGGGCTTTCAGGTATCCACTGTGTCGCCCGCATCTGTTCCCTCCACTCCCCAG
				AA		CCACATCTTGGCTCT
39	28	C	T	AAGACCCGT	CCCTCTCCTCA	CTGTCCGGGGAAGACACCGTGCAAAATGGCCTTAAAGTGCAGTGCAGGAGGGGCTGTGTGACTC
				GCAAATGC	GTGCACCTT	CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
					TTGCTACTAA	
48	41	A	G	CCTAGTGGCAT	AGTGGACATCC	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAAGGATGCATAGGATGTCCACTTTTAGTAGC
				TAAGGATGC	T	AACCGATGTTAATTCACACTCTCCATGTTAGTGGCTTACTTGGATTATCTCATTAAAACCCACA
34	64	G	T	CATGCTGTAA	GGAAACAACA	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/
				TACAGCTGTGC	AGCCTAAATGG	TCCATTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
				AAAGGATGAA		TTTATAAGCTGAATGAAAGAGTGCACACAGCGGACACTGTCTAAGTGGAAACAAAGGATGAAGCT
30	75	G	A	GCTAATCATG	TCTCTCCAGGG	AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTAA
				GA	AGCTTGC	TCCTG
35	39	T	C	CATGTGCTGG	CCTTCCACCAT	AAGGTTAATGGACTCACAGTTCATGTGGCTGGGAGGCTTCACAAATCATGTTGGAGGCAAAA
				CGAGGC	GATTGTGA	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
				AGTGGCATTC		TATTTAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC
16	123	C	T	AATAGCCTAT	TGAAACTCCCA	CCATAGGTTCAAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATCTCTTAACTCCATGT
				CTC	CATGGAGTT	GGGAGTTTCATAATAA

3	62	T	G	TAAAT	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTTGJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTCJCAAGACTTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA GG	
7	74	C	T	AATTT	GACTTCAAAG GAAAAGAACA	TCACTCOCOCA AGTCITTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA TTTATTGGCTGTCTCTGTAATAACAATGTGGTGAACAC[G/AJCTTAATCAGGACATCTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTCAAGGCACATAGGCTGATTATCAGTGG	
5	95	C	A	GGACTCA	CCAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	AGAAATTTTCTTTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTACACATCCCATCTGCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA CCAGCTGGAGGTGGAATAATGCGGCACCCACAGAAAACACACAGCTACACAGGCCTGCATT TGGCTTATTCJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAATGCT	
3	37	G	A	---	CATTCCCATCT GTCTTGCA	CCGACCAAGAT CCCTOC	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTATGTGTCGGTGATGTATGATGATTAATATCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA	
3	100	G	A	GTCTTGCA	GGCCTTGCAATTT GGCTTA	GGCCTTCTTTT TCAGGCAC	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTATGTGTCGGTGATGTATGATGATTAATATCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA	
b	97	T	C	---	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTATGTGTCGGTGATGTATGATGATTAATATCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA	
a	87	T	C	---	---	---	CACAACATTCAGAAGTTTCTGCATTGTCTCTCTGATGTCTAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCAAGGTTTCTCC[C/A]AGTATGGATTTCTCTGATGATTAATA AGCCCCGAATTCGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTCTCCAGTGGGAC TCTCTGGTGTGCACAAGAATGGAATTCGGCTGAATGCTTTCCACACT	
	107	C	A	---	---	---	TTTGTGGCTTG AGTTTACAAAT	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTGAA
1	32	G	A	ATGCAACAAG	GGGAACATCA ATGCAACAAG	T	TATTAGATAAAACCTTTGTTCCGATTTCAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTTAAGTAGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAACTTT GTGCAAGGCACCTCTGTGGCCTCACAACCTGCCCCCTGTGAGAGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG	
.	87	T	A	---	---	---		

		GACTGCTAAG GATTTAATTG TAAAA	TGAAGTGTAG ATGGCTAAGTA TAAAA	AAGAGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGATAGATTTTAACTAGCTAGCCATCTAACACTTTCAAGCATAAC
91 A	G GAT			AAGTGATGTCTCTACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTCACTGGCAATGATAATAAAGAAATATGATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTGGAATAATAGGAGTAA
105 T	A GAA	CACATGGCAA TGATAATAA CA	TCTATCCTCAG AGTGTAGTCTG CA	CATATGCTGCTTTATTTCTGTAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTAACCACTCTCAAGAAATGTTAGTATGTTGCTATTACATGTTT ACTTTTGATATTGTCTCATTACTATGTCTTATATAATATGTAATACAGTAAGTAGGTGATCC TGCAATTCAGGTAAAGCGGTAGGTGGAATCCAGATTTCCCTCTTGAGGAAAA
164 C	T ---		---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTTCAAGCTT GGCCCCACCATGGCCCTAGGGTGTCAACAAGTCCAGGCAATCATGGCGTTCTGGTATATCTGATCC AC
131 C	T ---		---	ATAGCTTTATTTGTCAACGAAGGCTACACGGGATCCTCTGGTTTGTGTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTTACACAGTCAAGTACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGAGTCCAGACTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGCTCCAGTGTGGTCATCCAGAAAGCAGCTTG
175 G	A ---		---	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTCAAGTCATAATAATGCATTTA TTCAGGGGAAACTTTAATCTTTCTTTCTCTCCAAAACAGCTGCTGGAAACACCTCAAAATTA GGGATGTTTCATCTAAACACCTTTACTGAACTTGATTCTTGGCCAGAGGAGGCTTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATGCAATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAGCTCTGTCTGCTGAGTCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAAGTTCTAGTCTCGCTCTCTCGATTTCCCTGCCAGCAGTCTTCTCTCTCTCTCTCTGGOOC TCTG
96 G	A CTCTGTCTG	CCCAGAGAAG CTCTGTCTG	CAGCCATGGCT ITGCAG	ATGCTTTTGATGATTTCTAATTTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGCTGTCATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGTCTCTCTGCTGTT CTTCCCTTTACATCTTTTGGGGA
b 193 C	T ---		---	ATGCTTTTGATGATTTCTAATTTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGCTGTCATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTCTCTCTCTCTCTGTT CTTCCCTTTACATCTTTTGGGGA
187 T	C ---		---	CTTCCCTTTACATCTTTTGGGGA

		GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTT	AAGGTTTATTGCATATGGAAATCAATAGIAGTATCTTTTACAAAAAAGGTAGAAATAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGGCAGTGAGACATCAACAA
28	A G A A			TTGTGCTCAACAGATGAAATTCATAACCTTGTCTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAI[A]GCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
b	112	T A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A]TATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
a	73	A T ---	---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
i	165	G T GCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAGATGGGC TCCTGGAGTCCAACAGGATGTGGACGTCCTGGTAGTCTCTTTTACACAACATTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[C]GCTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
.	195	C G ---	---	ATTGTAATTAATAATTACATGGGCCCTATTTATTAAAGGACATTGTAATGTTTCCACTTTGTTTTAA [C]TAAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGCG
b	68	C T ---	---	ATTGTAATTAATAATTACATGGGCCCTATTTATTAAAGGACATT[G]GTAAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGCG
1a	42	G C ---	---	AACCACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T]CJAGCAATGGATGCTGTGTCAAGACATACTGCCAATAAACITTAAGAAAAAGGA ACTCAATGAAGTTACTGTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAC
j	75	T C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGCTTT TTACTTAGCAAAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAITTTCTCAAGCACA T[C]ACCCAACTTGAAGGTGATTGAACCCCAAAATATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
l	134	T C ---	---	TGCTAAACACCACTTATTAAAGGAGTACTAGGAAAAAATACTCCAAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[C]TGGCTAATACACTGCAATATTTTA TGTTTAGCAATATTAGCTGGTCTGTGTATACCAGAGAGCGGTATCTGG
b	106	C T AGCCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

10a	28	T C A G A G	A A C A C C A C C A T T A T T A A G G	G C T G T G T T G G T A G T T T T C C T	T G C T A A C A C C A C C A T T A T T A A G G A G A G T C / A C T A G G A A A A A C T A C C A A C A C A G C A T G T G A A A C A G T T G G C A C G G T G T A A A G G G C A C A G A C T C T G G A G C A C A G C C G G T A A T A C A C T G C A A T A T T T A T G T T A G C A A A T T A A G C T G G T C T G T A T A C C A G A A G A G G G T A T C T G G
70	53	A G A C A T C A C A	C A A C C C C A A A A C A T C A C A	G C T T T T G G A G T G T A T A A T A G T A	G A T G T T A A T G A C A C A G A T C T T C C C A A A G T A A T C C A A A C C C A A A C A T C A C A / A G / A A T T A T T C A T A C T A T T A T A C A C T C C A A A A G C A A A A T A C T T C A A C T G C A A T C C
36	151	A G A	G C A T T C T T C C A A A A C A A A G A	C C T T G T A A G T G A C T A T T C C A A T	A T T C T G A G G C A A A G G T T C A G C A A A T C A G C T A G C A C T A A T C T T G A C C A A A T G G G T G A G T C A G C C T C A T C A C A G A G A T T T T T T T A A T T A G A T G A A A T T C A C A T T T A A A A C A T G G T A A C T C C A A G C A T T C T T C C A A A A C A A A G A A T / A G / A C A T T G G A A T A G T C A C T T A C A A G G A C
31	32	C A G	G A T C T A A C A G C T G C A G A A T G	A A A A G C T G G G A A G G A A G A G	C C T G A G A G C A G A T C T A A C A G C T G C A G A A T G G C / A / C T T C T C C T C C A G C T T T T G T G A C A A A A A C A A T T C T C T A A G G C A T C A G A A A G C A C T G A G T G C A A A A T G G G T T G T T C A G G T A C A A G G T C T C
14	225	T C		---	T A A A T A C T G C C A A C T A G C A T T A C G T C C A C T C T T G C A T C A T T A A A A C A A A G G T A T T C C T C C T T G G T A T T T C A A A T G A T G C A T T A T A C A A T A A A G A A G T T A G A C T T A A A T G C A C C C T G A T T A A T T A T G T A A A C T G G T A A T T T T T T A A A A G C A T A A T A A T T G G T T C C T T C T C A T A A A A T G G A A A T T T A A A T A T T C T C T G A T A G C T T G A G G T T / C / A T C A T T A G T A G T G C A A A G T G T G
24	112	A G		---	C G G T T T G C T A C A C T T A A T G G G T T T T T T T A A G G A T T T T T T C A G G C T T T G T C A G C A A C A C A A A C A A A G G T A C T G A T A C C A G G G T A C A G A G T G C G C C A / A G / C A C C T T A G A A A A A T T A C A T G A C A C G G A A A A T G C G C C T T G C T C C T T G A A G A G C T A C A G T C A G G A T T T G A C A A C T C A C A G T C T T A G G A A C T G G G C A A A G T A A G G C A A T T C T C A T C C C C T A G A G C T A T T G T G
39	139	T C A A T T C	G A A A A A T G A G A T G C A G T T A A	T C A C T T T G T G G C T T T T A A T T A T	G T A C A A A A A A A G C T G A G A A G A G C C A C A C A T G G A A G T G T C A A G A A A C A T T C T G A T A G G T A C G G A C A A A A G A G C T C C T T C A A T C A A A A G G A G T T A C A T A T T A G T T C T C A C C A T G C T A G A A A A T G A G A T G C A G T T A A A A T T C T / C / A G A A T A A T T A A A G C C A C A A A G T G A A A C T G T T G T C T G G G C C C T A T G T T G T A G A T T C T C T
11	216	T C		---	T C C C A G C T C A T A T T A T T T G G G C A C A G A G T G G G C A C T C A A A T A T C T G A T G A A C T T G A T G A A C T G A A A A G A G G T C T C T T A A C A A G A T A T C A T C C C G A A G A G A A G T C C C A C C A T A T A A A A T G A T A T G A T C A A G T C C A G A A A A C T T T G C C T T C C C A A G G A A T G T G T T C T A A T T T G G T T C A A A G C A C A C T G G T T C C C A C T T T A C C A C T T T / C / C A T G A C A T T G G A C A A T A G T A C T A C T C T T T T C T A C
13	112	G C		---	G C C A G T C T G T A G T A A G T C T A G G G A C A T G A C C A G A C C A G A A G C C C T G T C T A T A T A G A A C A A A C A G G T G C C A T A C T T G G G T G A G G G A T A C C G C T G T A T T C C C A G A T G / C / A A G A T T T G G T G G A A G G A G A C C A T G A C A G A T G A C A A A C G G A A C A G T T T C T C A A A A C A G A G G T A T A G A
57	74	C T		---	A A A A G C T T T A A A A A A A A A G T G G T G C T A T C T T T A G A A A C A C T T T C A G C A A G A T C A A G T A G C C C A G C T A C A G C C T / C / T G G T G C A T C T T A A C C C C C T C T C T T T

7	121	T G	---	---	TGCTCTTTTATTTCAGGTTTCACAACACACGCCGTG[G/TTGGCACAGTCTACCAAGTGCCCGCAGCGCCAGCTTGGCCGGAAGGCTCATCTGTTGCTCTCTATGGACTGATTGAATTTGGATGGCCAGCTOCAGAATGTTCCAGTGGGGCAGCTCTGTTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAOCCAAGAGGTTGCAGATGCAGCTTGAGTGGGTCCAAAGCCGGGTGGCTGTG
					AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTATCATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAATAAAGT[G/ATATAATCTTTGATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAATTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTTGAGG
					CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGTGACACAAATCAAGACTCACAGTAGCCTCAACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/CACACCACACCTGGTTAACTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACCAACTAAC
	114	G C GCTGGGA	T	---	CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGTGACACAAATCAAGACT[G/CJACAGTAGCCTCAACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCCACACCTGGTTAACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCCACACCTGGTTAAATTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACCAACTAA
	51	C G	---	---	CACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTTTTTCCTTTCTTTTCCCATATAACACAAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGTTTCAGTATGTTATGTAGAGTCACATACCTATGGCAAAAAATATTTTAAATTTGAGGGAATAGGCCCAATTT
12	71	C T AGCTTTT	TTAGAAATTTT GTGATTATAT GGAAAAAG	---	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGTGACACTTTGATAAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACATCTTTATGGAAACTGTTTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTGCACACACACAAGTAAA
188	36	C A CTCAGTACAA	GTTT	---	TGCTATTCATGACAGACACGTGAGACAAATATTTCTTATTTTACAGATGGAAATAGACCCAGACATTATTCAGTACTTTAACCACTAATAGTGGAACCCCTGAGACTTTA[G/ATCTGCAAGGGGTTTAATAATGCAATATCACATATATTTCCATTTTAAACCCATATTTAAGTTTCCATTTTCTTAATAGAAAAATGATAAAAAATGTTTTCCCCCAATAT
a	108	G A CTTT	CATTATTAAAC CCTTTGCAGA	---	TGTATAAAAAATCCAACTTGTTCACAAAGTACATATGTCCTATGATTTTATGCATACATCCATATACATATATCAAGGTAAAGTCCA[G/ATACAAAAAACAGCATTTCCATATGGCCAGTGTCTACAGAAGTAAGACTGTGCAAACTTTATCGTATAGTCAATAGATTGCACACTAAGGCAGGATGAGGCAGAGAAGCAAGTTGIGTCCA
337	87	A G AAGTCCA	ATGCTGTTTTT	---	



			GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTCC CAAAATATGATAATCTCTGCCACCACTACTGCTTTAAACACAAATAGAACTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
46	CT	T	TGTT	ATCACAGCAG AGTACCTTTCT	AGCCATCACAGCAGATACCTTTCTAACTT/CJATAAGATTGTGAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA
29	T	C	AAC	T	TCACCTATCTCTTTTGTGGTGAGAACACCTTAAATCTAAGATGATCAATTTCAATTAAGATGG TAGTGAGCGAACAAGAGAGGTTTCACTGACTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
b	112	T	A	---	TCACCTATCTCTTTTGTGGTGAGAACACCTTAAATCTAAGATGATCAATTTCAATTAAGATGG TAGTGAG/CJTGACAGAGAGGTTTCACTGACTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
a	74	CT	---	---	AACAAAAACAGACACCTCGGCTCTCTCACCAAGTCCACATGGTGCCAAACAATCCACATTCCT ACATCTCCCCACTGGCTGCCCTCTCACACCTCACCA/GIACCTGGCTTACCGGGAAGCATAAA GCCAAGCATTTAGTCTTTTATTGCAACATGGCTGGCTGCAATAC
3	107	A	G	CTCCTTCACAA CCTCACCA	ACTCACTGCTTGTGTTGATTAATCAACCTAGCC/GA/GCTGTGATGTGGGATTAAGATAAAATA AACACAAAAATGAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
3	36	G	A	C	TGCATTCAATTGCACCAATAATAACTTCTGTACAT/ATCATTAATTGTTATTCATTATCACAAAAAT TATGAGTGAGGATGATGTTATCCCTATTTTACAGATGAGAACACCTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCGGGATTGGAATCCATCACTGAATCCAGAGAAAT GTTCTGCATCACIGTACACACTGACTCTCTTTTCTCTCTTGAACAAAGGC
1	37	A	T	---	CTTCTGACCTGTTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/GC/JAAGTCAATTTGTAGGTGTTCTGGGGTTTGTACGTTTCCATTTCTCTATACACTGC CGTCTAAGGGAGGCTTGACAGACATTTATCAGATGGCTGTTTGTCTGCACTGTGCACTGAAG
11	70	G	C	CCA	TTTATGCAAGAGGTCCATGAGTTTACAGATCTCAAGGAAGAAAGCCCTAGAGATGACACCAAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATACTCTATCCACGTGCAGAAACTGGCAATAGTTTGTJ/TTTACTAAAAACACAAATGT TTAACCTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
81	178	A	T	---	CTATGTTATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTACAAAGATGAGAACAGGTCTTA GAACTCAG/GA/JATCGAAAGGAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCACTTCTTATTTTGGCCACCTGTTTGT TAGGAA
791b	76	G	A	---	

31a	44	C G	---	---	CTATGTAATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAGTTTCATCTAGTCCATAGACCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACCTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
36c	120	C T	---	---	CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCAGAAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTCTCAGCATGAGCCAGGATGTCAAGGTGAGAACCC/CJTJATGAGCCAC ACTTCTCATTCTCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCCAA G3
06b	118	C A A		CCAGGATGC AAGGTGAGAA	CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCAGAAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAGC/AJCCTATGAGCCAC ACTTCTCATTCTCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCCAA G3
06a	42	A G	---	---	CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCAGAAAG/GJGCCACTCCACAGATGCAACAG GCCTTTGAAGGAGCCAGTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTATGAGCCAC ACTTCTCATTCTCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCCAA G3
38	48	G C T G		TTATCTCC TTGTTTCTTT TCAAT	CCATCTCTCTCTCCCTCCCTTTATCTCCCTTGTTTCTTTTG/GC/JATTGAAAAAATACTGTT TTCTAACAGTGTGCTGGATGGATACTATGTTATAACATGCATAGTCTATAIGGGTATCA
15	54	T A T T	TCCTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAAATCGAAATGGA
37	41	C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAA	TGTTTTAACCCAGGAGACCTCCCAGAGAAAAATCCAAGAG/CJTCTTAAACCATAATTTTGTTT GAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
81b	131	A G C T G C A G T G	TGTCATTTATG CTGCACTG	TTACTTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGCTATTTATGCTGCAGTCG/A/GJA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
31a	29	G A A A T T	CCAATTTAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/JAATTTTACAGTATCTAATGCATGGGCATCTGTTT AACTCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGCTATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
92	38	T C	---	---	TCATGAGTCTTTCTCAAGATGCTTGTTAAAGTCCCAT/CJCAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACTTAGGATAATTTTGCAGACCAA

134	T C ...	CCCAATACTTT TTCAGGTGAA	...	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTCTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTAGTTC TTTCAAAATTAATGCCACCATAGAAATAATTTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTTACTCTTTACAC
40	C T A	GCAACATGGG	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACTTTTTCAGGTGAAAAAGGGAAAA[C/T]ACCCATGTTTGTCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTTCTGATGTGGGAAATAT TAGAAATTAAGCGAGAGAGGCA
97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG OCCAGG	TGTTTGTTCTGCACCTCCCAACAGTGGTCAATGAGCCTCAAGGTTTTGATTGACGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT[C/T]CCTGGGCAATTTGIGCAGTAGTGTGAGA TAAGTTGATTTAAACACTCTGTGCTCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGAT[C/T]CCATTTTGAAAAATTAAGCTTTTGAATTTGTTTCCCA ATG
b 161	C T ...	...	...	TCGGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
58	C T	GTTCAATAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TGCGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
134	G A ...	...	...	TGCGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
a 92	C T ...	...	...	TGCGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
b 125	A T TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAAC ACTG	TGCGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
a 44	T A ...	...	...	TGCGGTATTAGGATCGGTTCAACCTCGATGATGGGGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG CAGGACCTTGGAGCCTTGTGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
26	A/C	GGCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGGCCAATTTTATCCGCAATAAA[C/T]TCCCAAAGTCCCTCGATGGAGGCATTTTCAGAAATCGGG GCAGGGGAGGCAGAGGTTGAGACAGATGTGAAGAAC

5c	103	C G ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGCCTCTATCAAAAATTTAAAC/G/AAATATTAAATATTTTATTTACAGAGGAA CTCAGAGCCAG/AAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTCACGG
5b	99	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGCCTCTATCAAAAATTT/AAACAAATATTAAATATTTTATTTACAGAGGAA CTCAGAGCCAGAAAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTCACGG
5	165	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGCCTCTATCAAAAATTTAAACAAATATTAAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAATGACCAAGACACAGT/AAJCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACATAAATTCACGG
4	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ATATGT	CTCAGACATTCATTTTCATTAGTTGTAAATTTTGTGTATTTTCATAGCATGGATAATATTACAGAA AAAAATTT/GTACATATCAATGACTGAAACCTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTGAGCCTCTCAGTTTTTCCATCA/TTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCTGTTTCACTCTCATTTGCTGATGGATGGATGCATATAAAATATGGGTGATTC AGAAAATAAGTAAATG
3b	81	C G ---	---	TTAGAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAATA/C/G/C CATTAGGTATTAGATAAGCATCCCATAAACATTTGTGAAACGAGCCGAGTTTCGATTACACACA GTTGTCGTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAAA CATTGTTGAAACGAGCCACGTTTCCGATTACACAGTTAGTTGTCGT
3	187	G A ---	---	TTAGAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTGAAACGAGCCGAGTTTCGATTACACAGTT GTCGTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG/G/ATCCACCGAA ACATTGTTGAAACGAGCCACGTTTCCGATTACACAGTTAGTTGTCGT
1	52	A G GGAATCTTG	TTCTACCATG AACTTGCA	AATATCTGGCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/G/ATGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGGTAAAGACTACTCATTTCTCAGTCTCTCTGCTG
7b	148	C T ---	---	GAGTTTAATGAATCCTGTTCCCTCTCTAAACCTCTGTTCCCTCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTTCAAGAGGTGAG TAATGCTTGGT/C/TTTGTCTGTGCGGTATCTGCTCCAATCACCCATTCACATTTATTTGCTATTAT GCTGAATGAAACGGTTATATTACAG

37	165	CT	...			GAGTTAATGAATCCTGTTCCCTCCTAAACACCTCCTGTTCCCCCAACTTCACATTCAGCAGATAATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTTCAGAGTGTGAG TAATGCTTGGTACTTCTCTGTGCGGTAT[C/T]TGGCTCCAATCACCCATTCACATTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
93	53	GC	...			GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA[C/G]GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTGACAAACCTTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
41	80	T C	AGGTACTT	CTTCTTAATT AGCATCTACA	TGAAACCCCA GAACAGTG	GACTCTGCTCAAGAAAAAATAAATTGAATAATTGAATTAATTAAAGCATCTTTAATAAGCAT CTACAAGGTACTTAT[C/G]CACTGTTCTGGGGTTTCAATCCTCTTACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCTTTT CTC
150	45	T G	TGTCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTCTTCCCAATGACTTATTCTATATCTTGTACAT[C/T]GAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGGTGGGATTATTTTCACGGTCAATGTAATATGCATGTAAGACTA TTTTTACTGGCCTTCTTTTATGCATAAAACAAGGATTGCTCTATTTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGCTGCTACTAGATAATAGTCTTTATAGATATGTGTTTGAATAAAGCCACA AATTATCTATAAAACAAC[C/T]AAGGAACACAGGCTCAAAAGTGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
166c	141	G A	TTGTCTGG	TTTTCACAGTC	AGTCGATGCC AATTATAAT	GAAACTATCCTTTAGTGGTGGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/G]ATTCACTGAAGTATGTAATCAATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATAATTGGCATGGGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTT
466b	80	T C	GTC	GACTTCTGGG CTATGAAATA	TGCTTTTATG ATAACTAGTTC ACTGAA	GAAACTATCCTTTAGTGGTGGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/G]ATTCACTGAAGTATGTAATCAATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATAATTGGCATGGGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTT
814	104	CA	...		---	TGCTTTTAAATAACAAATGACCACCACCTGACACCATAGTCTGTCTCCATTGGCCACGCTTCTCCTC AGTAGAATAAGACAGGACTTTGGCTGGCTGCTATCT[C/A]TTCTCCTTCAGAAAGACACTTTGGCCCT CATAGGCATCCATAGATATTGTTGAATGAATGTGCTTTTGGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
1720b	55	A G	---		---	CCTCTAACAGAAAACTTGACTTCTCACTCAAAATACCTTCTCTAATAATTTTGAAGTAACCA AAATATCTCTCAATAAATAATCTTTTAAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAC

20a	47	A G	...	CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTGAGATATAATTTAAGTAACCA AAATATCCCTTCAAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
25	123	A T	...	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACCTTTGCATTGTCTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGTCTAAGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTCACCAGGGTTAGTTTGCAAT TAAGAAATGCCAGCTTTTCTCTGCATCATCTTGAACATTATCCACATG
18	74	C G	...	CCACTCAGTAAATCAATTTGTAGCACCTTATTTCTAAGATTCTAATTTTATAATGTTTACCCTTT GTCATTGCTCAGACCAAGTACATGTTTTCACAGCCATCTTTCTTTCTGGAAATCTTTCAGAAT TACAGTTATGATGCTCTTTTATATTCCTCA
43	91	T C	...	TGAGGCTATGATTGCAGATTTGTAGTACTAATACTTATTAGCAATTTCAATGTTGGGCACCTGTT CGTTGTGTTTATATCCATCTCTCTGATTTTAAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAAATTTGCAATTTACACCTTCTCTTTTGTCTTTAGGGA AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCTCTGAGTGAGCCTGTGAACCCACCCAAAGAC GGCTGGTCATCAGTGTCTCTCTCTTTCCGGACACTATCTTTAAAGAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCCAAATAATCTGTTTAAATAATCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTTACACAAAAAGGATTGCAAA
17b	84	C T	...	CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATCTAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
17a	83	A T	...	CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATCTAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
15b	115	C A	...	AGATAACCCCTGGAAACTAGAGAAATTAATAACGTGTTGCACTGTGACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACA/C/AJAGCCAAGAAAAAGCC TGATAATTAGAGGCACTTGCAATTA
15a	42	C T	...	AGATAACCCCTGGAAACTAGAGAAATTAATAACGTGTTGCACTGTGACACCTCACCAGAACTGGAAGG AGCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACACAGCCAGAAAAAGCC TGATAATTAGAGGCACTTGCAATTA
13	146	C T	...	CCTGTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCCATTTCTCTTGTCTTGA TTCCCCAAACCCAAAGGTTCTACCCCAATCTGATCAATGCTGACTAGGTGCTGGCTGGTTCAGGGTAA AGCATTTATGA/C/TJAGACACAAAGACAAAGAGGTAAAGTTGCTGCTCAAGAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

		19	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTGTTTATTATGTTGCTGCTATAAATCAATGGTTCTTA ACATTTCAAAATAGATCTTTTGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTAATJTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
		2	122	T	A	TTT	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTTAAJAAAAATACC AGACTAATGATTAATAATAATTACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGGCCCT CCTTAGA
		3	39	T	C	ATAAAT	TGTCATCTTGA CTCGTATTAA	AAATTTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAATAATAATTACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGGCCCT CCTTAGA
		b	170	C	T	TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATGCTGTTTAACTGCTGCTTTCAGAAAGGTTAGGTGTT T
		a	54	C	A	CAGGGAAGG	GTAGCAGGAT	CAAAATTATAT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/AAJATTATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTTGGTGACACTCTGTTTATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
		289	29	T	C	CAAACCTT	TCCTCTGTCCC	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCACAACTCTTATGTTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
		119	40	A	T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTTATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCAATGGCTTTAGGCTCTGTTTAAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAAGATTAACACTGGTCAGATGTTTAAAACTTGTGAACCTGCAGC
		316	104	T	C	CTCTT	CTGTTGATTTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGGGTGTAATCAGAAGCATCTATATTACCAGTCAACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTATJCTAACTTTGGATACATTCCAAAGCAT CATGGTCACTCCAGTTATGAAGGATGTTTAAAGGCCAGCC AGTGAGTTGTGCACAAATTTGGAGACATCTGTGACCCCAACTTAAACACTTCTCCCACATCTAC
		572	61	C	T	---	---	---	AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

38	31 C	T	TGAAGCAACC AGGCTTGT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGCTGCCTGAAGCAACCAGGCTGTGTCCTACCCCTCTTAGAGAAATAAATAATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTTGTTCTACCCCTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTTCAGGG T
31	32 A	G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCAAGTCAACTCTTGACTCCTCACTCCCATCTCGGTG TCTGCTTCCAGGGGACGATCTGACACAGCCTTTGCTTGTGTGACAAACAGAACATTCAGAAAG TGATGCTGGTGACCTCCAGGATA
146	A	C	GTTACCCAGA GTCTTCTAATA	GGGAGTTAGGA GTCAAGAAGTT GA	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCTCAATAAATATATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAAAC/AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
82	A	C	GGTGTCTCAAT AAATATTATT	GGGAGTTAGGA GTCAAGAAGTT GA	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCTCAATAAATATATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
60	T	C	GGTGTCTCAAT AAATATTATT	GGGAGTTAGGA GTCAAGAAGTT GA	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCTCAATAAATATATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG CTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
84	C	G	GGTGTCTCAAT AAATATTATT	GGGAGTTAGGA GTCAAGAAGTT GA	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCTCAATAAATATATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG CTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
33	C	A	GGGAAATATTC TATCTCACCTA	GGGAGTTAGGA GTCAAGAAGTT GA	CGTTGGGAATATTTCTATCTCACCTAAATTTATG/C/AGTGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGTCATATTTAAGTTGTCAGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
125	T	C	CACAAATGTA ACAAGAATTG	GGGAGTTAGGA GTCAAGAAGTT GA	GTTGTGAAACTCCAGTATCATTTCCCTCAACCCAGCTTAAATCAAAATCACTTTTCTTCTCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAAACAAAGATTTGATCCTA/T/C/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
58	C	T	CAAGTGAATT ATGACCAAAA	GGGAGTTAGGA GTCAAGAAGTT GA	TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATTATGACCAAAATGAGA/C/T/AAAT TTGTTAAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTTCAGGTTCAATATTTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTTCTTTTCTTTTGT/G/C/TCTTA GAAATCAATTTGCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGAGGACTACTTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC
56	59	T	CAAGTGAATT ATGACCAAAA	GGGAGTTAGGA GTCAAGAAGTT GA	TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATTATGACCAAAATGAGA/C/T/AAAT TTGTTAAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTTCAGGTTCAATATTTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTTCTTTTCTTTTGT/G/C/TCTTA GAAATCAATTTGCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGAGGACTACTTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC

154	T G T T T T	T T A A C C A A G A G T T T T C A T T C	C T A A C T T A A A A A T C C T C A T T C A A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A T T A A G C C T A A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A G A G C A G A C A T T G T T T A T C A T G T G T T C G A T A A T T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
95	A G T T G A A A A A	A A T A A G T G A A A G T A A C T G A C	A A A A A A G C A C T A C T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T C T A T C G A G A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A T T A A G C C T A G A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A A G A G C A G A C A T T T A T C A T G T G T T C G A T A A T T T T T T A T A T T T G A A T G A G G A T T T T T A A G T T A G C A T
5	A G T T G A A A A A	A A T A A G T G A A A G T A A C T G A C	A A A A A A G C A C T A C T T	C A A G T G C T T G G A C C T T G G A T A G G T C A G C C G C T G A A G G T T G G A C A G T T G T T G G T T A G G T T G G A G A C C A A A A T T C A G T C A T C C T G T A A T A T A G A T C T T G T T C C T T T G G G T T A C C A C T A G G G T C A C T A A A G A G A G A T G G G A G A C A G T C A A T C T T G T C T A A T A A T T C C A A A T A G C C A T G G G T T G G A C A A A A T A C A A G G T A G T G T C T C T A A C T T T A A T G G G C A T A
133	C T A A G G	T G C C C T G T C C A A G G	... C A A T C T A A A T T C A T G T G T A G A C A C A	A A T A A C C T G T G G C A C A T A A G G C A A A T A C T A G C C C C A T A C A G A G T G T T T A T G T T A A T A T T A T G A A A A A A G T C A A G A G A A C A A G A T A T A G A T T C T G C T A G A A T A C T T G A A A T C T G A T G C C C C T G C C A A G G C T T T G T G T C T A C A C A T G A A T T T A G A G A T T G A A T G A A A A T T G G C A A A A T T C A G A A A A G G G
77	T A A	A A A T G A T T C T T T C T G C T A A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T T C T A G A A T G C C A C T T T A C A G C C A C T G A A A T A T A T T G C T C C C A A A T G A T T C T T C T G C T C A A A G A G T A J T T T T T T A A G T T A C T A C T T A T T A T A T T C T G C T T T T T C A A A A A A A A A T G T G A G A A C A G T A C A A A A T G T G T T C A G T A T A G C A A A T T A A A T T A A A A A G T A A G A A A A A A A A G A G C C A A T T T G G G C
144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C	G G C A T T T T G T A A A G G A G G A A A	T A G A G A G G C T T T C A G T T T C A G G T T G G A G G G G T G G T G A G T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T C T G A G A A G A A C T C A G T T C T A A A G T G T C A G T C T T T G C A A A T G C T T T A T G A G T T T C A G T T T C C T C C T T T A C A A A A T G C C A T C A A T T C C T C A A G G A A A A A A A A A A A A G C T T T C T T
23	T C C	T G A A T T C A T C C A G A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A A C A G C T C G A A T G A C A A C A A G A G A G A A A A G A G A A T A A A G G T T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T T C T G T C C C A G T G C A T G G A G C A G T G
115	T C G C C A T T C T A G	T G A C T C T C A A G G C C A T T C T A G	G C A C T G C C A G C A G C C	C A G G C C C A A C T C T G T C A T T A A G T G T T T A G A A C A G A C A C C T C A G T C A C A C A A A G T T T C T T G T A T G T G C C C A C C A T A A A C A G T T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G T C G G C T G C T G G C A G T G C T T T T C C A G C C T G C T G C C C A T A C T A A
40	A G C T T G C C A	T G G C T C T G C T A C T C A	G A A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T T G G C T C T G C T A C T T G C C A A G A T A G A G A T T A T T A T G T G G G A G T T T C T G A A G A T T C C C A T G G T A A A T A G T A T T C C T C T C C C T G C T A G G T T T G A A G A A G T T G A A



25	C T A	GCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGGAAATCATTTACACTA/C/TGGAAATCAGCAATGCTAAATGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCCTGGAATTTGAACTATTGTTAAACATTACCAGCATACCAGTGGG CTGGGTACAACTTGGCTACCGAGGAGAACCTGACACAGACTTCGTAAATGGCTTTCACAGGCTACTGGA AAGCC
75	C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTTATGCCATAATTAAATTCATTACACTC/C/TACATCATATTTTCTTAGCAATACA TCTAGACACCTGGCACTCAGTAAGGATATCTCTGGCAGATAATCATTTATCATTAGACATTGCA GGAACCCACCATATGGATGGATAATGTGTTGTTTAAAGGCAAGCAATTA
26	165 A C ---		---	TTGCATGCATTTATACGAAAGGAAATTAATAATCTCTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAGTATAGTAACAAATGAATTAGAAAAATTGTCAAGTGTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/C/GACATAGTTGCTAAGGATATTCACAAAAATTAT TTCATGA
78	A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAAACGTAAATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/C/G TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGTTGATCTGGAG
89	C T GCTCTAGACC	GGGACACACT	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC/C/TTCCAGGGTCCCTCAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGATCAGGGCCCTTAGCTCTCTGGGACAGTGAAGGGCCACCCACC
10	C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCTTAGGTCCTGTAGCAAGAGAGGAAGCATCTTCATGGGCAGGAATTC/C/TCAATTT CTGTGTTCTTAGGGTTTGCGCTGGCCATCAGTTCACTAGCCCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
128	23 T C ---		---	GGACCAACAGAAATTACTTGGCAT/C/JAGGGTTTCTTAAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTAGGCTCATTTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
132	G C AGGCTCTOC	CATTAACTGCTGC AGGCTCTOC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAAGGAGCCATCCACGCTGCTCTAGCACAAAAAATAGATACATCATTTCTGAATG GGCAGATTAACTGCAGGCTCTCC/C/GCTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAGGGCTGCTCCGTGAATAC TAGTTCCG
134	C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTGCCCAAGACCAATTAACAAGATTTAATAGTTAAAGCCAAACTATA AAGAATTAACTGTTCAAAAGGTGTTAAAT/C/TCTTAATACCAATTTATAGGGCCACCATTAACTT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
37	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTAT/C/JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGGTATTTCTCGTTACCCATAGTCACTGCAAGTGTCCACCCCT

		TGTTACITTTGA	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCITTTGCTCTGACAGCCAGTTAGCTGTGATTGTCAGAAAGTTTACATTTGTTGTTG
6	81 A	GGA AGCTAACTGG	TTTCATGCTCTGCTCTTCCCTGGAAATTTCTTTATTGAGCGGGGAGGTGGTAGGCACAGAAGC CAGTCATACGTTTAAATTGACCCCAACCATTAAGTAATAGCATTTCA
0	77 G	CCAGTCATAC TTTTAAAGCA	CAATGATCCCCCAACATTTCCAGGAAAGGTCTGGTCTGTTCTTCCAGCTCTGTTGGTGGCT GTCAATCTTTGACATTCCTGTCTTGACGTGTATATCCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGGTGTCTGTG
1	55 G	GTCTGTGTTCT CCAGCTTCT AGCCACCAC	GGGGGCACAAATTTAGCTACAGTGCATATTAAAGATAACATAGAAATATCATAATAACTTGGTTTAC TGAAATCTGAAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAAAC/CCTGAAATTC AGAAATAAATAGAAAGGTGAATCATCTTATATCAATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCCA
5	122 A	C TACTATCCAA TTCA	CACCAGCCACCACCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GA/GCTGTG GTGCCAAGGACGCATTATG
7c	192 GA	---	CACCAGCCACCACCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GA/GCTGTG GTGCCAAGGACGCATTATG
7b	179 GA	---	CACCAGCCACCACCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GA/GCTGTG GTGCCAAGGACGCATTATG
7a	128 GA	---	CACCAGCCACCACCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATG/GA/GCTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GGCTGTG GTGCCAAGGACGCATTATG
0	71 GA	GCAACCTACT GACAAATTTAA TTTTAGTT C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG/GA/GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
3	123 TC	TGTTTAGGAA ATAATGACAA GAAAAA G	CTGTAACCTACACACATCTCTCTGTAACTCTAGGTTACTTGTATACAAAACACAAATGTAATGCT ACATAAATAATTGTACATCTATATTGTTAGGAAATAATGACAAGAAAAAGGCTT/C/GTACAT GTTTGGTAGAGTTGTACCAGCCATTTTCCCCCAATAATTTCAATCCACAGTTGGTTTAATCCACAG AAACCACGAATG
3	46 C/A	CAGAGTCTGG GGGAGAAGA TATCTCGTT	ACAGTTAAGAAAGGCTGCAGCGGTTGCAGAGTCTGGGGGAGAAAG/C/AAACGAGATAAAGCATG GCAAGACCACCGTGAAGATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTGAGAAAGAACAGAGGAGCGTT

3b	77 T A	---	---	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTTGCTGGAACTTTGCCTGGAAATGCTC TTTCCCTCTTAGAGCTTTGCTGGCTTACTTTCTTTTCCCTTAGGTTTACAGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAAA
6a	50 A C	GACACCTTCAT TCTGCTGG	AGAGCATCCA GGCAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTTGCTGGACCTTTGCCTGGAAAT GCTCTTCCCTCTGAGCTTTGCTGGCTTACTTTCTTTTCCCTTAGGTTTACAGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAAA TACTCCTCATTCCTCATGTCCTAGACGTAAGTCCATGCTGATGCTGCTGAAACATTTATTCCTAAAT TAGATTTCCACCCCAAGCACTTTACACAGAAACAGCATGGAGCTGGCTCTAGATGAGTCTGCTGAAAC GAACCTTACTTAAGGACAGTGGTTTCCATCTGCTTCCATCTAGAGATCTAGGGTGTCTTTGGAAACC ACCTTGG
6	175 C T	---	---	AATACCCAGCTCCTAACACCATCACACTGATCAATCAGGTTTAAACATATTATCTGGGAGG ACACAAACATTTAGACCATAGGATGAATTAACATAGATGTGTTAAGTAATTATTAACATGGTA CA[G/A]CAAACTTCAGTTTAACTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATG TGA
1	136 G A	GTGTTAAGTA	TTG	CTGATGTTTGGGAAGCACTGCTTACATCTCTAAATGTGAGCAACCCAAACACAGAGACCCQ[G/A]T GAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTCCCTGGTGCATAGTAGACACT
10	62 G A	AGAGACCCC	CTCA	ATGGATCTGCTCAATTATAGTCCAGATAACAGCCCTCTCCCGCCCACTTATTTTACT TAAGGGTTTAGCAAAATCACCTGACAAAGATAGTTAGTTTCAACATTTGACCTCATAAAGTGATTTT TTCTCTTCTGTTTGTCTTCTCCCTCTTAAAGAGATAGT[G/A]CCAGAGGGCAATTCGACTTTCTGT AGCCACAAGATT
14	177 G A	TAGTC	GGCTCTGG	ACAACACAGCAAAATCAACACAGATCTATTAGATTCTT[A/C]ACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
37	37 T A	TAGATTC	TGAGATGGTG	CAAGCACACATTCAGGCAGTGGCAGGTAGGGAAGTGGGCAACTTGGCAGCAGAGAGAGGGAAG AAGTTGAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGCAG ATAAAGA[G/A]CCAAGCCCTAGTTGAGTGACACTGTTGGGGATTCAAAG
38	140 G A	AGATAAAGA	AGGCCTGG	ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTCTCTG[C/T]TTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCCA
75	47 C T	TTTCTCTG	GTAAG	CTGCCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTCTTACAT[G/A]CAAAATGCTC CTTTTAAAGTCCCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCTTAGGA
02	55 G A	ACAT	G	

3	33	C T G T C	CCAGTTGTA GCATTAGAA	ACGAGCAGAA CTACCTCTAAG AG	TCGTGTTCTCCTCAAGTTGTAGCATTGAGAAAGTCGTCCTTTAGAGGTAGTTGCTCGTCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCCAACAAAGTGTACCAACAGCATGTTAAG GAAATGTGCAATGCTTGTACCTCTGACGACACAAATTAATCCCATTTGCTTAAAAAGACCAGG
3	70	C T A T C A G A G A A	TTCTAGGCC TCAATTTTCCC	CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTTGAAAAATCAGCTACTCTTTAGGCCCATCAGAG AATCTGGAAGTCATGGGAAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGCATATATATGGAG AATACAGTTTACAGGGGACACAATCCCATTTCCAGAGCCATCATCTGTAAGAC
4b	109	G A ...	...	...	CATGCTAGGTAGATCTGATCATGAAGTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTGATTTTATGAGGTGGTGTGGGAGAAAAATTTGATGGTTGGG TAGTTGAGTTTCTGTCCACC
1a	90	A G A C	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTGATTTTATGAGGTGGTGTGGGAGAAAAATTTGATGGTTGGG TAGTTGAGTTTCTGTCCACC
2	79	C T G G A T G T C T	CCGTTCTAACC TGGATATAAA	GGGTGACCTG TTCCAT	TTTGACCCCATACATGAGATAAACCATAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCCTGTTGAGGACAGGGTCAACCCAC
0b	146	G C C A T C T	GGTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGGATA TAACATCTGCTGATGGAAGGCTGCACCTGGATGAGGTCAAAA
0a	78	T G A T A G T T C T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCAAAA
8	125	G T ...	...	...	TAAATCATGCTTATTTTCAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTATGATGCACCTGTCCTTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTCCAAAAGCCTTTATGCTTAC
7	67	A C ...	...	...	AAAGCGATGTTGAGATACCACATTCOCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA TTC/AAAAAAGTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATTCAGAAATACCTCTGTCAATCTTAACCTTGTGACAG
5	72	T C A A A C	CCTCAGTTATG TATCAAAATGA	GGCTCACCAT CAATGTTTT	TC TAAATGTGAAACCAAGAAATCCTGACAGGACCTAACTGCCAGTCTCAGATTATGTATCAAAATGA AAAACCTG/CACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAACCTC

19	51	C T	...			GAAAGCAGGAAGCCAGGAGGACAACTTTGAAAAAGTCTTTAGACACAC/TTTCGGTGATCCG AATTTAGTGTGATTTGGCAGGCAATGGGGGTAAACATGTTCCAGTGTTCAGTGTTCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAAATGAATGTGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
16	116	G A	...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTTCATCATCTCTGCTCTG/GA/GCCCCCAGGATAAAGCA GGCA
37	49	T C	CA	TAAGATAACC ATACTAGGTAC ATCOG		AGCAATGAGTTAACTCCTTACATGAACAGTCAATTAGTCTTCTGACAA/T/CJGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAAGACACAGT CATTAAAGTGGAGAACCCAGCATTTCTAATCAGGCTCAGTGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
38	25	A C	G	TGACCAATGTG TTTAGAAGCA CTCTCC		CAATGACCAATGTCTTTAGAACGAG/ACJGGAGAGGACACCCGACGACACAGAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGAGCGAGCCACAAAGGTGAGGAAGAGCAAGGGTGTGGCCACT
01	114	A G	...			GGACATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAAOCTCGGCTTCTCACCTGACAAGTGG/AGJATCATGTGCTACACTGC AGTGTATAATGCTGCAT
14	99	C T	CC	TGATTCTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAGC/CTJACCATCCTTCAATTGCTTCTAGACCTATACTAG ACTCAAGTCCAGCAGGCCCTTAAAGGTAAAGGTAAAGTACAAAGTGTACCCATGGGAGGTATGTAGGCTA CAAAAGAG
19	33	G A	A	CCAAGAGCGT CCTATGAATC ATG	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCTATGAATCATG/AJCATTTGTTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
91	84	A T	GT	TTGAGGCTCTTA GTGATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTGTGCAATTATTGCTTCTTATGTAACACAATCACCACAATTGAGG TCTTAGTCATTGCATG/ATJGTATAACAATAATTGTCACCTTAATAGGAACTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
60	117	A G	CAACAGAA	CCATATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/JG/GGCTATATTAGAAA ATTCTACCTGCATCCCTGGATCTGAACGTTCTTCATGATACT
68	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA/JJCTGAAAAATCTGTTTGGCAATCTATTAAAGG CAAATATACCAGCAGTGGTGTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

7	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATATACCTTCCAAATGACTAGTATGAATAGCAGCGTATTAAATTTACCTATTATATTT ATT/CJATCATGATTTGCTGCCCTCTTTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
3	51	A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCCACTCCCCAAGTTAGTCAATATAAAAAA/CJACACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
3	24	C T	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACGTGCTGCCCTG/CJGGTCTGTTCTCTGTTCTTCAATGTTCAACTGCTTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTTT GGAATTGCAACATTTGGGCAT
3b	117	A G	---	---	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTCAATATGAGTCTTTGTGAACAGGGTGGGAAGGATCCTGTAAAGGATGTTAAATATTGTTTT CCATAATATTGAAGATGTG
2a	94	G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTCAATATGAGTCTTTGTGAACAGG/CJGGTGGGAAGGATCCTGTAAAGGATGTTAAATATTGTTTT CCATAATATTGAAGATGTG
5	68	G C	TGCTCCCCCAT CACCT	AGTTGTGTAAG G	TAAATGTCCTGGGGAGATAATAGAAAGGTCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT /G/CJCTTACACAACCTTGAAGTAGGCCCATCCAAACACTGTGTCAGAGAGTAACTGTGCGAC
8	57	C T	---	---	ACAGCCTCTTCAAATGGCACAATCAAAGACACAGTAAAGAGCAGGCAAAATCTGG/CJCTCAC CATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAAATGATTGGCCTT
5b	71	C T	---	---	AGTTCACCTGCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCGCCAC GATG/CJTTACTATAGATAATCTTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
3a	58	C T	---	---	AGTTCACTGCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCGCCAC TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
7	158	A G	---	---	TGGGCAGAAAGTGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCGTGCAOCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCTCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCCTGTATCTGTTACGGCCC/CJGGAATGCTACCGGCTCACAACCTGCGGAGGTAGGAATGACGA G
6	117	T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGGCAAGTCTGGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACCAGTGGGACACCAGGGGTACTTGTATCACCT/CJCTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCAGGGAAGACTCCTTACTTCCACTTGAGAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA



10	110	A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTTCTTAAATTTGGIGCCATAGTACTGGCTTCTGTGTGCAATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAGCACCATGTGGCATCC/GTGTGATGGCTGCATTTGTCCAGTC AAATGAGACAACACTTCTCTAT
12	226	T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAGGCCAGTTTAACTTATTCTCTGTACACA AATAACTTTATGGGAGACAGCATTTGATTCAMATCAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCTCTCTGTAGAAACCAATTGAT
35	105	G C	AG	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/GC/JAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
8b	99	C T	TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCATAACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAATTTAAACGCCCTAC CAATTTTCACTGTTTCTATTGACCGTACTTG/C/JTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
8a	38	G C	CTACGTGTT	TTTTAATTTT TGGGGTGTCT	TGTTTAAACCATAACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAATTTAAACGCC TACCAATTTTCACTGTTTCTATTGACCGTACTTGCTTTTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
16	69	T A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGACTTTGCTGTAAGCAGAGAAGCACTGTGA CT/AJCATTTATTAGGCCCTCTCTCGCTGAGCCCTGCCTAGAGCAATTTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCACTATTGTGACAAGATTCTCTTTTAAACA
12	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAAGAGTCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTTGCTTTTACJATCCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
16	61	A G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCTTA/JGJC CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTTTGTCATTAAAGTCTCTATTCA ATTACCAATTTATCGGGGTAATTAACACTGGAAGTAATGCCAGGCTAATTTGTAGATTATGATAAT TACACGCTCTTTGCTATGCT
7	77	C A	GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAATACCAGTGTGGCAGAGGCATG AAGCAAGAGG/C/JCTTTTCATCTGCCCTTGGGGTTTTCAGTAACAGCAATGCTTTTGCCTCC CGGATGAAAGATACCCCTCTATGACTCAGCAATTCACCTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
19	50	C T	TTCCGAATG	TGACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAATTTCTCTCTCAGTGAGACCATTCTTTCCGAATG/C/JGATGATTTCTTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTGCTACCTGAAATTTGTATTTTTTAA AAATCTCTCCCAATATTG

[illegible]

					TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACTACCATTTGCTGTATTGCTCTTCAGIGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGAAGTATTA ATTAGATTCTATTGATA[C/][GATGTTCTTTCAAGAGGAAATTTGTGAAGAGGATTCCCAAT TGCAATTCATGGC
155	C	T	ATTAAITAG	CA	TCATTGACATTTTAGAGTTCCTCAGTCTTTATGCTTATTCTTAGGAAAAAAGTGGTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAGATACTAGAAAAATGC[C/][GAACAGAAAAAATAACCA GAAGATTCATTATGGTTTTTCCAGAACGATTAC
113	C	T	AATGC	GTTC	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATCAGTCATAGAAATCATCTTGTAAAGTTC[C/][G JTGAAAAAAATATGCCAAAAATTTAAATTTTATCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
65	A	G	TTCC	ATAA	CTTACTCCAAAGTGTTCAGAGACCACCTTCATTC[C/][TTTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAGGTGAAATTTAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
38	T	C	CACTTCATTG	CAAAAA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTATGTCCACACATGAATAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGGCCCTGT[C/][G]TCTCTGGCATA CATATAAAGGAAGGCTAA
121	G	T	GCCTGTT	GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTATGTCC[C/][G]CACATGAATAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGGCCCTGTCTCTGGCATA CATATAAAGGAAGGCTAA
43	A	G	C	AATAAAT	TTTTTCCATTTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATTAACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[C/][GGACTCATTTCTCTTGCATCTATTCTAGGTATTTCAGCCCCGAGATCTACCCAGG
139	T	C	GTAGCAGGT	C	AAATGAGTAACCCAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[C/][ATGAAT AAATGAGGTAGTGGAAITGCTTGATAACTGGAGTAGTGCTT
56	G	A	AAAGATAACA	CA	AACATTTTTAACCATGCTACATTTACAAACACTGAAAGACAG[C/][G]AAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACCTGGAAAGGAG
44	A	G	---	---	GCCTTTTGGAGTTAAGTCTTTTGGAGTGTCTTTTTTTTCCCCACCTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAAAGCGCTGG[C/][G]GATAAACACATCTTC
93	A	G	---	---	CCCTGCTATAGGTGAGTTTAAAAATCCT[C/][G]CCTGCTATGGTTGCTTTGTAAGCCACATCCACT GAGGTATTTCTGCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG
29	G	A	---	---	

		AATAAGATGG TACCTTAACCTA	CAAGATTGGTA CAGAGAAATTC	TGCATGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CITTTTGAATAATTAACCTGTATCCCATCATGGTTCATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAAACAAT/CJTITGAAATCTCTGTACCAACCTTTGCTTTTC
70	143 T	CATATAACAA	AAA	GATCCTTCATCCCTCTCCAGAAGAGGAGAGAGGAAACACAAGAAAGCCTGGTGACAGGCC CCAATTCCTACTTCATGGATGTGAATGCCAGGTGAGGAGAGCGCTTGGTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
11b	423 T A		---	GATCCTTCATCCCTCTCCAGAAGAGGAGAGAGGAAACACAAGAAAGCCTGGTGACAGGCC CCAATTCCTACTTCATGGATGTGAATGCCAGGTGAGGAGAGCGCTTGGTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
11a	390 C A		---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCACCTCTCAGTTTATTCCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
702c	345 G A		---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCACCTCTCAGTTTATTCCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
702b	344 C T		---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTGAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCACCTCTCAGTTTATTCCTAACTTTAATGATCTCTGTGGA CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTG
1702a	179 C T		---	TATAGTATTTAACGAAGCCTAGAGCAGCGCTGTGGGTGGTGGTTCAGTTCAGTTCAGCCTGAGGTTGCAG ATATAATAACCTTTGAAGCCATAACTTTTAAGTGGGTTTGAATTTCTTTTAAATTTTATTTGGGA GGGTTTGGATTTTAACCTTTTAAATGTTGTTAAATATTAAGTTTTTGTAAAGGAAACCAATCTCTG TGATTACCTCTCAATCTATTGT
3N21	49 C A		---	AGAAATGGCTACTTTCATAGGGCAGAGCAGCCACCTTTTGGCTAAATTTTAAACATCCAAAGCTAAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAAATATGTTCTATTTGGGAATACCTTAATATCAG ATACTAACAAGTACAGTGTAGATAAGAAATAAAAGATAATAATACACATACCTTCTAGGTTAGTAGA AAAGC/G.TCTTCTAGGTTAGTAGAAAAGTT
14V30	203 C T		---	



46	G A	---	---	TTTTGTTGCTGTGGACACCCACTGCTCCAGGATGAAGGAGAG[G/A]ATGAGATCAGTTTGGACACTTCTCTGAAATATAAAGAATCAACAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAAAGTGCATCTTGGGGAAAGGGCTCCAGTGTATCTGGACCAAGTCTCTTTCAGGTGGGACTCTTGATCCAGAGAG[G/G]GACAAAGCTCCTCAGTGAGCTGGTGATATATCCAGACAGAACCCAAAGTCTCCGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTCACACAGCCTCACTTCATTCACACTATTCTGAAAATATTCCCTGAGAGAGAACAGAGATTAGATAAGA
78	A G	---	---	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGTGAATATACCAAATTCIGCATCTCCAGAGGAAAATAAGAAATAAAGATGAATGTTGCAACTCTTAAAAAA
43	C G	AAGGCACCCA GCCATC	GCTCCTCGCTG GGTCA	AGCAGCCATCACATGATCTGTTTTCCACCCTTCACTGAAGACACCATTTAT[AG]TACCCAAGGGCAGAAGTAGAACTTACTATTAATGTTTGACACAATTTGGAATTGTC
53	A C	TT	TCTACTTTCTG OCTTGGGT	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCCAATACCATCTGTAGAGTTGGAACATGCAATCTTTAAAGTTTATATGTCATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTTCCATTGCTTATCTTGAGCACAAATGATAATTAATTAACATTTATACATCACCTTTTGTACTTTTCCAAAGCCC
293	T G	---	---	TTTACAGCTCTGGCATTTTCTCGCCTAGGCCCTGTGAGGTAACTGGAT
38	A G	GGTAAAGTT CTTTTGCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTAAAGAA[AG]AAGGAAGTAAAGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAAGGATGTTGCCACTGGCAATGTAACTGT
249	C T	---	---	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCCCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGGAGGCCAGGGCTGGAGCAGCATGAGGCCAGCAAGMAGGCTTGGGTTCTGAGGAAGCAGATGTTTTCATGCTGTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACGAGCATCTTTG[C/T]
157	C A	---	---	GGAGTTGCCCCCTTCTAAGGGAAGGAGATCTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCCCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGGAGGCCAGGGCTGGAGCAGCATGAGG[C/A]CAGCAAGAGGGCTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACGAGCATCTTTGGCT
34	C T	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTC[AG]TGCCAGCTCAGCCCTACACCAGTTTCCACCTGGAGTTTCAAGGGCAAAAGGCAGTGGCATGCAAGCTGTTAA
61	C T	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGGTGACGTTAGCATTACCCCCAACCTCAATTTAGTTGCCCTAAGCATTGCCTGGC[C/T]TCCTGTCTAGTCTCTCCTGTAAAGCCAAAGAAATGAACATTC
93	T C	---	---	CCCTGTTCCCATGCTGAOCTGTGTTTCTCCCCAGTCATCTTCTCTGTTCCAGAGAGGTGGGCTGGATGTTCTCCATCTCTGTCTCAACTTAT[CTG]TGCACTGAGCTGCAACTCT

b	44	C T	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCTCCCAAGTCACTTTTCTGTTTCTCCAGAGAGGTGGGGCTG GATGTCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
					TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGGCT CAGTGGCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCCCG TCCTTTTGGCCCAAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC AIC/AACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
b	206	C A	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGGCT GCTCAGTGGCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCC CCCTCTTTTGGCCCAAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAC CACACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
la	56	A C	---	---	CTGAATCCCTCTCTGCTGGCTGGATCCGGGGACCCCTTGCCTTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCAAAAGTTGTGAAGCAGAGAGAGAAAGCTGGAGAGGCCGTGGGCCAAT GGGAGAGCTCTGTATTATTAATATTTGTCGCGCTGTGTTGTGTTA
3	54	C T	---	---	ACATATCTGAAAAATGTTGAAGCCTAAGCCAGGAATAAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGTATTACAAAGACTTCATGC
1	62	G A	---	---	GTGTGAGACCATCATGTGCCAGTCTAGGACCCCATCTCCTATTATTCAGTCTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
4	47	T C T			AAGGCCAGATGCACATCCCTGGAGGAGCATCCATGTTCCGAGAGAAACAGATAGATCCCTGTATT TCAAGACCTCTGTGCATTTATTAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
3	52	A G	GAAGAACA	A	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTGAGACTTCCCTTTTCATCTT
6	76	G A	CGCA	T	TTGGACAAACCTAGAAATTTCTCCCTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGTCTGCTTAAAGCA[G/A]TACCCCCCTACACACACACCCCTGTCTCTC
3	94	G A	CA		TTTGATTGATATCGTGAATCTCTCAGCCGAGAAATGGGCTGGATTGCTGCTTTGGTTAATACAT CTTCCCTAAAGAAGATAAACACAAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
5	48	C T	---	---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGGCCAC[G/A]GTCCCTAATGACACCCACTCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGGAGGAGCAGCAGCCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG
4	37	A G	AGGAGCCAC	CATTAGGGA	

32	C	GATTGA	CAGGTCCCA	CAC	TGCCAC	GTGACCTGTGAGGTGAGTCCCGAGATTGAG/GC/GCTGAGTGTGGCAAGTGTGTCAAAAGGGG
				ACTCAGAC		TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTTGAGGCCGGAAGATCA
				GCTCTCAGAC		TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCAATTCAGTAGTTACTGAAAGAAAACCTCTGCTA
				CAAAATAACA		GAATGATAAATGTATGTGGTCTATACTCCAAATAAACAAATGCAACGTTCC/T/C/GATTTCATAAT
120	T	C	ATGCAACGTT	CAAGATTAGA		CTTGGTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCATACCAGCT
				AATC		TCCATTCTTTTGGCCCTGCAGCATGTATGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGAT/C
				AAACAATCTA		GTAAAGCTTTCTGTTAGATTGTTTACCTTGGTGATCATGCTTTTCCATGTGTAGCTGTAATATT
65	T	C	TAAGTACAG	ACCAGAAAGCT		TTCCATCATATCTCAAGTAAAGTCA
				TTAA		
				CCCAATTTTA		CAAAATCTTGGAAATATCTCAAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT
				TTAAAGTTTA		AAGCATGTACGTGAATTTTAAAT/T/GTATAGATGTAACTTTTAAATAAAATTTGGGGTGTGG
91	T	G	TAAAT	CATCTAT		GAAGATTAAAGGAGGTGTGCTGTGGTCTCTCCCTCCCTCTCCCA/C/A/GTGGGAGAGACC
						TGTGATTTGCCAAGTCCCTGGACCTGGACCAAGCTACTGGGCTTATGGTTGGGGTGGTAGGCAGG
						TGAGCGTAAGTGGGAGGAAATGGGTAAAGAGTCTACTCCAACTAGGTCTATGTGACAGACCAG
						ACCTAGGTCTCTCTAGGAGGAAACAGGGAGACCTGGGGTCTCTGTGGAT
50	C	G	CGTACCTCCAA	---		CAAGCGTACCTCCAAACATAAATTGATTG/GTATCTGCGAGACTTACACTCAAGCAATCTGAGG
			ACATAATTGA	GCTTGAGTGA		AATACTGAGGAGGCGCTGGCTACTGTCTCTGCACTGTCTGTTG
4	A	G	TTT	AGTCTGCGAGA		CACACTGTCTGTTCTCAGTGTGAGGTCTCTGCGAGGTGAGGTGGGTAGCCGGGTCCACA
						GGGCCAGCCCTGGAGGGGTCTGGCCCCCAGGTAGGCGGAGAGTCCCTCCCTCAG/GTAACT
						GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACCACTCTGAAGCCAGCTTGCCACCTCCAGT
						TTGCACAGGGATTGTCTGAGGGCTGAGGGCTGTCCCAACCCCGCC
7	T	G	GAATGTGAC	CAGGTAGAAT		GAGGAATGTGACTTCACTTTGGTG/C/TCAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA
			TTCACTTTGGT	TTCTGTCCATT		GTTCGGAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAA
4	T	G		G		AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTGTGTGATTAAAGTCTTAAAT
						TGTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTAGGTGGACCTAAATCCTTATCATATCTTTATT
						AATTCAGCCAGTGTATCCACCAGTTTTTGTGTTTAACTGAATAGATAGCGATGA
13e	T	C	---	---		AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTGTGATTAAAGTCTTAAAT
						TGTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTAGGTGGACCTAAATCCTTATCATATCTTTATT
						AATTCAGCCAGTGTATCCACCAGTTTTTGTGTTTAACTGAATAGATAGCGATGA
113c	T	C	---	---		AAGGTGAATATCGTTTTTGTAACTGAATAGATAGCGATGA

68	G A	...	...	...	ACTGGTGGAGACTGTGAGGATCCAGGATTCAGTATTCTGGCCAGAGGGCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCTGTGTGCTCCCTCTCTTATGACTGTGTCCC
142	A G	CTC	GCTA	CAATTTATTTG AAAGCTATTCA GACA	TTCTGAAATATAACACGCAATTGAGCTATTTAAACTGTAAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAACATTAAATGCTAACACATTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAAATAAATGTGAATGGT
70	G A	ACTGA	ATGATCACOG	CCACAGAAC TATTGTAAAC AA	TCACGTTGGTCTCTCAGATTCTGAGGAATGCTTTGTTATGTATATTACAATGATCAACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGAGGGCTGTTTTTGT
314	C A	...	...	...	TTACAGAAACTTGCCCTGTGCTGTCCCTCATGCTAGGGCGGAGGGTCTTTCTCTCTCTTCC TACCTACCCCTTTCTCTTGGCCAGGGCTCTGATCTCTACCTTTCTTGTCCCTGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGAACCATGGCTGCCCTGGGAGGAACCATAGCTCCCT
96	G C	...	...	...	TTACAGAAACTTGCCCTGTGCTGTCCCTCATGCTAGGGCGGAGGGTCTTTCTCTCTTCC TACCTACCCCTTTCTCTTGGCCAGGG[G/C]CTCTGATCTACCTTTCTTGTCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCCTGGGAGGAACCATAGCT
182	T A	...	...	...	CCAGATGTGCCATCACGTTTTTCTGAGGCTTTGACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTTGAAGAAATATGTT[A/C]AGAAACACAAAGGCTT GAT
78	C T	CTCTGCCA	CCAACAACAT	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAAA
104	T A	...	...	...	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
75	A G	...	...	...	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTACATTTTGTATTAT GCTCTTA[A/G]TGATTACAGACTGATGCCAGACAAACCTTGGGAAGA
79	T C	TGG	CTTAGAAAA TCTGCTTTAAC A	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGGCATCTGTCTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT[C/J]ATCTCTAATTGTTCCCTAGGAATGACTGTCCAAAG
107	T C	GTTCC	GGTCCAGAAGA G000G	GGTCCAGAAGA G000G	TGCTCCCTGTCCATCTGAGTGGACCCAGGCACCCCTTTGAGGAGGTGGGTGAAGTCTCTCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTCTC[C/G]CGGGCTCTTCTGGACCTTGACCCGTG GATACCAGCCATGTGCCATGGTATTGGGTCTGGGAGGGTGGGTGAATAAAGGCATACTGTCT

4	131	T A	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGAGGGGAAAGAGCAGAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAACATCGCCCAACCTAGAAACGTTTTTCATTGTCATTTCCAGAGAGAGAGGAAAGAAAAA TT/AJACAACTTTCATTTCTTTTGACGTTTCATAAACATTTCTACATA
5	118	A C	---	---	TCCTGCAAGAAGTTCTCAAGCCTTTTGAATTTTGCAATAAAGTACAGCTTTCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTTCTCTAAATTTAAGTGAGA[A/C]TCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATTAAGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA
3	242	T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTGTGCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAAAGTGCCCATTTAAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTTAAATACATGCTGAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/AJTTCAGAAC
0	165	G A	---	---	TACACAATGAATGCTTTTATTCGGTATGCATCCACATTTAGCATTTAGTGGTCTGAAACAGCAAG TGGAAAGACGAGCAATTTGCCAGGAGGTCAAGCCCAATTTGCGGATCTGCTGTGCACACCCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG[A]GAAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
'5	148	G C	---	---	AACAGTCACCACCAACACATGACAACTCGCCAGGAAGGCTTGTCTCCCTCCCTTTCGCTCC ATGTGCCTAGTCAGCAAGGTGCGGGAGGCACCGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA[A/GC]GGAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTGCTTTCAGTAACCTGGTATGCTGAA
21	41	G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGGAGCTTTTGTGTTGTTGGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAA GAATATTTGGGGAGAACCCCTGGAACCTGGCCACGAGGACATCCCAATATCCCTCTCTCAGGG CTCACCCCGACATCTCAGCCAAATGAAGGCTCTGAA
25	215	T A	---	---	GGTGAGACGGGTTTATGTGCACATTTACACAGGCTCACAGGCTGGGCTGGGCGGCCATGCTC CTGTGTCGGGCTGCTCTACAAGGGGTTCACTTTCTTCCACCACACTATGTACAGTCAGTGTCCAA GGTGATGGGCTACAGTGTGCATCAGTGTGCTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAA[A/T]AAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAA
20	202	G A	---	---	AACCTGTTTACAAAATAGGCTTTCAAAACTTCACTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATTTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACCTGCACAAAGGTGCAAGGAACCGGAACCATTTGTGTACACTGTCTTCACACAG [G/A]GCATTTCTTCTACCTTAACCTGCAGCTGTGCAAGATGCCTCAGTGTG

3	184	G A ...	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAATGGCTTGTGTTCCAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAGGCGATGTTCTTAACGTGCCCGTGAGCAG
3	204	G A ...	---	ATGTCAGAAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCTAAATCCACA GATCTGAAAAGTAGAGCTCTCCAGGTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
3b	201	G T ...	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGCTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
3a	85	T C ...	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[G/C]GCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGCTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
1	149	G A ...	---	TTAGTGATAAGGACAGGCTAGAACAGCGTTCCCAACCCCTGGACCAATGACAGTTTGGACCAAA TAACCTTTGTTTCAGGGGACTGCTCTACACATTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACCAATCATGACAATGAAATGTCCTTAGACATT GCCAATATAOCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
5	110	G A ...	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGAAAGAGG GAAGTCGATAATTTTAAACATATGGTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACATTGAATGCA
3	199	T G ...	---	ACCAAACCGTTGGCAAGGCTCCCCAAGACTACGACCCCCAACCTTGGTGCTTACCTATGCCGGGTG GGATTGAAGAAATAACCAATAAATAATGCTACAAATTTTCCAGTAGTTACCAGGCCACCGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTCTGGCTTGGTCCAGGCATAGAGTT/G JGGCCTACAACCCATTATCAATGAACCCCTCAGAACCATCCAGTTGGGGCT
1b	157	G A ...	---	TGGTATTTTCTTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAATAAAGTATAGTTGAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG JGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAGCACAACCCAGAAAAAAGTGTGT JGGCTTAAGGGAAGCCAAAGGAAGTTAAGT

1a	48	A G ---	---	TGGTATTTTCCCTTCTAAATGTTATGATTAAATAGTGTCTTTGTJAGJGAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGAAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAGCACAACAGAAAAAAGAGTGTGT GGCTAAGGGAAGCCAAAGGAAGTAAAGT
6	61	C A ---	---	TTCTATTAAATCCTGTGCCCATTCGAAGACTGCAITCAGTCTGCATGAGCCTTAGTTTCJAJTAA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGAGGTGAGCAATTTCTCTGTATTA TACAAACTGGGACCAAAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAAGTTATTAACTT
1	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTTCTAACGCTCCTCCTCCTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGACTGTGTCTTCJTGTTCCCTGTTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
6	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTATACITTCITCTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGACTTCTACATCTCGAAACCTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATCTAGAAJGJAJAAACACCTAATTTGGCTCATCTTGGATCA
0	49	C T ---	---	TTTTGTTAAGTCTTGTGAAGCCACACAGAAAGTATCTACTCTCTTACJCTJAAAGTGTACTTTGCA TATATTTTATGGGGATGATTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCCCT TTGTTCAAGGAGTTCTTATTTGGCCTCTTTCTAAACCTTAAACCTCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
5	31	A C ---	---	GAAACCTCGTTGGCTCAAGGAACTGTAGJAJAAATTCITTTTTTTTATTTTTGTTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGTGATGGCAGCCTGCTCTTTGTTTGGTGAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAATGGAAGAAAGGTTAATGGA
12	41	A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAAACACTCCAAGAATACJAGJAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTATGCTGATGAGGCGCATGTGACACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGTGCTTGGCCAGTCCCATAGTAGGTTGCCATAAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAAAGAAATTTCA
52	179	C T ---	---	GATTCCTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCAATTTGGAAGGAACGAGCCCTA ATTATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTCAJCTJCTGTGACAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

1	167	A G ---	---	TGTTGAGGAGCTGTAAAGGCTGAAGAAATAGTCTCTGCTCTGGTCTTCTGTTGGAATGGATGAGTCTCT TTTACAAAATTTTCTCTTGGCCATGGGTGTTATGTTTAGAATCAITGGAGTTGGAAGACTTAGATTCA ATTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
1	198	GA ---	---	GGTTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGATAG AAAAATGGTGCCCACTATTGACTTGTATACACCTTACAAAACACACATTAAACCTCTCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
3	164	CA ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCATTTAATT TGCACCTTACTTTGTTGGCTACACACATTGCTTCCAAATTTGTAATTTCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCCTTAAAC[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACTTCCCTGTATTTCCCTATTTCAGCATTTCAATGATTA
3	72	A G ---	---	AAAAAACAACTTCATTTGACATTTCTAAGAAGATAAGAAAAACACGATCCACTGTGTGTTGCTT GATTTN/G/GGAGATAAACCTGATCTCTAAGAAAATTTAAACCAAGCAGTACACTAAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGAAAGCAATCCAACTAAGTTGCTAAGAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAATATAGCA
5	111	CA ---	---	TGAAGGACCATTCGAATGCCCTACCAAGGTAAAGTAAATCGGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCCGGTGC[C/A]AAAAATGTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTTAGTAGTAACTAATGTTTAGATA TGATTGTTGAATTTGTTGCTGTGTTCTGGTG
8	177	A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTGATGAAGGTGGGGCAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGTA/GTCTCTCCAAATTTCAAGGGCTCCC GTGGGATGTTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
1	34	T G ---	---	GGGATTCATGTGTCTGTCTCATCCAAATAGCACCT/GJCATGACCTCAGCCCCCATCTTTCTTCCC TATGTTCCAGAGACAGAAATAGACTGGCCCCCTTCTCTAGGGGATCACAAATTTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTTCTAGTTGA
7b	88	T G ---	---	GTGAGAGCGAGGCTGAGCCTAGACATGAACCTTTCTGGCCCTGCTTTCTGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATTT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCTGTTTGTGTTGGGTATCTGCCAGTGTGTTTGTAAATAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAATGAATATATAATTTTTTATGTTTTGTTTCTGA

a	44	T C	...	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCT/CJTTCGTTAACTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTCCTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
	197	T C	...	TCCAGAAATTTCCCTCTTCAGCTCATTTTGTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAATTAATTTCCCTTCAACAATAATATTTTACAGAAGCAGGAGCAAAATATAGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAAATTTT[C/JAG TTTGCAATAGAACTAATCTGGTGAATAATTTACCTAAACCTTGGTTAT
b	57	GA	...	AGCCGAGCTGGACTCATGGATGTGACCCCTTGTCCCTGCTCTTCTGCCCTGG[C/JCTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGTGCCATCTTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGGAATGGAATGAATCAGGGGGCTGCTACTAGAGCC
	69	GC	...	CTCTCTCTTCATCCCATCACCCCTAAATAGGTAGGTGAGGAGGCTGGGAAGAGGTGGAGGAGG G[C/JAGAAGTGAAGGAGATAGGAAGGATATACCTCTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCTATCAGTGTAGAGGCCCTAAATTTATATCTATAATATATAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTTGTCAAAAGTTTAAAT
c	242	T C	...	GAAGGCAGCTGGATCACTCCGCGAGTCTTGGCAGCGCTTGTGTGGACACAGAGCTCCTCCT CAGGGCCCTGGCACTCACCTTCTATCTGTATGATGTTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCCTAACTGTTTAAATATGTAACCTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA[C/JACAACCTT
	3101	T G	...	CTCCCTTCTATGTCTCAGCAGCAGCTTGGGGCACACTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAATAAATACGTACATTTTCGAGGTAATGGTA
d	131	T A	...	TTTTGAGTCAAGACTTAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAC[C/JA] ACTGAATGAAGAAGTATTTTGGTAACCAAGGCCATTTTGGTGGGAATCCAAGATTGGTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
	99	T C	...	TACAGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTGTCTTGGTTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG[C/JAGCCCCAAAGTACAGCCTGGACCAACCTCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGCCATTGCCATTGMAACTAAGAGCTCTCAAGTCA

5	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGATGATTTTTTTTATAAATATTTTATACACTCTTGTGAATTTGGATCTTT TTTACTTTGAGCATATATTTAGAATATGTGTAAGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGAGGTTTCAATTTGGAATAGTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CTACCAAAATAGCCAGTAGTATCTGAAAAATGAAAAATAAATGAAGTAT
6	137 G T ---	---	GGCCAGGAGATTAGCAACAAGGATTCTTCTTACTTACTTGGCCCTTTTATCTTCCCTCTTGCCC CAGTCCCTTCTCCAGCTTCAATGAAAGCTCTGCACAGACACACTCAGTGTCTTGCGCAGTGTCT [G/CTACTCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAAAATGTCATCAG
	252 C T ---	---	ATTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTCAATTGGATCCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTGGCCAGAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAATTTTAGTTTAAAAATGTGTCATTTTGTCTGTATTTGGCATTCCTTC/
	218 C T ---	---	GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTCTGGCAOC CATGATGGAACCTCTTGCCATGTTTAGTACCTGGACCAAGTAGTATCCATCCTGACTTTTAAAA TTCTAACAGCCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC/TTTAAACAAAGCATAGAAATTTCTGAACAAC
3c	146 T C ---	---	TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGTC/CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
3b	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGTC/CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
4	165 G C ---	---	GAAGACTGAGTTTCCAGGAGGTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCAGTNCCTTCCAGAGGCTCTCAGACTACCTCCTCCATCTCCCT CTCCCCACACACACAAATACAGAGATTG/CJAATTTCAGGAGCCAGTTTCTAGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTTAGTTTCTCAANTGGGAAATGG
6b	25 A G ---	---	AGCTTTTGAAATCCAAAACCCACATG/CJCTTGACTCTCTTATCTCCTCTTGTGTACATCTATCC CTGAGGCAAGAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTGCTATCCCTGATGACTGGGCAAA

2c	25 A G ---	AGCTTTGAAATCCAAACCACATAG/GCTTGACTCTCTTATCTCTCTCTGTTGTACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGGCTGCCTGAACGGAGGATGGGGGGGAGACAT CGGTCAATGATCAAGCATCTCTGGCTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTGCTATCCCTGATGACTGGGCAAA
	59 GA ---	TTTCCCAATCCACAGGTAAACTAATAATGATGATAGAAATTTAGAACTACTCC[G/A]GTTT TTCCCTGGGAAATATTACAAACATTTGGCTGCTGCAATCAGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGTACCCTGCTGAGACTTTATGT ATTCAATTTAGAGCCAGGCTTGGCTCTGTCACCCAGCTTTCAGTGCAGT
2b	106 T C ---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCGTGCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCTTTTATTAATAAAAA AAAGNTATCTAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
	106 T C ---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCGTGCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCTTTTATTAATAAAAA AAAGNTATCTAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
2	103 T C ---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCGTGCTC AATACACTAGATATAGTTACTGTGATTATATATTT[T/C]AAATGGTCTTTTATTAATAAAAA AAAGNTATCTAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
	103 T C ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
17c	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
17b	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
97	136 A G ---	TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT
	136 A G ---	TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTAAAT

				TTCAAAATTAACACCAATTGGGTATATTATAATTINGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCTTCTATTGTCTTGACGTATTAAAGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCAATTCGTGACCCCTCCCTCCTACCCCTACTTGGCTCTGACTTCCCTTCTGCGCT GAACCTTCTCTGTGGCTGTGCGCTTCTCTCTGCTGGCTCCAAATAC
66	GC	---		TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAGTATCTACCCCTTA GGATATTGTGAGAAATCAATAAGTTTACATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
b	156	AG	---	TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAGTATCTACCCCTTA GGATATTGTGAGAAATCAATAAGTTTACATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
	156	AG	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGACATCTTTCCCTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
b	119	GA	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGACATCTTTCCCTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
	113	AG	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGACATCTTTCCCTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
	119	GA	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAAGGAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCATGTTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA
b	123	CG	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAAGGAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCATGTTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA
	123	CG	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAAGGAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCATGTTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA

198	T C	---	AGGTTCTGGACTGATGCTGGGAACAATTGGGTCGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAGGTATCCTAGTCCATCCCTTTATAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATATTCJG ATCCCGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
205	G A	---	CACATCCCAAGGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGGAGCGATTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCAGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
205	G A	---	CACATCCCAAGGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGGAGCGATTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCAGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
90	G C	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCTACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGNAGATTGGCTAACG/CJCATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACACANTAGGTGCACACANNNGGGTT TTCTCTGGTCATAGAAATCTCTAAAGGGAATCATGACAGATTTCTTGGCTTTA
90	G C	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCTACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGNAGATTGGCTAACG/CJCATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACACANTAGGTGCACACANNNGGGTT TTCTCTGGTCATAGAAATCTCTAAAGGGAATCATGACAGATTTCTTGGCTTTA
167	C T	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACCC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
155	G A	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACCC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
181	T C	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATATGATGTCCTAGGTACATTTGTTTTTATTTGTTCTG CGAATGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCTACTATTCJGCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTTTATTGCTCTGGCTTCATTTTGAAATNG

17b	204	G A	---	---	TTGCCATTATTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAAACTTCTCCTCCTCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
18b	147	C T	---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGTGGC TAAGTGTGGGG/C/TTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
18a	124	C G	---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
14	124	T C	---	---	AAGTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGNT/CJGNCAANT AAAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
15d	202	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05c	46	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
15b	153	T C	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA/CJTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05	202	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

				TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
b 248	A G ---		---	TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
			---	TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
240	A G ---		---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGGCAATTCGTGAGATTGCTTT CCTACCCCTCTTAAATGTATCTTNCNTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCTGTAAGNTGTTT
b 118	T C ---		---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGGCAATTCGTGAGATTGCTTT CCTACCCCTCTTAAATGTATCTTNCNTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCTGTAAGNTGTTT
			---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTACCCCTCAGAACTTCTTGAAGGCGAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
b 169	T C ---		---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTACCCCTCAGAACTTCTTGAAGGCGAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
5	165 C T ---		---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAAA ACACCAAGTGGGTTAATGGAATGCGTATGTGTGAGTNCATATTACGAGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTCTGAAAGTTGGTAGTACAGGCTGCCCAAAATGTAGT TCTTGNCGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG
7b	162 T C ---		---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAAA ACACCAAGTGGGTTAATGGAATGCGTATGTGTGAGTNCATATTACGAGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAAGTTGGTAGTCTGTTACAGGCTGCCCAAAATGTAGT TCTTGNCGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG
7	175 C G ---		---	TCTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG

41b	136	G A ---	---	TATCAGCATGATTGGCTGTGGACACAAAGTCAATTTGTACITTTGNTGNNNTCCCTTTCTNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTCTGTTAAATATACCCCAAGC G/AJGGATTGTGATGGATCTGTTATTTCTCTGTCTGTGGACAGAGAGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
49e	192	G C ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGA(G/C)TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
149d	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAATA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
349	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
1403b	57	C T ---	---	TGGTATTGGAAATGGGTTTCAGACTCCGGTTCCTGGCTCTGACCTTTGGTAAGTTGCTTTCCGAAT GOCACCTTTATAAAGTTAGAGGTATTACCTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAGGGTTGTCTGATTGT
1403	58	T C ---	---	TGGTATTGGAAATGGGTTTCAGACTCCGGTTCCTGGCTCTGACCTTTGGTAAGTTGCTTTCCGAAT TGCCACTTTATAAAGTTAGAGGTATTACCTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAGGGTTGTCTGATTGT

c	31 C T ...	...	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCGGTTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAGTCGC
b	31 C T ...	...	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCGGTTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAGTCGC
			CCATGAGCAACAGCATGTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGCTCTCCGTGGTNAOCTTCTCTCCACCATCACCTGTGTTTT
2b	122 T C ...	...	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTT/CJATTCACTCT CTGCCACATGCTAGTAACGTGTGAGTGATGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATATATTGGCTAAGGTATTCATCATATTGGCTAAG
2	114 C T ...	...	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTT/CJATTCACTCT CTGCCACATGCTAGTAACGTGTGAGTGATGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATATATTGGCTAAGGTATTCATCATATTGGCTAAG
0	97 A G ...	...	GGCAATTTAATGACTCCAAAGGTAGTAATCTCTTCCCCCAAAAAAGGTTTTAAATCTGTGTGGA CATAATGTTGAATTTGCAGTTCACTTGGAGTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCTTCCA
10	31 A G ...	...	GGTACACAAAGAAATGCTTCTGGAATCTAC/AGTACGGCTTAACATTTTGGCTGAGTATTATC TGTACATGTGTAATGTGAACCACTGAAGCTGGGCAAGAACAAATCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTATGTTCCTCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAAGAATAATCATAAAAAAT
13c	77 A G ...	...	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/AGTAGGTAGGATGAGCATCACACTTGGGAGGACATATTTCTGGAGTACATATCCTG GGTGTAAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTAATAACAGTCTTATTGAGGAAAAATAACTGGAATCA

103b	77 A G	...	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATCTCTGCTCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
137b	112 C T	...	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TTCTGTCCTCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
137	112 C T	...	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TTCTGTCCTCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
340b	79 G T	...	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TTGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCTTAAGAGCCATGAAGAAATTAAAGACT ATCGCA
840	79 G T	...	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TTGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCTTAAGAGCCATGAAGAAATTATAAGACT ATCGCA
879b	110 C T	...	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAAGTTCCTGTTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAG/AAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
879	110 C T	...	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAAGTTCCTGTTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
900b	119 C T	...	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATATGGAATAATCACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/TTGCTCTGAGAGGT AAAGTGCCTGCCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTCTGCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAACCACTTTCTTTTGCTCC

10	119	C T	---	---	---	---	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCTAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGTGCTCTGAGAGGT AAAGTCCCTGCCCAACGGCAACAAGTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCATGAGAAACCACTTTCTTGTCC
13c	165	C T	---	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCCCTCTCTGAACTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAATCCAGATGACTCAAGCCCGGCTGGAGTAT
13b	165	C T	---	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCCCTCTCTGAACTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAATCCAGATGACTCAAGCCCGGCTGGAGTAT
43	164	C T	---	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCCCTCTCTGAACTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAATCCAGATGACTCAAGCCCGGCTGGAGTAT
60c	270	A T	---	---	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTGGAGTGAAGGATCTGGAGAGCACCCCT GCAGAGCTTCAATCTGTTTCAAAAGTGTGCCATGCANGGCTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAACCTTAAATGCACCTCCCAACTTT
60b	270	A T	---	---	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTGGAGTGAAGGATCTGGAGAGCACCCCT GCAGAGCTTCAATCTGTTTCAAAAGTGTGCCATGCANGGCTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAACCTTAAATGCACCTCCCAACTTT
177	203	T C	---	---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGATCA TTCTGGGCATTCTTCATAGAGTNTGTTTTAGTCTGTAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C/TAAACAAACACTGGCTGAGGCTGTTGG
112	102	T C	---	---	---	---	AAATCTAGAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAACTAGCTAAATCTT/CJTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

					CTTTAGAGGTGGTCATTTGGTTCCTTCTGGAAAGTGATTGCTGTTTAAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/TCTCA CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTCAGCTTCTGAGCCCTGTTACTGCAATCC
3	127	C T	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC/GATGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTTAGGCTACCTTCCTGTAATTGCTTCTGTTTTCAAAGGG
32c	166	G A	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC/GATGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCAATTGGTTAGGCTCA/GCTTCTGTAATTGCTTCTGTTTTCAAAGGG
32b	219	C G	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC/GATGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCAATTGGTTAGGCTCA/GCTTCTGTAATTGCTTCTGTTTTCAAAGGG
32	219	C G	---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGTGCCTAGAGCNAGGACAGAGTGACCTTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGCTC/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54b	188	C T	---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGTGCCTAGAGCNAGGACAGAGTGACCTTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGCTC/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54	183	T C	---		TGGGATTAACACCTGTTTCTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTCGCTT/TCTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAAGTCATATGGCTGGGCTTGGACGAG
73d	129	T C	---		TGGGATTAACACCTGTTTCTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTCGCTT/TCTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT TGAAGTGAATGATTGCTTGCACAAAGTCATATGGCTGGGCTTGGACGAG
73c	165	A/C	---		

3d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTCAAGGTGTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTATATGGCTGGCTTGGACGAG
3c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTCAAGGTGTTCCGTGCTTTC/JTGA CATCTGATCTTCCCAACAGGGCTTATTTC/JTGGCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTATATGGCTGGCTTGGACGAG
3b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTCAAGGTGTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTATATGGCTGGCTTGGACGAG
3a	129 T C ---	---	GACTTCATGCTCATGAACAAGCAATTGCTTAATTTACAGACATTAGAACAAGCTTTC/JGJCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGCTTCCCAATGATGCAGCCAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAATAATGAATATCGATATAC
38b	60 A G ---	---	GACTTCATGCTCATGAACAAGCAATTGCTTAATTTACAGACATTAGAACAAGCTTTC/JGJCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGCTTCCCAATGATGCAGCCAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAATAATGAATATCGATATAC
68	60 A G ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCGGGAAATTAGAGCAAGGAATTGATATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTATGTCCACTTCTCTGCTGCCATCAC TGGGCTTTTACAAGGAGGCTTT
70b	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCGGGAAATTAGAGCAAGGAATTGATATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTATGTCCACTTCTCTGCTGCCATCAC TGGGCTTTTACAAGGAGGCTTT
370	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCGGGAAATTAGAGCAAGGAATTGATATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTATGTCCACTTCTCTGCTGCCATCAC TGGGCTTTTACAAGGAGGCTTT

14c	49 T A ---	---	TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAAAT/AJGAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
34b	41 A G ---	---	GAG TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAAAT/AJGAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
34a	38 G T ---	---	GAG TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAAAT/AJGAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
71b	62 T C ---	---	GAG ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCTCCTTAATAAACCTTAAG ATTCTCTTTGTTCCCTGACATTCTGAAGGCCACGCTGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTGTCT
71	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCTCCTTAATAAACCTTAAG ATTCTCTTTGTTCCCTGACATTCTGAAGGCCACGCTGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTGTCT
95d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
95c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA AATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGT
95d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95b	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95a	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
47	85	C T	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACGAG ATCTCACTTAGCTCCTT[C/]/CCTGCCATATCCTGTTTTCCTACTCTCTATCTCTGAGACTTCTTCTCT GAATGAATTACATGCACCTCAATCCCTGCCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
34b	68	T C	---	ATCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATCTACTTAT T/CJGACAAAGCAAGAAACACACAGAAAAGCCTCTGTTTGAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATCTTATCATCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT
34	68	T C	---	ATCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATCTACTTAT T/CJGACAAAGCAAGAAACACACAGAAAAGCCTCTGTTTGAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATCTTATCATCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT



19	64	A G ---	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCCTAGTATTCCTTTAGTGAAGATTCAACAG[AG]
				AGACCAGTTTGCCTTCACTTAGTAGGGCCCAATGATAGACTTTTAGGTGCTACCACAAGGGTACCTGC
				ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCTGCCTTGGTC
				TTCCCTGTTTACCATAITTAATGATGACATGCAACACCTCAGAGCCCTTTTA
74b	133	G C ---	---	ACAGTACACATGGCCCATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAA
				ATTTAACTACCAGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAAT[G
				/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTGGTCAAATGATTGTT
				AAITCTTAATTAATGTTTATGTTTATGTTTINATTACTGCCAATCACAGCCAAAG
74	133	G C ---	---	ACAGTACACATGGCCCATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAA
				ATTTAACTACCAGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAAT[G
				/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTGGTCAAATGATTGTT
				AAITCTTAATTAATGTTTATGTTTINATTACTGCCAATCACAGCCAAAG
				CAATAGACCAATGACTGCCACAAGAGAAAAATAGTGGATCTACATTTAGAAACCACATGTTTTT
				ATTGGCTCTCTCTCTCTCTCTCTTTTATGCTCTCTCAACACCAATTCACITTTATCTTTTCAA
				T[G/AJAGCAATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTTCACAACAGTATACATTA
82	137	G A ---	---	GCCTGCAAAAGTCTTATATGCTAT
				GGTATGTTGAGGTCAGCTAATGGTCACTGTGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGG
				CAAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATACTC
				TGGTTCAAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA
54b	194	G A ---	---	GTTAAATGGCCGTGTCCTCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
				GGTATGTTGAGGTCAGCTAATGGTCACTGTGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGG
				CAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATACTC
				TGGTTCAAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA
54	194	G A ---	---	GTTAAATGGCCGTGTCCTCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
				AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTTATTTCTCTCTACTGCCTTCAOCTT
				CCATTAAAGAACTCTGTGATTACATTGATGTTTGGTTGCTACACTACAGAAATCCAAGATGACCTC
				CCCATCTCAAGGTCAACTAATTAACACCTTAAATCTATTTGCAATCTTTGTCATTACCATAACATATT
39	210	G A ---	---	CATGG[G/A]TCTGGGATAAGGGTAGACATTTTATGGAGGCATTA
				GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATTGGAGTGTATTAGAAAACTGATAGT
				AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCTCTTCTCTTCTTATTTTGCCTT/CJACA
				GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG
10b	130	T C ---	---	GTAGGACAAGTNCAGAAAAAGGGAGGAGGTGGGGGGTTTCTGGGAAGA

					GAAAAATGATGTTTTGATTTCCCTCCTATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAACTCTGTCTATAATTAACCTTCCTCTCCTGCTTTATTTTGCCTTC/JACA GTTTAGGTAATAAAGATGCCCAAGAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGCACAGTNCAGAAAAAGGAGGAGGNGGGGTTTTCTGGGAAGA
0	130	T C	---		ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACGCGGGAAGAACAGGACAGAACACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
9b	168	GA	---		ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACGCGGGAAGAACAGGACAGAACACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
9	168	GA	---		CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAGTG[G]TTTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATCTTCGTTACATAATTTGATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTGTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3b	51	T G	---		CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAGTG[G]TTTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATCTTCGTTACATAATTTGATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTGTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3	51	T G	---		TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTCTCAGCATCTCTATATACT GTGCTG[G/C]CTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAGT AGGAGAGACAAGACAGATGTGGGGTCCCATGATATAAGGTAATTG
9b	145	G C	---		TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTCTCAGCATCTCTATATACI TIC]GTGCTGTGCCCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAG TAGGAGAGACAAGACAGATGTGGGGTCCCATGATATAAGGTAATTG
9a	137	T C	---		TAACACACTTTTCAATTTGGTTTCTTACTGCAGTTAAAGGACCATCCATTATATACAATTCCTC AGTTCTATGCTTTAGAGTNCATTTATAGGACTACTGAAAAATTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGAGGACTGTGGTTAA[G/A]ATGTCTCTCT TGCCCCCTTCCCAAGTTCTTAATCTAG
82	188	GA	---		

10	93 T	---	---	AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAACTGCGCAATAATAACAGCACACTGACT TTTCCATGGTAAAGAGATTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTACCTTTGAAATTTTGAATTTATGG
11	118 CT	---	---	GAAATCCATTGAAGTTTTGACCTTGAACCTGATCTCATTAACTTTTNCCTGTAGTGGTTGTATTT CATTTTGACAACAGAACAGACGAAAAATTTCCACTTAAATTAATTTCTC/TAAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATTTCTTCAGAACTCTAGGAATGGAAG AA
71b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
71	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
89b	156 GA	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCCACATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTCGATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/JTNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89	156 GA	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCCACATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTCGATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/JTNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
188	31 A G	---	---	GATGACAAATTATTGTGATTGGCATTTTAAAJ/GJGTACCATCCATTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGATTGCTCCTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCTCAAACTGATCTTTAAGAACAATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
191	145 GC	---	---	ACCATCAATGTATCACCTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCCTGGACATTGAAAAATAAACATTACTATTGGTCATTTCTGCTACTTACAAGGTTACTGCACCTA AACAAGTTAAG/GC/GJGTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTTGTCCTATAAATAAATTTTACATGCT

84	144 A G ---	TTGGTTGGCAATTTAGCCTCATAACAACTATTTACAATCAATAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGCAAGATTTGAAGCCAGGAATCCATT CACCGGTAC/GJGTGCTACCTGGGTAATAAATGTTTAAATTAATCTATGGCATTAGATTTTCAAGA GTCCTAATGTGGTTTGAATAAGGTGTCCTTAAATTTGTTTATCAGTAIGC
39	185 C T ---	TTTTCGCAATTTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATTCACCATTTAC TGACCATAATGACTTGGGGAACATTATCTCACCTATCTGAGCTGTATCC/CJTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAAATGAAATAA
127	63 A ---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGAJ/- JGATTAATCAATAAGCATAATTAATTTTATAATATGGAAATTTAACTAGATAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTTCGGATGACATGATGAACGTGTTCTAAGCAGACAG
390	87 C T ---	GCCTTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGCTTCTCATCTGATTATTTTGTGTAT TTATTGTTCACTTATTAATTC/JGTGCTGCTCCCTTCTGGTATGCTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTCGTGGCTCTAGAGGTGTCAGAAAAGTTCCGGTGAATAGAAATTG ACGAATGGGTTGAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
404b	87 G A ---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATAATTTTAAATTTG/AJAAAGAAACTTGTTCGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCTCAGCAGTTCCATGGTGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGATTATATAACAA
404	87 G A ---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATAATTTTAAATTTG/AJAAAGAAACTTGTTCGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCTCAGCAGTTCCATGGTGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGATTATATAACAA
545b	77 A C ---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTCJ/CJCCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCAATTCA
5545	77 A C ---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTCJ/CJCCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCAATTCA

-860b	134 A G ---	---	---	ACTCAAGTTGGGGATAAATCAGAAAGTTCTATGTACAACCTTAAATTTTGTAAAGATTTTATGT TTCTTTTATATAAATTATGGATTTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTACJ/ GJTATACGTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAATCATCAACTTCTGTAT
-860	134 A G ---	---	---	ACTCAAGTTGGGGATAAATCAGAAAGTTCTATGTACAACCTTAAATTTTGTAAAGATTTTATGT TTCTTTTATATAAATTATGGATTTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTACJ/ GJTATACGTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAATCATCAACTTCTGTAT
-3106	208 C G ---	---	---	GCAACAACCTATTATACCTGATCCAAACCCAGGTCTACTAACCTTAAATCAACCTAACCAATAC TATATATTGCTGTTCTGAATTTATTTAGAACTCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACCTGCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAGTCTATATTGTGAAGGAAAG
-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ AAACCTATATTNCTGTCCTGTCGATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG GNAAAATTATCCCTGAAATTTTATACCA
-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTCGATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAATTTTATACCA
-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ AAACCTATATTNCTGTCCTGTCGATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG GNAAAATTATCCCTGAAATTTTATACCA
-6109a	129 T C ---	---	---	AATGCCCTATCACCTCCATCATGCTGCATACTGATTGATTCATATGCTTATTTAGCACCTGTC TTCCAACACATGCTGTTTGTTCATGAT[C/G]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTAAATCAATAAATTAATCAACTTGGCATATGCAGG GMC
-6112	96 T C ---	---	---	GMC

44	103	T C ...	...	...	TAATTGCACAACATTACATATCAGGGTTCTGATTGAAAGGAAGAGAAATATTCCTTTCTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTTAGTGAAGAAGG AAATTGAGTGTGGGAATTAAAGCAACAGGAGACATTTTATATACTCTACAGTGGGGGAAGACTT CCTATTCTCTTCCCAAGGATGGATACATTCTTAC
68	124	C T ...	...	...	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCACAAAGATTTCCTCCTAGTAGGGCTTGGGTGTGGCACCGTTGGCTCATTCCTACTCTCCCT GGGTCTTATTGACTTTTACGGGAGCCTAGAAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTCTGATTGATTTTAA
136b	234	C T ...	...	...	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGCTGAGAGAGCTCACTCCCCC ATATATTCCTCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
336	234	C T ...	...	...	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGCTGAGAGAGCTCACTCCCCC ATATATTCCTCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
381	92	C A ...	...	...	TTGGATACAAAAATTCAGTTACACATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAAACA[C/A]GTAATTTAAAGCTCAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTGAAITGCTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGGCGCAAAAGATCAGAGTTTACAG
436	198	C G ...	...	...	GGTTGAGGCATTGGAAAGGCGAGAAATTTAGGCGAGTAGAAATGGACATTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGCATATAAGAAGTTAGACTTTGGTGGTTGTTAGTAGTTGTAGTAGGTTAGCGTT[C/
449	186	C T ...	...	...	GJATTGGGTGATTCACAGACAAGGTGATGTTCTAAGATTGTATTTATTGT GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCAGCTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCATCTGCATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTAATTTTCTGTGGTATTATA
449	186	C T ...	...	...	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCAGCTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCATCTGCATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTAATTTTCTGTGGTATTATA
449	186	C T ...	...	...	TCTTATGTCAGACCTGAAGTTCCTAATTTTCTGTGGTATTATA

63	72	T C ---	---	GCTGGAGAGAAAGACCTCCAAAAGAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTTGTGTCCATT TAAGAAATATTTTGAATGGAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTCTCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
174b	76	C T ---	---	AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAAGCATAACTTAGGGTACCATAA
474	76	C T ---	---	AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAAGCATAACTTAGGGTACCATAA
478b	175	T A ---	---	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
478	175	T A ---	---	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
3559	149	G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTT[A/G]TCAAAATTTTAAAGAGAACAGGAATAAGGAAGGCCTAACAGAGGAG TTAAATTAATTGTGCAAACTTATCAGTCTTC
3564b	54	G A ---	---	TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCAATTTGATTATNATTTTTTTGTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
6564	54	G A ---	---	TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCAATTTGATTATNATTTTTTTGTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

08b	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAATCCCGACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACAGAAAAAGGAA AGC
08	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAATCCCGACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACAGAAAAAGGAA AGC
166	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A/C/A/AAATCCCATCAACACAGCTCATGCTGGAAGGCATTCTGCTACTCTGTTGGTTTCATGTAA ATGTTGGGTGACTCATTCGCCCTCTCTNTCTCAAGTCCAGGCTCTTGGGTAGACCAAACTA ATACACAATGTTAGGCACACAAAGAGA
370b	120 A G	---	---	AGATTAAACATAATTACTGGGCCATTGTAGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT AGATTAAACATAATTACTGGGCCATTGTAGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT TTTGAAAAATAAATTCATGCCCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
704c	33 T C	---	---	TTTGAAAAATAAATTCATGCCCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
704b	33 T C	---	---	TTTGAAAAATAAATTCATGCCCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
704	28 T C	---	---	TTTGAAAAATAAATTCATGCCCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

				CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCCTTAAACACATTTTGTGAGGCTGGAATGATCCCGATAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTTACTGAGTCGACACAGGATGTCCACAGTGAGCCTC ATCTCCAGTCCATGGAGGAGTTGACTTAGACCTTCTCTGGACAGGAAGGGTC
10	106	GA	---	AAAACAAATGGTGCATTGCATAATATTGGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCCTCTTC
66b	148	GC	---	AAAACAAATGGTGCATTGCATAATATTGGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCCTCTTC
66	148	GC	---	ACAGATAAAAGTCTTTATCCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAAATTCAC[G/TTT]TACTGCATAAGATATCTTCATGTACAACGTG ATGCTTTGTCTTCTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTCAATAGGGCAGAGTAGANTACTACAGGMAAGAGTAAATTCAGGT
787b	97	AG	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCAATTTACATTATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAAATCAATCAGTCAACCCCG[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGTGGCTGTAGGAAGTAGGGTTATGCCCTCTAATCCCGGAAAGGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
793	105	CG	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT[C/J]AGAAAGCAATTTTAAATTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGGCCAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
3810b	37	TC	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT[C/J]AGAAAGCAATTTTAAATTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGGCCAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
3810	37	TC	---	GCATGATTAACACAGTGCAGAAAATAACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACAATGAGCT GCAGGGTAAAC[C/A]JTGATGATACCCCTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAATCTTGGTTCAGGTGCGGCTGTGCAG
6817b	145	CA	---	

					GCATGATTAACCCAGTGCAGAAAAATACCAAGTACATTGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAGATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC(C)ATGTGGATACCCCTGTGTCTCTACTNGCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAACTTGGTTCAGGTGCGGCTGTGCAG
317	145 C A ---			---	GATGGAAGCCATTTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTAGCAACACAGCAATACTTTTGTGTTCTCTATATGACACCTAATATCCAG
319b	221 C ---			---	GATGGAAGCCATTTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG TTGCTTAGCAACACAGCAATACTTTTGTGTTCTCTATATGACACCTAATAT
819a	175 G T ---			---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT(G)GAGCTTAAATAATATCAAAATGCAATATAGATTGGTGCACTGT TAAGCTGAATGCAATTATGGCAACACACACTGGACTGGGTATACGTTG
826b	154 A G ---			---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTGCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT(A)GAGCTTAAATAATATCAAAATGCAATATAGATTGGTGCACTGT TAAGCTGAATGCAATTATGGCAACACACACTGGACTGGGTATACGTTG
3826	154 A G ---			---	AGTGCAAACTATTTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCAGATGAT(C)JATTTAAT TATTGATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAGTTTGGCAACTGTTTGGGCTAATT
6857a	122 T C ---			---	TTATAGAATACTTATGGGCATACGNGTAAATGAACCTGCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGTTGCTGAAATCCTCCCTGCTCACAACAGCAGCTACTNGGTTTTCTAAAGACGTA ATTTTGCAGGCAACTT(C)ATAGAGCCATTCGTGCAGAAAGGAGGAGGAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGGCTGTAGAACTGAGCTCATTA
6865	153 G A ---			---	ATTGAAAACTGGTAGCAACAGATAAATTAACAATAGAGCTGGATATAAAATGAGAGAAGATGC AGACTT(C)TAAAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTATTTGGAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTTAGTTGCCCTATTTTATACATAIC
-6909	73 C T ---			---	



396b	242	G T	...	ACTTCTAGTGCCTCTGTACACACCTCTAATGCCCTTGGTGGCGGACCTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGAGCGCGGACGTTCCCTG CAGGAGAGAGAGGGGCTGTGGACCAAGGCTCAGTCCCTCTGCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTTCTCTCTCCGCTGCTGGGATC
996	228	T G	...	ACTTCTAGTGCCTCTGTACACACCTCTAATGCCCTTGGTGGCGGACCTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGCGCGGACGTTCCCTG CAGGAGAGAGAGGGGCTGTGGACCAAGGCTCAGTCCCTCTGCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTTCTCTCTCCGCTGCTGGGATC
021b	112	G A	...	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATG/GA/CCCGACTGCACCTTCTGTG CTTCAAGCTCTTCTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7021	108	A G	...	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATG/GA/CCCGACTGCACCTTCTGTG CTTCAAGCTCTTCTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7056c	118	C T	...	GGCAGTAGGACACAGTGTGGGTTCTGCTGGACCTTGGAGAGCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTGTCTAAGTTCAGCAGATGCCACATAAGGGGTTTGGCAATTTGATA
7056b	118	C T	...	GGCAGTAGGACACAGTGTGGGTTCTGCTGGACCTTGGAGAGCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTGTCTAAGTTCAGCAGATGCCACATAAGGGGTTTGGCAATTTGATA
7091b	153	A C	...	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATCCCAATCACTGTG CTTAATTTAAATAGCATT/C/TTCTATCATTTATCAGCCTTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATGGTCTCTTTTATCTGGTTCTATATGAATGCTAT
7091	153	A/C	...	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATCCCAATCACTGTG CTTAATTTAAATAGCATT/C/TTCTATCATTTATCAGCCTTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATGGTCTCTTTTATCTGGTTCTATATGAATGCTAT

[illegible]

75	194	C T	---	---	CTCCTAGACTAGTGCCTTACCTTTATTAATGAACCTGTGACAGGAGCCCAAGGCAGTGTCTCCTCACCA ATACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGTCATTGTCCATGCCTA[CT]AGAT AATTATTTTGTATTTTGAATAAAACATTTGTACATTCCTGATACTGGG
78b	273	G A	---	---	TGATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAGTGACCCCAAGAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAGAAATTCACCTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCACAAAGCCAGTGAATGTGAAGGAA
78	273	G A	---	---	TGATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAGTGACCCCAAGAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAGAAATTCACCTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCACAAAGCCAGTGAATGTGAAGGAA
182b	116	A C	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTTACCTCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAAGTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTCTGAAGCCTAGTACCCCAATT
182	106	C A	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA[CT]TCTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAAGTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTCTGAAGCCTAGTACCCCAATT
191b	273	T A	---	---	ATAATTGCTGTTTCTAGCCTGGCAAGATATTTCTATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACACCAAGCACCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTTCATGTGGATTTTAAAGCACTCTAGAACAAATGAAGCTTCTGGCATATTTAAGGAG CTCCCAAAATGTGTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGCACTTT
199c	112	T C	---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[CT]GGGSCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTGTCTAA
199b	112	T C	---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[CT]GGGSCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTGTCTAA





WI-7252a	520	T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTCCACACTCGCAGCAGCGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCGGCCCTGGCTGGAGGCTGCCCGGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCTCTCCCA
WI-7265m	252	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCTT/
WI-7265l	231	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
WI-7265k	121	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
WI-7265j	174	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
WI-7265i	227	T C	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
WI-7265h	80	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
WI-7265g	170	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT

7265f	231	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAGATTGCGCT
'265e	227	T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
'265d	174	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
'265c	170	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
265b	121	T G --	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
265a	80	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTGCGCT
281b	183	C ---	---	GATCACCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCAAGTCTGGCCAGCCCTGCAGGCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCGCGAGGCCGAG GTGTGTGAAGACCACTCGTCTGTGGTTGGGCTCTGCAAGAAGGCTCCTC
281	171	C A ---	---	GATCACCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCAAGTCTGGCCAGCCCTGCAGGCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTCAGACTCTC/AJTGGCAAAAACGGAGTCGCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGGTTGGGCTCTGCAAGAAGGCTC

WI-7282b	159	G C	...			TGTCACCTGGCACATTCATTTCTCAGTTGAAGAGAGAAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCTCACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTTCATAAAAACCAAACT[G/C]TAGCAAGATGCAATGCATGGCAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C	...			CTTGATTACTTCCACTGAGGTGGAGCATCTCCAGTCTCCCAATTATATCTCCCCACTCCACTAC TCTCTCTCCACTTCAATTTTC[C/T]TGTCTCTTCTCTCTAATCAGTGTTTTGAGGGCTGACTTG GGGACAACGTATTATGATATATTGCTCTGTTTCCTCTTCCCAATAGAAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG AVJCGGTAGTAACATATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG TGACGGTAGTAACATATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T	...			AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGTATGGTGGTGGACCGGATATGGAA ACCAAGGTGGTGATATGTTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG TGACGGTAGTAACTATGTTGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205	A C ---			AACTATGCCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAATGAAGAGGAAATTTTGA CGGTAGTAATGTTGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACACAGCAATCA AATTACJTGGACACATGAAGGGGGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	G A ---			CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTGTTTTT
WI-7314b	49	G A ---			CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAA/JTJTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTGTTTTT
WI-7314	36	A G ---			CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAA/JTJTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTGTTTTT
WI-7321b	199	C T ---			ACTCAGGGAAGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATCIC /TJGTTGCTGGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---			ACTCAGGGAAGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATCIC /TJGTTGCTGGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---			AGACATTCGCTTCCCTGAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGTCCAGAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTAAATTCGAAATTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACCTTCATGGATCAGATCTGGGGCAGCAACCTATAATCA/CA/CA
WI-7338c	221	A G ---			CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTCTTACCTTGAGC CATTAATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATCAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACAC/CA/GTATACACACAGACATCAGAAAATTCGTGT

WI-7338b	125 A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACJCCCTTG AGCCATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATTCGT
WI-7338	125 A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTTTACACACAGTATACACAGACATCAGAAAAATTCGT
WI-7338	221 A G ---	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCAATTTTAAATAATCTTAATGATTATTTTATTACTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384c	146 T A ---	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCAATTTTAAATAATCTTAATGATTATTTTATTACTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCAATTTTAAATAATCTTAATGATTATTTTATTACTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	---	TGAAATCCTGGTCTCTGGCTGCTCTAGCTGGTTATTTTACTTTGCCOCCCTCCCACCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACTATTTAAAGGTTTTGAATTCAGATTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAAAGAACTTTTCCCCAAAGATGTGTATAGTTATGG
WI-7388c	106 A T ---	---	---	TGAAATCCTGGTCTCTGGCTGCTCTAGCTGGTTATTTTACTTTGCCOCCCTCCCACCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACTATTTAAAGGTTTTGAATTCAGATTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAAAGAACTTTTCCCCAAAGATGTGTATAGTTATGG
WI-7388b	106 A T ---	---	---	CTTGTGCTGTCCAAAGAACTTTTCCCCAAAGATGTGTATAGTTATGG

WI-7388	94 T A ---	---	TGAAATCTGGGCTCTTGGCTGTCTGTAGCTGGTTATTTTACITTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTGTCTGCCAAGAACTTTTCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	TTAGATTTAAATTGGCAACCCAGCACTGCTGCCACCACTTCCACTGCAGATCTNCTATTCTCTGG[AVG] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTCTGTTCACTGTAACTAGTTTGTNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCTCCTCTTGCCAATGGAGGAGCCTGTGGATGGTACCAACAACAAAGCCCAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTTC[TC]GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCTCCTCTTGCCAATGGAGGAGCCTGTGGATGGTACCAACAACAAAGCCCAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTTC[TC]GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAAAGGGTGGGCATAGCAGTTGCCA[GC]CCAGAAGAGCTTTCACATCAT GAAAGAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7464b	168 C A ---	---	AATTTGAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAAAGGGTGGGCATAGCAGTTGCCA[GC]CCAGAAGAGCTTTCACATCAT GAAAGAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7464a	103 C A ---	---	AATTTGAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTTCTCTATGTA GTACAACAGAGCCACAGCACAAAGGGTGGGCATAGCAGTTGCCA[GC]CCAGAAGAGCTTTCACATCAT GAAAGAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7499b	134 T G ---	---	CAATTCTCAATCCAACTAGTCTGNTGCCTTAACCATTCAGACAAACTTCCACTTCGAAGGTTTTTA AATGCAATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAT /GJTATAGTCCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATTCTCAATCCAAACCTAGTCTGNTGCCTAAAGJCCATTCCAGACAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCAGAGGCACATCAGGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGTC GAAGAAAATATTTAAATATTGGACCACCTTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGTC GAAGAAAATATTTAAATATTGGACCACCTTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCTTTGCGGTTCTTGATGTTCCGAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGGTGGAACACATCCCGGTGATAGAAATGCT AAATTGTC[GT]GTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAATTCGG AGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCTTTGCGGTTCTTGATGTTCCGAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGGTGGAACACATCCCGGTGATAGAAATGCT [C]AAATTCGTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAATTCGG AGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGAAC AGTCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTTCTTCTTGAAGAACCCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGAAC AGTCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTTCTTCTTGAAGAACCCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGAGAGGTC[CT]CTA AAAGAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGATCTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAATAAATGAAGCTGACTAGAAATTTCTATTGACAGGCCAAAGTACATTTAGT ATGGCAITGAGTTGGATATAGTTTCAATTTGATGTGCAATTTGAAATTCAG

WI-7555b	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGGTC/TCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCAGCTAAGTCTGCATTCCTGTTAAAGCCACTTTGGGTG ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCATTTTGAATTTTCAG
WI-7555	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGGTC/TCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCAGCTAAGTCTGCATTCCTGTTAAAGCCACTTTGGGTG ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCATTTTGAATTTTCAG
WI-7567b	290 GT ---	---	TGAGCCATCACTAGAAAGAAAGCCCATTTTCAACTGCTTTGAACTTGCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCTTGG ATCGCTAAGCTGGCTCTGTTGATGCTATTTATGCAAGTATAGGCTATGATTTAGGATGGGCTAC TCTTCAGGGCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63 T C ---	---	AATGATCCCCCTTTCGGTCCAACAACAGGAACCTGACTGGGCGAGTGAAGGAAGGATGGCAT/CJ AGCGTTATGTGTA AAAACAAGTATCTGTATGACAACCCGGGATGCTTTGCAAGTAACTGAATCCAT TGCACATTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTGGGTTTAAAT ATTGATGAGTTCACCTTGATCATGCGCTACCGAGGAGGAAGGAGGATTTG
WI-7574c	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTTGTGTTTGCAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTTACAGTGAGTCCACTACCTCACTGAAAATCATTTTG TACCACCTTACATTTTAGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/AGJTCGTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7574b	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTTGTGTTTGCAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTTACAGTGAGTCCACTACCTCACTGAAAATCATTTTG TACCACCTTACATTTTAGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/AGJTCGTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7574	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTTGTGTTTGCAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTTACAGTGAGTCCACTACCTCACTGAAAATCATTTTG TACCACCTTACATTTTAGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/AGJTCGTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7576c	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGCTGTGTAACAAGAAAACATAAGAGAGC CTTGGTTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTTGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAA/ATJGTTGAAGGCCCTTATCTACATTTCCACCTAC TTTGTAGTGAGAGACAGAAGCAAAANNNNNNNNNAAGAAAAAATAAAG

WI-7576b	168 A T ---			AATGATGATAATGATGATGACGACGACAAACGATGATGCTGTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAATAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTGT TCTGTTTGTAAACCTGCATCTGACACAAAAAA[A/T]GTTGAAGGCTTATTCTACATTTACCTACCTAC TTTGTAAAGTGAGAGACAAAGAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATC/CAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---			AACCATGTTCCCTTCTTTCAGCACCAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577i	77 T C ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577h	50 G C ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577g	157 G A ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577f	48 A G ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577e	84 G A ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577d	93 T C ---				AACCATGTTCCCTTCTTCTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577c	154 C A ---				ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC

WI-7577b	117 A G ...				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTAATTTCTCTGAGGGTTTGTAGTAAAGACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAACATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577	107 G A ...				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTAATTTCTCTGAGTGTAGTAAAGACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAACATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7619g	106 C G ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC CTCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC CGCTTCTTCTTACAGAGAAACATAGCAGATACCGAGAAACCTATTTC
WI-7619n	237 G C ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC CGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG TGCGAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ...				ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCC C G CTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619j	206	T G ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACT C G CTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CGCT G TCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619i	106	C G ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACT C G CTGTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619h	150	T C ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCT C G CTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619g	228	A G ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACAT A G C ACATACCCGAGAAACCTATTTC
WI-7619f	237	G C ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACATACCC G C AGAAACCTATTTC
WI-7619e	99	C T ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAAC G AGACTCTCTGTGCTGGGGTGTCTAATTACA TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619d	189	T A ---	---	---	ACAAGGGGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCAT A G CTTTTCCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC

WI-7619c	90	C	---	---	---	ACAAGGGGACTTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGATGGGCCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCATCTTTTCCCT CTCTGGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206	T	G	---	---	ACAAGGGGACTTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAATGGGCCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTCTCT CGCT/GTCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189	T	A	---	---	ACAAGGGGACTTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAATGGGCCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105	A	G	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[NG]TTAAACCCACATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626c	155	C	T	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C/J]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626b	28	T	A	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAG TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626	144	T	C	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTGCCA TACTAATGA[T/C]GAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7689c	134	A	G	---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCAGCAGGTGGGC TCCCAGTGGCTGCTGCCAGGCCCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTGTTCTTAAAJA /GJTAAGGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTTTCATATGAC

WI-7689b	134	A G ---	---	---	TCCATACCGCTGATTCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGCTTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCGCCAGCAAAAGGTTGTCTCTAAQA/GJTAAGGCGAGAGTACACTGGGGCAGCTGATCAAAATTGCAGACTGTGTAAAAAGAGAGCTTAATGATAATATTGTGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGCTTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCGCCAGCAAAAGGTTGTCTCTAAATAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAATGATAATATTGTGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	---	TGGAGAACATTCAATCTTCCGCTCACTATTCAATCAATGAAGATTAG/ACACTGAGATCCAGAGAGCTGGATGACTTGCTCAAGTTCACCAAGTGTAGTGGAAGAGAGGTCAGAGTCCCTGGCCCTTGATGCCAGCTCAGTCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCACAGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACACTGTCACTGTCATCC
WI-7703b	164	T C ---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCACAGTATCAAGTATTTTAAATTTGGTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATTCAAA
WI-7703	156	T C ---	---	---	TGCTATAAACCAAACTGATGAAGTAAAT/CJGGTCTCTCACTGTTTATTTAACTCTCTAAATCTTTCAATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCACAGTATCAAGTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATTCAAA
WI-7743d	275	C T ---	---	---	TGCTATAAACCAAACTGATG/CJAAGTAAATGGTCTCTCACTGTTTATTTAACTCTCTAAATCTTTCAATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	---	TAAATGAGTGTGTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGGTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGGTCAGGA
WI-7743d	275	C T ---	---	---	GAGGGCAGAACAGCGGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGGTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGGTCAGGAGAGGGCAGAACAGCGGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGGTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACTGTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGGTCAGGA
WI-7743e	106	C A ---	---	---	GAGGGCAGAACAGCGGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGCAGACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAAGACATCATCAAGTG GAGAGAAATCAGTAGTTAAAGTCAATTAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGAGTAAATTTGTTTATTTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126 G C ...	---	ACAGGGCCTTTGGAGGTGCAGCCCCCACTGGCTTTGACCTGCCTCCCTTCATGTCATGGAATTCCT TCATCTGGACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TAGG GAAAGATCCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAACCAAATCACTGACCTTTGCTGAGCCTGTAATAAAGGTCGGA
WI-7773b	237 C G ...	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGATCATCAGATTATTTTAAGTTTATCCGTAATTTT GATAAAGATTTTCTATTCCTTGTTCTGTCAGAGAACCTTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGTTTCACTGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTGAGCTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170 T C ...	---	TGCAACCTCTTTTGGTATGGGAGCCTGCTGGTCAGACTCCAGTAGCGAGAGAGCCACCCAGAA CAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGCTGTTCCGGGAGGAACACATTTTAA TTACCCCTTTGCAGGACCACTTTAATCTGTTT[C/J]ATACCTTGCTTATTAAATGAGCGACTTAA ATGATTGAAATATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165 G ...	---	GCAGAGCCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCAATGGAATAAACTGTCTCCCCCATGCTCTATGAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCTTGAATGATTTATTTGTAATGATATCTTGGTCTGC
WI-7785b	165 G ...	---	GCAGAGCCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCAATGGAATAAACTGTCTCCCCCATGCTCTATGAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCTTGAATGATTTATTTGTAATGATATCTTGGTCTGC
WI-7785	156 T ...	---	GCAGAGCCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCAATGGAATAAACTGTCTCCCCCATGCTCTATGAACTGC ACATTGGTCATTGTAATANN- /JNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCAATAATTTATTTGTCCATTGA TGATTTATTTGTAATGATCTTGGTG
WI-7789c	84 G A ...	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTCTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTTACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCTCTGCTGACTCGGGGCTGCTCAGACGACTAGGCCAGGACCCATCT
WI-7789b	84 G A ...	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTCTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTTACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGCTGACTCGGGGCTGCTCAGACGACTAGGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	<p>             TCTCCCCCTATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTACAGAGACTCTCCG              TGACG/GA/JTGGAAATTTAAGTTTAGGGTCCCTAAAGCAATTTGACACACAGATTTGTTGAATGACTGAC              CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT              GCCCTCTGGTACTCGGGGGCTGTCTCAGACCACTAGCCCAAGGACCCCATCT           </p>
WI-7790b	190 CT ---	---	---	<p>             AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTCTCTAAGGTTACTCTTCATGAGATTCAATCCATT              TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG              TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACCTC/G/JTCTATACTTT              AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC           </p>
WI-7790	190 CT ---	---	---	<p>             AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTCTCTAAGGTTACTCTTCATGAGATTCAATCCATT              TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG              TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACCTC/G/JTCTATACTTT              AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC           </p>
WI-7795b	81 CA ---	---	---	<p>             CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT              CTTGATGATGATC/G/JTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT              TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCTCTGAGGAAAATGTCCAAA              TAAGATGAATCAGTTAATACCGTATCTCTTAAATTTGAAATATAATTCTG           </p>
WI-7795	81 CA ---	---	---	<p>             CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT              CTTGATGATGATC/G/JTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT              TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCTCTGAGGAAAATGTCCAAA              TAAGATGAATCAGTTAATACCGTATCTCTTAAATTTGAAATATAATTCTG           </p>
WI-7814c	41 GA ---	---	---	<p>             TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/JTTCATTTAGTCATGTGACCCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAAATATGACTTGTATATTTTAAAGAAATAACAGAA           </p>
WI-7814b	41 GA ---	---	---	<p>             TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/JTTCATTTAGTCATGTGACCCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAAATATGACTTGTATATTTTAAAGAAATAACAGAA           </p>
WI-7814	28 GA ---	---	---	<p>             TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCAATTTAGTCATGTGACCCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAAATATGACTTGTATATTTTAAAGAAATAACAGAA           </p>

WI-7830d	150 C T ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTTGGA
WI-7830c	54 G A ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTTGGA
WI-7830b	134 G A ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTTGGA
WI-7830	44 A G ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTTGGA
WI-7865e	25 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T ---				CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T ---				CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25	C T	---	---	CCACCTCTATCTGATTTTCCAG[C/TTAAATGAGCGCAGGAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGTAGCTATTAGAGGGTGGTGG GGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191	C T	---	---	CCACTTCTATCTGATTTTCCAGCAATGAGCGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGTAGCTATTAGAGGGTGGTGGGT ATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/TTGAAAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92	A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCCACCTTCAGCCTCACTAGTCCCC CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCATATAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCCACCTTCAGCCTCACTAGTCCCC CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCATATAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGCTTACCCCTATTCAAGCA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT /C/TTACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCAATTAATATTTCCCTGCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T C	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTATTAGAGGG GTGGGTGGCGGGAATCCT[C/TTATTCAGACTCTGTAATTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAAATGAAATCCAATGAGCACTAGAATATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTTAATCAATTTG
WI-7870b	85	T C	---	---	

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGGC/TGGGAATCCTATTATCAGACTCTGTAAATGAATATAATGTTTTACTCAGAGGAG CTGCAAAATGCCTGCAAAATGAATCCAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTCAGAGACTGGCGCGGCCAGGGCCCTCT GGCTCCCTGCCCAATCCCTCGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCCAAGGCTGTCTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTCAGAGACTGGCGCGGCCAGGGCCCTCT GGCTCCCTGCCCAATCCCTCGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCCAAGGCTGTCTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC/AGJTATGTAAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC/AGJTATGTAAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGCT/CTGCCATTGAACAGTGATTAAAGTTTGAATCAAGCCATGGTGACACA AAATGCAATGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGCT/CTGCCATTGAACAGTGATTAAAGTTTGAATCAAGCCATGGTGACACA AAATGCAATGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGCT/CTGCCATTGAACAGTGATTAAAGTTTGAATCAAGCCATGGTGACACA AAATGCAATGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC



WI-7901	33 CT	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C]/TAGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTGGTTGGGGTCTGGTGGTTATTGGGCAGCGCGCTGGTGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 TG	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCCT TTTTAAACAACTCCAGGCCCTGGTTGGGGTCTGGTGGTTATTGGGCAGCGCGCTGGTGTGAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTGTTGTT
WI-7926c	150 CA	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C]/A/JATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 AT	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTACATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 CA	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C]/A/JATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 GT	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCATAAGCAGCCAGACCCACAGGCCAGTCCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/GTTCCTCCCTGGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7947	203 GT	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCATAAGCAGCCAGACCCACAGGCCAGTCCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/GTTCCTCCCTGGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7963b	145 TC	---	---	CATGTGCTGCATGAAGAGCTAAATTTAAAAAGCAAGTAAGACTAATTAATTTAAAAATAAAATGCC ACAAATTTCTCTCTCTTAAGTATTACAAATGGAGTTTATCTCTGCCCTAAAAAGTGAAGAAAT TGAGTGAATGA/T[C]/A/JATTTTGTAAATTTAGGATAAGATCCAAAGTATTTTCCCCAACTCTTGTTCCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTCAATTAAGGCCAGAAAGCAGCGGAAA

[illegible]

WI-8021b	57	CT	---		ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGGTGTGAATCTCATCTGGAAAC/C/TTGATCCC ACGCTTAGAACCTTCAACCAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTCTGA ACTGGTCTTCACTTTGAGATCTTTCTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGATTCGAATCGGTGAATTGCCA
WI-8021	57	CT	---		ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGGTGTGAATCTCATCTGGAAAC/C/TTGATCCC ACGCTTAGAACCTTCAACCAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTCTGA ACTGGTCTTCACTTTGAGATCTTTCTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A	---		CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCATTCCCATGGGAAGACAGAAGAGAT GGGCCCCAGAGATGGAAGGACCCAGTGTATCAACCAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG/A/G/CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAAGGAAAGAGC
WI-8024b	206	A	---		CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCATTCCCATGGGAAGACAGAAGAGAT GGGCCCCAGAGATGGAAGGACCCAGTGTATCAACCAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG/A/G/CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAAGGAAAGAGC
WI-8077	167	A	---		GAATGAGCCTTCTAGCGCGGAGGACCTGCTGTGTGTGGCTGCACATGCAATCTATGGAATGC TTTTTGGCCAAAGCGGGGCACAGGAGTAAAGCTCTGANNNNNNNATCTCGCCCAACTCCTTTCT AAGGAGTCTGGGTGTATGCCCTACAACCC/A/G/TAATCTCATCAGATGGATTTTAAACGTT GTGATTTGTGACTTACTTTCCAACTTGACTCTGGCATAACAAAGGAAAAA
WI-8118f	114	GC	---		TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTTG/G/TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	---		TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---	---	---	TCTAGGTTAATCAAAGCAATTGCAANTTTGGATTGGAATGAC/TTCACCTCCCTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTCT AAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	---	TCTAGGTTAATCAAAGCAATTGCAANTTTGGATTGGAATGACCACCTCCCTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAAC/T/CIGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTCT AAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGGCAGCAGGGCCTCGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACATGAAGAGGATGATATAAAAACAATCACGGCA
WI-8171c	46 A G ---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGMGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACATGAAGAGGATGATATAAAAACAATCAC
WI-8171a	46 A G ---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACATGAAGAGGATGATATAAAAACAATCAC
WI-8171b	298 T C ---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACATGAAGAGGATGATATAAAAACAATCACGGCA
WI-8314b	85 G C ---	---	---	GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTTAAGGG/GC/AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTCTGACCTATTCAATAGGGTTAACCCT
WI-8314	78 C G ---	---	---	GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCT/GC/TAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTCTGACCTATTCAATAGGGTTAACCCT

WI-8321	178	GA	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTGTCTAGTTCTAGTTTATCAACCTACTTTTAGCTGAACGTGTGGC
WI-8321	178	GA	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTGTCTAGTTCTAGTTTATCAACCTACTTTTAGCTGAACGTGTGGC
WI-8332b	123	AC	---	---	TATGACTCACITTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTGCGAGCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCACTGCAGTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGGAAGCAGTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	AC	---	---	TATGACTCACITTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTGCGAGCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCACTGCAGTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGGAAGCAGTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCAGTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACCCAGGCCCTCTCCAACACCGTGGG
WI-8378	308	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCAGTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACCCAGGCCCTCTCCAACACCGTGGG
WI-8426	184	TG	---	---	TTTAGCACATATTTAGCATTAAGCCTCAACGATACAGCAATATGTTACATCTCTTGTGAAAAACAG TTGTGTAGACTGTTAANNNNNNNAATGTAACCTCGACTTGTGCTTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGGNGGGTGTGCTTGTGAACCTCCATCTGTG/GJGCTTGTAGCTGGTG AGGCTGGAGTATGGANGNCCCGGGCCCTGGCNATGNATCAGTGAG
WI-8450h	61	CA	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTAAGA AAAACCTTCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTC/TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTC/TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTC/TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTGAGTCTTCATAAACCTTTCAAAGAGTTACAAAAATACGTTATTTTAAAG/CTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTCGTCACACACCATACCACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGGAACCTTTTATGTCACAGT GACATCCATTCCGCCAGACTTAATGTTTAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATAAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATCAATTTTTTATJNNNNNNNNCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATAAATACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTTTNNNNNNNNCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATAAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATCAATTTTTTNNNNNNNNCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATAAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATCAATTTTTTNNNNNNNNCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGAGTAGACTTAATTTTGATAAAAAAAT TAAAAAGCATG/GAATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATTTCTCCCTTTGTTTGTCTTTTAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGCAGCTCAGTACCTGTC/TGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGCTCGGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAATGTCAGCTCAGTACCTGTCGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGCTCGGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAAG
WI-9446b	75 T C ---	---	---	GAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAATG/CJCTCTAAAGNGACACATGCCCAAAATGACCANGNCATAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGNCCTTACNTTATCACTGTGCTCTCTGCTTTTGTCTACCTA TGNGAACTGCACATACTGTGGCAATATTGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGNAACCTTACCATCCATAGACTATAAAGANCAATTA TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCCAAATGACGANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGNCCTTACTNTATCACTGTGCTCTCTGCTCTTTGCTACCTA TGNAGCTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAGGCAACCAAAATAACTAAACTTGAATAATGAAG
WI-9497	185 A ---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAGGCAACCAAAATAACTAAACTTGAATAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAAGTTTCTATTCTATCCATCATACATAATAGATTGTGCTAAGATCATTTTGGAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTA/CJAAGTG AAAGCTCTCAGCTTGGAAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAAGTTTCTATTCTATCCATCATACATAATAGATTGTGCTAAG/CJAATCATTTTGGAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTACAGTGA AAGCTCTCAGCTTGGAAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATGCTGCTTNCITAGTTGTTTATGTAATGCTGTAGATAATGCAGCCCATG CAATACACCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GT/CJGCTGGATACCACTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTCATAAACATTTATTGATCCTTTTGGAGTAAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/GJA/CTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTGAG GGNTAAATGGTACAAAAAAGGCTTAACCTTTTNCITTCACATTGATCACA
WI-9625b	172 A/T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTGATCTNCCTCTGGGAAAAACCTTTGGAAAAAATAACACGCACA TAAGTATCATAACTGAGGGTGTGGACAAGTTACTTCTA/TJGTTTACCATTTTATATTGACATAA AGTAGCAGACTAGTTATTTCATTTAAAAAAAACACACTGCACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAACAACGCGACA TAAGTATCAATAACTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTAGTGATGCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTATGCTAGACCTAAAAATCCAAGCT TACAACTTC/TGTCTTACCTGATACATTTATCCATTTACTTTTCAATTTTGAATTTTAAAAATGTTA ACTTAATACGTCCTTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGAGG C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGCTGTGCACAGTCTCCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCTATGTTGTTT

WI-9676h	134	C A	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676g	202	C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676f	184	G T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676e	173	T C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676d	134	C A	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676c	114	A G	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676b	92	C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676a	84	A C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT

WI-9738b	40	CA	---	---	TGGACCAACACAGACAGATGTTCTCTGGTGCCTGTGTA/C/A/JATTACAACATCTTGTATGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCCTTTATTTCTGTCCCTATGTTGGTGGCACATGICGTATGCTGTC
WI-9738	40	CA	---	---	TGGACCAACACAGACAGATGTTCTCTGGTGCCTGTGTA/C/A/JATTACAACATCTTGTATGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCCTTTATTTCTGTCCCTATGTTGGTGGCACATGICGTATGCTGTC
WI-9756	47	A	---	---	ACTGAAATGTAAATGGCCAAAGGCACCCAGGACCTTAAAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACATAACAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCTTATCAGCTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAACACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATTCTTCACITTTTATGATTTAAAACTCTCCGTGG
WI-9758	135	A	G	---	GATGGTCCCTTAAGGATTTGCATTTGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGCAAGGCAATTTTATACTATTTA A/A/GJTAAAATAACTCTGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTTCTAAATTT ATTACG
WI-9778	127	GA	---	---	ATTAAATCCAGGCGGGGAAAAATGGATCTTTCATATGCTCTGTACCCCAACTATAAATTTTG GTTCTCATGCACCATTTTCAITTTTGGCTCTCACTCCCAAGTACCACTGATTTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAAATGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	CA	---	---	TCCTCCCTTTGCCCTCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACTGCAGGACTTCTGACAATGCAATTTTCTC/AJTGATCCCAAGGAGGA CTCAAAAAAAGTGGAAATGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAAGCATGGAAGGTTGGCTTTGGC
WI-9841	101	A	G	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTAGATATGTCATGGAGAAATGCAGATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/A/GJTGATGATGATATATATATTTAACACTT AGGATATATACACACAATAAAACGCTCTGTAAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	GA	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATAICTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGGCACATGAA AATGGAATGAAATAATGA/G/AJTGACATAGGAATTACCTACATATTTTG

WI-9880b	157 C A ---	---	---	GAACCTAACACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGA[C/A]TATAAGATCCCTTTTAAAAATTATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108 C T ---	---	---	GAACCTAACACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCCTTTTAAAAATTATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127 C T ---	---	---	ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTAAAAAACACGCCCGATATCACAGTTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAGAAAGCTACACAAAATTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAAGAAATACTTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAAGAAATACTTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102 C A ---	---	---	ACAACGCTGAACCTTCATACAGTCAATGGTACAGTCAAAACATCAGATGTACAGACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAC ATTAAGGNTCCCTGNNATATTTCTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161 C T ---	---	---	CGTCCTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAACTGACAAATGGGTGTCCOC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51 G T ---	---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTCTCTT[G/T]AATTTGTCAGTTC ATTCCTGGAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCAAGTGCTGAACCTTCTCCCTTCTGTCAATGGTTGCTGTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTCTTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	---	TATCTTTTATCCTGGGCCACAGTCTTGATTATCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAAACACAGAC/CJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTCAGATTGAGC
ESTC1	33	---	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	---	GCTACTACCACGGCTGCTGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	---	GCCATCAAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCG ACTTGAA
ESTC107	20	---	---	---	---	TGCTGCTCCTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	---	AAACCAGGAAGGCCTGCCCGCAGAGGCACATGNACAGGCGCAGTGACAGTGACC
ESTC110	23	---	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAAATTACAAAAAGC CTCCA
ESTC119	24	---	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAAGTGG
ESTC129	20	---	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAAAAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGCTGCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCTTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGNGCTTTTITAGCAGCATTTGCG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGNATGCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTAATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGCG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTTCTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCCCATTTTTTTCTTTTAAATACMACTACTGGTGTCTNAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGNTTGCAGCAATTATAAGTGGATCAACAAATT ATATTATTGATACAAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCTGGCTGCTCGGATGGAGCGGGGGGGGCTCA CCACCCTGCAT
ESTC158	35	---	---	---	ACCAAGCCTGGGATTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCAAGGCTGCTGCTGCA GCTTGAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCAACCACAAGGACAGGTT TTCTAGCATTTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCACTGGGCCCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	
ESTC162	36	---	---	---	CTCTCGTCGGTTTGCAGTTGCTTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG TCATTCTCCATAGAATAATTGGTTTTGTAACANGCAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC164	31	---	---	---	
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCGCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATTTCTATTAAATACCTTTTAT TCTCTTTATTTCCCATAAAAGGCAACCAA
ESTC177	42	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC18	29	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC181	21	---	---	---	GCITGACTAGCGAGGCTACATCAAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTCAGCTTG ATTTTTCACCTCA
ESTC186	43	---	---	---	
ESTC187	24	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGATATGGCTGG TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACATCACTTGCTTCCAT CTTGC
ESTC188	25	---	---	---	
ESTC189	27	---	---	---	AAAGTACAAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA TCCTCAAAATACCACCTTCCCCCTAACCTTATCAGCTAGTAAGCNITTTCAAAGGAGGAAATGGGTTAC CTTCAGGGG
ESTC196	42	---	---	---	
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNGCAAAGTCTCCACAAAGCACA AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC20	33	---	---	---	TTTGGTGAATCCCAATATATGAGTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG
ESTC200	44	---	---	---	

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTTAGCAACATTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGCGGCTGGGTGGCCGCCAGAAAGGCTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACAGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAATA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAAGAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAGTC
ESTC22	41	---	---	---	---	CTCCAGAGTCCTCTCTCANACCAGGGCAGGAGGAGTTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAACAAGTTTCAT
ESTC23	27	---	---	---	---	AAACACACCCCA
ESTC230	43	---	---	---	---	GTACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAGGAAGC
						TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTTAATTGNGAGATGCTTAATGTCACAGGCTACA
						TAAGGGCC
						CTTCTGAAGCCCAAGAGAGGGGGCAGANGTAGTTCTTGATTAAAAAACAGAAAGGGAGGAGGA
						CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
						TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGA
						ATGTTAGGATCG
						TTCTACTTTATTTCATATTCACCACACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
						TCCTGAAGGG
						GGTCTCCACGAATTTGAAGACATATTGGTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
						CAAAAGGGTAGTCATATTCCTCCANCAACAGCATGATAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGCAGCATCTGACNTTCTTCCTCTATTCTCTATAAAAAAGGAGCAAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGGCCCTCAATTCATATTTTATCTTGAGCCGCTTGGTCAGGTTTGATTCGCACTCC
ESTC31	32	---	---	---	ACAGCCCAACAGAACTATTGTAAACAATATTNTCAGTCGGTGATCATTTGTAATATACAAAGCAATTCCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCAITTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAAGAAACCATTT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGCTGGAGTTTGTCTTTGTAACNCTCTCATCGAGGCTATATATTAATCTGTCGGTGAGCCCTGCGCTGTCCTCATGGGCCAGACTGTTACCTGT
ESTC50	56	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAGNAGTGGAGGAAAGGACACCAAGT
ESTC56	45	---	---	---	AAGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC57	20	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTCTCAAAATNGTTCAGACTTCAGGAAAATGATTTCCACATGGTAAGGCC
ESTC59	38	---	---	---	TCTGCAGCATTTCACCTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC6	27	---	---	---	AGTGATTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACCACTCAAG
ESTC61	57	---	---	---	ACAGACACAGCATCACACCANAGGGCCCCACGGAGGGTCGGGAGACGACACTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC63	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACITTCGCTAA
ESTC69	20	---	---	---	AGTTTCCCTAGAGCTGTGGGCGCAGATAGCTGTTCCCTGAGTTGCANGCAGCATGGAGATTTGGACACTG
ESTC7	45	---	---	---	G

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ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGNTTTGGGGTGACGCCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCATACNITGGGTTGAAAVGTTG GAAGA
ESTC77	40	---	---	---	ATGACTTTCCTGTCCTCCATCGAAACCAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGTCTGAGATGNTCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGCTGCTGGTTGGGGAGGCTACAGCCTGACCACATT TTTGC
ESTC89	22	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTTCTCTCGCTTGGCATTCGCTCCTCCTCNGCCAGTGTCCACCCAAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCTCTCTCAGTTCACAGTGGAGACTANGGAGATTACAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAAGTTGNAGACGCTATTATTAGTTTGAATATCTGTCG
DWU-100	127	CIT	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAATCTTCCCACTGGCCAG ATCTTATCAATGATCTTTCACCTAAGAAACAGCAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGGGATTTTTCACAAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	AG	---	---	TTCCATCTAGATATCTACTCAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGCAGGGCTTTCACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATTACCA GATGAAAGGATAAAACAAATGTGGTCCATCCATACAAATGGAGTATTACACAGCCATAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213	A/C	---	---	CAAAATCCTGGACTATCAACCTTGTGTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAATTCACAGGGTCCACCAATCATGCCAGCTTCTGTCAATGATGAGATATACATTT ATGCTGACCTCCCTCAAGACTGATTTTTCATGCTGGAAGCTTACAATATCTCAAGGAACAGCAATG TCAACAGGGAGCTGGGAACCAAGCCCTATCTGAGTCTTGGCTCCCTCC

DWU-252	94	A G	---	---	AGTATACAAACATTTAAGCTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGIGT CAGAAAGGAGCTACAAACCTACCCCTCA/GT/GAGCATGGTACTTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCCTGTTGAATGACAAAGTATGTGGTTTGTGTA AT
DWU-330	85	C T	---	---	GAACATTCTCTGCAGCACTTCACTACCAAAATGAGCAATTAGCTACTTTTCAGAAATTTGAAGGAGAAAA TGCAATTATGGGACTGA/C/TCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTCTTTTGCAA CAAGACAAGCAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAAA CTCGATGAATGIGTTGATTTGAGAAATTTTACAGACAGAAAIGCAATCTCCCT
DWU-370	231	A G	---	---	GAAAAATGTTAATTGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTTGGTTTTAAAAGAG AAGCATCATTTCCCAACAGGGCACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGAAAGGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCCTA/G/GCATCTATTTCCTCTGTGC
DWU-1537b	89	A G	---	---	CTCTAATTCAGTCCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCACAATAGCTCAGGTAATC CAGGACCAAAACCCAGGAGC/GTGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---	---	CTCTTAAGTTCAAGTTCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCA/C/TTATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGGAGCTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAGAGCCCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTCTCTCCCTGTTGGGAAT CAAGCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTC/GA/GCAGCTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC
ESTD-ADAa	184	A G	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAGAGCCCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTCTCTCCCTGTTGGGAAT CAAGCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTC/GA/GCAGCTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC
ESTD-ANT1	160	T C	---	---	TCTCTGTCTATTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGAGCTGCCCAACTCGGAAACAAAGAGGGCGCAGTGGAGCAGGAGATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCT/C/GAGCTCAGATGATCTCTGT
EST10398					TGCCTGGGGTGGCAAGGCTGCAAAACAGGAGGCCAACCCAGGAGGCTTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACITTCACACGCGGAGAAG CATTGTTTCTTCGGGCCAAGAAAGGTATCTACC/N/G/ATAGTGTCTATTAGGCATTTG
2b	168	A G	---	---	

EST10398 2a	147 C T	---	---	TGCTGGGTGGCAAGGCTGCAAAAGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAG CATTTGTTTCTTCTTGGCCAAAGAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C	---	---	ATAICGTGGCCTTAGCCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-				CTTTCATGCAGATAGGCTTCTCTACTAAACACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG
D4S95	90 T C	---	---	ATAATGGGGCAATCACCTTTCTTTTCTTTAGAGTCTACCGG
ESTD-				
GPPK2L	38 G A	---	---	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTTACCCTGACGAGAACTGCTCGATATC
ESTD-				CTGGGCTCGCCCGCAGCAGCTGCTGGACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGGTCG
HRASb	82 A G	---	---	TATTCGTCCACAAATGATGTCATCTGGATCAGCT
ESTD-				CTGGGCTGCCCCGACAGCTGCTGGACCTGGACGGGCTGGGGCCAGGCTACCTCTATAGTGGGG
HRASa	37 C T	---	---	TCGTATTGCTCCACAAATGCATCTGGATCAGCT
ESTD-				GGAGGCAGGAGGTGGGGAGGGGCTGCTGCTGCTCCAGGTCCACAGACCAGAGAGCGGCTCAGTG
NRAMP	81 A G	---	---	TATCCCCACCCCAATGTTGGGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G	---	---	GTGACCTTCTCACITTAATGAACTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC
EST36751				AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTATGAACA
7	36 C T	---	---	CCAGTCGTTCAATTTAGCTTTCAGGTTTAACTCTGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
				CACGTGGAAGGAGCTATTTTGGAGGCTTAAAGATAAAGAACTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTTCACTGGATGCATTAATAACAAATGATGTTTACCTTTTGAATAATAA ATGAAGGATTTGACCTGCTTCCGCTCTGGAAGAGATCCGTACCGTCCGTGACGTTTGAACAATACA GATGCCCTTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST40552	109 A G	---	---	GCCTCTATACCCCTGTGGTCCCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCCCTGAATGTTGGAGCCAGT GTGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAGGTAAGGCAACCTCTCTGCTGGCTC TGSCCCTAGGACTTAGTATCC
EST18288	121 C T	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTTTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-AK- 168	31 C T	---	---	
				AATCCCAGCACITTAGGAGGCTGAGGCAGGCATATCACAGAGGTCAGGATTTGAGACCAGTCTGA CCACATGTTGAAACCCCATCTCTACTATAAAATACAAAATAGCCAGGCATGGTGGTGCCTGT AATCCCAGGAGGCTGAGGCAGGAGATCGCTTGAACCTGGAGGGCGAGGATTTGTTGGTGAGCCGA GATGGCACCATTTGCACTCCAGCCTGGGCAACAGAGTAAACTCTGCTTC
ESTD-ALB	180 A G	---	---	

EST70523 3	182	G T	---	TTCCGCGCAGCCCCCATCTTGGCACCCCTGTGCCCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCGGTAAACATCCGGCGGGCGCGCTCTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCCCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101	C T	---	CCAGTGTGTGGCAGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGCGGGAGGTTCAGTGAGCTGACATCGCTGCGCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTTGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGACCTCTAGAAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTGTACACTACATTTCTGATTGGTGGACTCTTGTCTGAAGAACCTT
EST74167 6	137	C	---	AGACCATGAAGGAGTTGAAGGCTTACAAATCGGAATCGGAATCGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCAAGGAGCTGAGGGCGCGAGGCCCGGCTGGCGCGGACATGGAGGA CGTGC GCGCGCGCTGTGTCAGTACCGGCGGAGGTGCAAGCCATGCTGGCCAGAGCAACCGAGGAGC TGGGGTGGCGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGCTCTC
EST43211 8	132	C	---	CGCTGTGTGAGTACCGGGGAGGTGCAAGGOCATGCTGGCCAGAGCACCGAGGAGCTCGGGGTGG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGCTCTCCGCGATCCGATGACCTGCAGAAAGCGCC TGGCAGTACCAAGCGCGCGCGCGCGAGGGGCGCGAGCGGCGCTCAGCGCATCCGCGAGCGGCTG GGCCCTGTGTGAACAGGGCGCGTGGCGGCGCGCACTGTTGGGCTC
ESTD- ARSB	126	A	---	GGAGAAATGGAGCCTGTGGAAAGGAGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGTCTGA AGCAGAAAGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGAGCTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTAATTTTTCATTGAGAACACCAATAATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATAGTGGGTTTCCCTTTCTCTTCTGATCAT TCTTACAAGTTATAGTCTTATTGGAAGGCCCTAAAGAGGCTTATG
EST26021 1	137	A	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGTAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATCTCTGACGACTTCACTACCAATGA GCATTAGCTACTTTTTCAGAAATTGAGGAGAAATGCAATTTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGTCAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A G	---	GGGCAACATAGTGAACCCCATCTCTACAA/GJAAAATACAAAATTAGCCAGGTGTGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAACCAAGATGGTGCCACTGCA



ESTD- CB22	119 C T ---	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAAATATGGCAATGAGAGACATCACTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGCAGTGCCAAACCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCT AGTACATAATTGTGCTTATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	---	TAGNACCATCAVAGAGGAATAGGCTGGTACCCCAAGCAGGAGGACCTAGTAACATAATTGTGC TTCAITATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCCCTAGCCCATTAAGCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCACCCGA GGTGGCTGTGTTGAGCCATCAGAGGAGAGATCTCCACACCCAAWA
ESTD- CB24	145 A ---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCCCTAGCCCATTAACCTTCCCTTCCAGAGGAOCTGAA AAACGTGTTCCCAACCCGAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCAGAGGCTTACCCCGACCAACGTGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	---	GTTTTCTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTTTCTCTCTCTCTCTCGCGTG TCTGCTCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTGAGCTACATGCTCTGTTCTGTCACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGGCGTG
ESTD- CB27	125 C T ---	---	---	TTTTCTGTTCCCTGAAGATTGAGTCTCCAAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGTTGCAITTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCT GCTTCTCCTGTTTCATCCTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	---	TTTTCTGTTTACCTTGTTGAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTTCTAAACAATAAATTGAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTCATGCAGTAG
ESTD- CYP206	61 A G ---	---	---	CAGGCCAGCGTGGTCGAGGTGGTCAACATCCCGGCAGAGAACAGGTCAGCCACCCTATGC/AGJCA GGTTCATCATTTGAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	---	AAAAAACA TTTTAACACCTTTTCAATCATATACACCATA/AC/ATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAAGTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAATAATTAGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	---	CATCCCCCAAGCCCATCCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTGTAGTCCATGGAAAGGCTCTCTGGGGGGGTG GGGTGTGTGGCTATGTTGGTCTTGTGTAG/CT/CGGGGCTTTGGTTTCAAGTGCACATTGCGTT ATTGCAGATTGCTTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ...	...	CATCCCCAAGCCCATCTCTAGCCACTGGCATTTTGGCCCTTGACAGATACACTAGGCCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTGTGGCTATGTGGTGCTTTGTAGACGGGGCTTTGGTTTTCAGTTGCACATATTCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ...	...	TTTGAGACCACCTGGCCCAACATGGGGAATCACATCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGAGGAGAAATGCTTGAACCCQA /GJGGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G ...	...	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAATCCAAATAAAGTACACTGTAATAAAGAAATTAACAGAAATATCATTTGT TTATCAAACTATTTATCACTTATTTATTGGTAAGCCACTACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ...	...	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCQJ/GJGGAGCCTTGATGTCATCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ...	...	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTGGAAAGGATGCTGCTGGT
ESTD- D3S2a	248 G ...	...	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTGGAAAGGATGCTGCTGGTATGT
ESTD- D7S399	83 A G ...	...	TGAATCTTAATTGCTATCTCTACAAAATGTAATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJ/GJGCTCTCTCTACATCATCTTTTCAAAAACATTTTTCATCCATGGACTCCATAC TAGAATATTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ...	...	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTJGJCTGCTGGTGGAGAACCAACTCTGCGCTGTGGGTAGGGGCAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ...	...	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCACJG GJTTCCATGGGTGTGGGCTGGGACCTCACGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAACTCTGCGCTGTGGGTAGGGGCAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAGAGAGAACAGAGT

ESTD- DRD1	154 C T	---	---	TCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAGATCCACCCATCAC ACAAACGGTACGACCCCAACCTCGAATCGCATGAATCTCGCCACACATCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C	---	---	TCTGCCCTTTGGTCAGGAGGCTGCCGGCAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACCAACGGTCTCCACAGACTCCCGACAGCCCGCCCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGAACCATGCCCAATG
ESTD- DRD3	109 C T	---	---	AAGACGATGGCCAGGATAGCGCGCAGTAGGAGAGGGCATAGTAGGCGATGTGGCGGGCTGGCTGG CACTGTGGAGTTCTCTGCCACAGGTGTAGTTCAAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- EPB82	93 C T	---	---	TCTTTAGGATCCGATCTCGGCTGGTTGGCATCGCTCCGCTAGGTGTAGCGGCTCCACAGCTGG GGTGAGGGGTGGTGGGTGAGTGC/TGGGGCGGGTGCAGACCCACCGGGCTGGGAGGACTTCA CCCGCCTCACCTCCGTTTCTCGAGCAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGACCC/VGJGGAAGCCGCTCTGGCGCTG GCAGTCCGTGGAGGGATGTTCTGGCTGTTGAGATCTCAAGAGCGAGCATGCTGTGGACACA CAGAGACTATTTTAGATTTCTTTGCCCTTTGCAACGAGAACAGCAATGCAAAACTCTTTGAG AGGGTAGGAGGTGGGAAGAAACCAACATGTCATTCAGAAGTTAGTTTG
ESTD-F9	111 A G	---	---	AGATCTGATGATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTAAAGTATGATGTTT/VGJGTCAAACCTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACAGAAGAGAAATAAATTCACAGTCAA AGAAATCAAGCACITTTTCAACACATTGAAGTTGTTTGAACCTTGGTGTCAACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G	---	---	CGGAGACCGGTGAGTGTGGGTGGGAGTGTGGAGGGAAGGAGGAACTGGGGGTTAGGGACT TTCCGGGGTGACTTTCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGAAGGGACCTCTGGTGCACCGTGTCTGTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGCACTC/ GIGACTGTCTCCGGAATTCGAGAGCT
ESTD-GCK	88 A/G	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAAGCCCTGCTGAGCCCACTCTGTTCAACCATGAC AACCACAGGCCCTCTCAGGA/VGJACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGGGCTGAGCCCGAGGAGGAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCTCCCGAGGTACAG

EST34088 2	62 A T ...	...	GTGGGGCAACAGTGGGAGAGAGAGGGGCCAGGGTATAAAAGGGGCCACAAAGAGACCGGCTC[A/T] AGGATCCCAAGGCCCAACTCCCGCAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ...	...	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCAAC[A/G]GGCATCA TTGAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCCTAGG
ESTD-HT2	154 G ...	...	GGGCTAAATTTCCGAGCACTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGCAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTGCTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ...	...	AACACAAAGCCGAGGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCTTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGTTTTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTCTACAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ...	...	CTGAGAAACAATTGGCAAAATAAGGAATTGGCACTCCCAACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAAGAGAAAGAAAGG[A/G]CCCCAGA AATCACAGGTGGCAGCTCGCTGCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATGCAACGGCTTGGCAGGAGTGC[CT]CTGGGAGAGAAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGFBP1	43 C T ...	...	TTTACTATTTCAATGGATACAGAAATTGGGAGTCACTATATCTTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTGCTTACATTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGGTGGG TGCAGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACGAAAGT ATGTAATACTTCACAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD- IGHV4-6	120 C ...	...	CAAAGTAAGCACCCAAATAATGTTAGCTATTACTATCATTTATTTATTTATTTATTTTGTG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCTCTGGGTTGATGCCATTCTCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCAACCCGCC ACTGTTCCCGCTAAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1A	110 A G ...	...	CCACTACAGATGGAATAATGGGTACAATGAAGGGCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTTGGTGGTCTCTCTGCTC[A/G]GAGGCTCTCTGCAATTCAGG
ESTD-IL1B	99 A G ...	...	TCCAGGGTGGCTGGACCCAGGCCOCCAGCTCTGCAGCAGGAGGAGGCTGGCTGGCTGTGAAGCATG TGGGGGTGAGCCAGGGGCCOCCAGGACGGCACCTGGCTTACGCTCCCTCAGCCCTGCTGTG[A] TCCCAGATCACTGCTCTCTGCTGCAATGGCCCTGTGGATGGCTCTGCTGGCTGCTGGCTGCTGGCC
EST74082	134 A T ...	...	CTCTGGGGACCTGACCCAGCGGAGCCTTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T	---	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTCTATTAAGTGAACATGACATGTCATCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGGAAGATCCACGTGTGTGGCCATATTGTAACA CATTTTTCTGCAAATC/TACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G	---	---	---	TGCCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTACCAATTAACCAGAAAT CCAGTTATTTCGAGCCCTCAAAATGACAGCCATGGCGGCGGGTGCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGT GAGGTTAGGTGGCTGTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T	---	---	---	ATGCAGGATGAAGGTGGACAGGAGGATGAGGGCCAACTGTCTATCCAGGGCTGCAGATGTCTG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTG/TAAAGTCCAGTATCCAGAGTTTTGGTTTTTGAAGTAGCAATGCOCTGTGAA AAGAACTGAATACCTAAGATTTCTGCTCTGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGTCT TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T	---	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCATCTCTCCCGTCTCAGGTTTACCAC/TGTCAACATTGACACA
ESTD- KRT8a	21 C T	---	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T	---	---	---	CACCTGTGTGTCTAGATCTCCTCAGTGGCGGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTGGCCGCTCTTGAGGTGTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACCGTAGCAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGATGCTGTGTTATACCTGCCTCGCCATGCAGCATCATAGCCTGT GGGAACCAGGGGCTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGAGTTATTAGCATGGTTACCTGTGATCTCCAACTCTTGGCGTTCCACCGATG GAACTGCGGGCAATCTGACACGTGTGACCCAGCTGTACCAATTAAGTGAACATGGCTTCGAG AGAGTTGACACAGATTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACACTTTCCTTACCCATTCACTGAAACGACTTCG/GCAAACTGGAGCCTTGAGGMAITGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGGTTTGTCTTAATTCATTTCAATGTCTCTTCATCTTTAGCTGTGGGGTTTGTGTTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACTTTTATAAAATTTTTTACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCTGCCCTCCAGCTCTGCTCCCTAGCCT/GAAGCTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTGGTCTAAGTGTGATACCTCTGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGCTGCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCACAGACTGATATGGCTGGT AACATGGACTGTATATTGTACAAAAAAGTTTTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAAGGTGACTTATATCCACACTGCACACTGCCTAG/GGCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTTGGAGAGGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTCAG/GTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGAACACAGTGACCATAATTTCTTCTGCAGGCATATAGAAITTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGATATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG CTJATTCCTGTGGTTTTTAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACCCCCACCCAGCACACCTCCACCTCAGCCAGACAGGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGGAG/GTCAAGCGGTGATCATCGAGCGCGCGGG CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAH	100 A G ---	---	

ESTD-PAR	120	A	---	---	---	CTCTCAGGAACACCAGTCTTCTTACCAACACGACTTATTGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGAGTGTTTCTTTCACATTTCTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
ESTD- Per/RDS	74	A	G	---	---	ACCTACAGAGCTGGCTGGATGGTGTGTCCAACCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTG CTGGAGA[AG]GAGCGTGCGGAGACCTGGAAGGCCT
EST68308	5	29	C	T	---	GGAAAGAGATTTAAGAAGCTTGATTGGAC[CT]AATCTCGTCTTTGAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGAACTCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAGTAGACTTTAAAGGTAAAGTAAGAAAGTAGTTATTTTAA
EST54045	6	39	A	G	---	GGAAATATAAAATATTTTAAATACCTCCATTTTGCTT[AG]TCCCTTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATTGTCATGTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGGCTTGAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88	A	G	---	---	ATGAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAA[A]GAGCGAGCTGTGGTGACAGGTGTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTAATCTT
ESTD-RDS	127	A	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTGCTGGAGAGAGCGTCCCGGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGGAGCCGAGGGCGCAGACGCGAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTCACT CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94	G	T	---	---	TTGGGAAGTTAGAGCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCACAGTTC[G/T]CTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45	A	C	---	ATCACAGGTCTCTGGTCTCTGGCCATCTTCTCTGGGAGAGATGG[AC]TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTGATG
EST19590	55	C	T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGT[CT]GGCTCAG GATGCCGGAAAATGAC
EST76136	39	C	T	---	---	TGAAGCTTCTGCCAGCTTGCATTGTTTCTAGGAGAAC[CT]GGCTCATACCTTTATCTATAGCCTT CCCTAGGCTCT
ESTD- SPTB	176	C	T	---	---	TGAACACCTGTGTGTCGGAGCCAGGTGTGTTCTCTCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCGCGGCACTGCTGGTTGAGCTGGACATACACCTTCACCTCTTGGCCGGGAGAGAC ATTACCCACCTGGCCATGTCCTGGCTGTGTGACAC[CT]CCTCTGTGAAGACCCCAACCCCTGC CTCCCCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCTGATCCACAAGAAGTGGTACCATTTTCATCAGGCGCATCAGTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTCTCTCACCTAGAACGTTTGTTCACAACTTTCTCCAGTATGGATGGGATATGATGGGGGG GAGAGCAAAATTTAAATAGGACCATGAGACACATCA
ESTD- THPB	125 A C ---	---	---	TGGGCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCAGACAGGATCAGCTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAGAGGTCAATAATATTGATGTGTTAA CATGGGTGTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 G T ---	---	---	AGTAGTGGATGAAGCTAACCGCCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAAACAATGCCCTACTCTCTTATGCATTAGTATCACA AACCCTGGTGAATATAATAGATTGAGTTAATTAAGTATTTCTTACCTTTATTACCTTCTTCT AATACAAGCATATGTTAGTATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCGCCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAAACAATGCCCTACTCTCTTATGCATTAGTATCACA AACCCTGGTGAATATAATAGATTGAGTTAATTAAGTATTTCTTACCTTTATTACCTTCTTCT AATACAAGCATATGTTAGTATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC[AVG]TGGCGGGGATGGCCGGGGAGTTC TGGTTGGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTCGGTTGCGATGCGCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGCGGGTGCATGCCTGAGATGTAGATCGGCGC
ESTD-VWF 6	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTACGTCAAGCCTCAGCACCCAGATGCTGTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTGGTGA AGGAGTGGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
ESTD- TNFα	152 A G ---	---	TTCTGCATCCTGCTCTGGAAGTTAGAAGGAACAGACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTC[AVG]GAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTTGCCCAACTTCCAAATCCCCGCCGCCCGGATGG
ESTD- TNFα	88 A ---	---	TTCTGCATCCTGCTCTGGAAGTTAGAAGGAACAGACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTC[AVG]GAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG GTGTGCCCAACTTCCAAATCCCCGCCGCCCGGATGG
EST52418 6	113 A G ---	---	CAATTACAGGGTCACTGCTATGATGTGTTTGGAGCCCAGTACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGGAGTACGGGCTGAGGCATACACT[AVG]AAGTGAAAACCTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACCTATTGCCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGC[AVG]GGGCTGGCTTATCAGCCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGCCCCCATGCGGGGGGACGTGGAAAGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[AT]CTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCCAGTGCATCTGTTCTCGAGTTTT CTCTGCCATGTGCTATTGACGACGGACCTGTCCCAGCCAGATGATTTACCATTTCCACAGTGGT CCC[AVG]TTAAACAATCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCTCTGTATAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCTTAGCA CTGGTCCCTGTAGTCTGTATCAGGTAGAGGAGATGGACAGGTGGAGAGGAATTTTGAAGGGCA TTGGAAATCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTTCCAGGTATTGTGCAGAAAGCCGAGATGAOCTCTATGTCTCAGATGCATTCOATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTA/C/GJGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGTGGTGAACCTGCTCTTGGCATTGCCGGCCCTCTGGGGCCCGTGG TCCTCTGGTGTGGTGTAGTCTGGAGTCAACGGTCTCTTA/GJGTGAAGCTGGTCTGATGGCA ACCCTGGGAACGATGGTCCCAAGGTCCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGGCCCTGCTGGCCAACATATGCCTCTCAGA ACATCAOCTACCAGTGCAGAACAGCAATTGCATACATGGATGAGGAGACTGG[AVC]AACCTGAAAA AGGCTGTCTTACAGGGCTCTAATGATGTGAACCTTGTCTGAGGGCAACAGCAGGTTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cd	112 A G ---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGTAGACAACA GTGGTACATAGCTGTATTTATGCTCTCTTCTCTGCTCACTTCA/GJGGGTTCAGGTTGGA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACA/C/JTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTGACCAACACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGGGAGAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCTTCTCATCATGAAAAAC TGGGAGGCCGGCATTA/GJGTGCTCATGCCTGTAAATCCAGCATTTTGAAGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGATTTGAGACCAACCTGGCCCAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTTAGACTAAGTTCTTGTCTCCAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATTTCTTCCCTCCTTAGGATGAGGTG A/GTAGTAATGACCGATGGGTGAGAACTGTCTGTCACTGAGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCTTCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCAAGGCACTGGGCTCCGAGGACTCAACCACTGCCOCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111 CT	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAGTTTGTCTTGGCTGCCTGTGTGGGATATTTGAAAGAGATC/TJTTGCCAGTCCAAATGCTCTAGAGATTTTCCCAATGTTTCTTGTAAAGTTTCATAGTTTGAGGCCCTAGATTIAGTCTTTAATCCATTTGATTTGATTTCTGTGA
ESTD-FYR1	109 A G	---	---	CTTCGTGACGGGAGGTCAGTCTCCGCTCTTTTCATGGACATATGGATGGATGCTGTGACCAATTTCCCCTGTGACAGTGATGACACGGCAGACTTGTCTACTATGAGIAGI/GGGGAGCTGTGTGCACTCATGCCCGCTCCCTGGAGGCTGAGCCACTGAGATCAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGGCCACTCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTGCTGCTGCAAGGATGTGCGIAGCTGTGGCTGGAGTAGCCCCGACTCTTGTAACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100 C	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGCCGTAGGGGAAGCTGGGGGATCTAGGGGATGGGTGAGGAATGGGCCAGCCAGTCCCGGGTGGCTGGGTCCCAACAGAGAGGGCGGTGGAGGAGACAGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G	---	---	GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCAAGCTTCAAGGAIC/TJGTCCTGTCCGACCTAAGCGAGAGCCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G	---	---	CCCTCTCATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAAIAGI/TCTCTACCCGAGCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD-CTLA-4	48 A G	---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGIAGI/TJCAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACITGAAATGTTATTCAACTGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACITTAGCTTAG
ESTD-ACE	96 CT	---	---	ATGGCTTGCCTTGGATTTACGGGGCACAAAGGCTCAGCTGAACCTGGCTIAGI/JCCAGGAOCTGGCCCTGCATCTCCTGTTTTTCTTCTTCTCATCCCTGTCTTCTGCAAGGAATGCAGTGGCCCAAGCCTGGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88 A G	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAAGGATCTGCCI/TJGTCTCCCTGCGTGGGGGGCCAAACCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTCGTGAACATCTGCACAAATCGGCTGCCTCTGCTGCTAAITTTGAATGATATTGTGTGTGGGACCTGAGCACITTTATGGCACAAATGATCACTATTTTCTTGACCCCTACTTACIAGIATCTCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTGTGCTCTATAGTCCCAAGTGAA

ESTD-PS-1	99 A G	---	---	GGGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTAGTTCGTAGCCATATTAATGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCCTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTGTAT
ESTD- B3AR	104 C T	---	---	GGCTGCCAGGGGTTCCGTGGAGGGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGGTATCGTGGCCATCGGC/C/TTGGACTCCGAGACTCCAGACCATGACCAA CGTGTCTGTGACTTCGCTGGCCGCGAGCCGACTGGTGTAGTGGGACTCCTGGTGGTGGCGGGCGGCCA CCTGGGGC
WI-567b	48 A G	---	---	TCTACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCCTGGTTC/GJAGCCCTCATCTCTTTTA CAGGATCCGCCACAGATCCCACTGATCTGGCCTTAGGCTCTCTTCTCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTGTCTTCAAGCC
WI-801c	58 G T	---	---	ATGGAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-801b	58 G T	---	---	ATGGAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-1099b	76 A G	---	---	GAAATTCACCTATACAAGAACTATTTCTCTAAATTAATTACATTAGTCTCATTTCTGAAATATTAT TTTTTACA/GJTACCCCTTGTATATTTTGTATTCATTTGTAACGAGAGATTACAATACGTAACGC TGTTCAATTGATAGTGTATCACAAATGTCTAAATACITTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CA/C/TJCTTAACTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAAATAAAGTGAAGAGGTAAAGAGGAGACAACCTGTGCTTT TTAAGAAATAGAAAGATCATTCTTATAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G	---	---	TAGGGCTGTCTTCCCCAGAGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCTATGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAGCAGCAAAAGGAGAAAGGAAGT

WI-2625	98 G A ...	---	---	GGCAGTCTGGCTGTAGGTAGACAGCACTGAAGGATGGAGAGAGAGAAAGACAGCAGAA GCACGTGGTAGTTAACAGGCTTATTTAGGA[G/A]CAAAATTGATGACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTCTCTTA	GCCTTAAGTGT AATCACAGGG	TCTGTGTCATATTTCCCTCTTTGACTCTGACCTTCTCTAGTCTTCTTTATAGG[G/A]ACCCTGTGATT ACACTTAGGCGCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCC:TTT	GGCTTGCTCA	CTTGTGAGGG AAGGCT:TTG	CCATTGTGAGTTGGTGGGTGCACCTGTGCATCCCTCGCACTCAACAAAGTGGCTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAAATGCTTTCCATGCTCCCGTGTCTTTGAAAATTCGACT TTATCCTGAAAAAATCAGCTGCAGTGTATCTCCGGTATAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTATGCGGC	TCAAGTATTGC CTTGTGTGG	CTTGTAACCATGCATTTACAGCATACACCCTCAGTGAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAGATTTTGGATGGATGAAAGCAGAGAGGAGATGCTAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA	CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAGGAAGCAATTTAGCCCTAGGGA[G/T]AGAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCAATGCTTGGCTCCCC
WI-1796b	29 A G ...	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCAATGCTTGGCTCCCC
WI-1796	29 A G ...	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAAAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTCT TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCGAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGT[C/T]GGGTAACTGAGAGTGGTTTTTACACCCCAA
WI-1959b	87 C T ...	---	---	GTTGTGCTGTAGCAGACACAGAGGCA[G/G]AGAGGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAAATGCAAGATGAGCTAATGGTCTAGAGGTAAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ...	---	---	CTTGAGTATCGGTGGATTTGGTATACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATGTATCTGTTCTACAATTATACAGTAGGAGACATATGTTCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGCGCTATAAATAGC
WI-1980b	140 C T ...	---	---	

WI-2015b	190 A G ---	---	TGTCAGATAGTCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCGACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACTA/GJCATATACCTT CTAATACCATAGAG
WI-754b	49 C T ---	---	GAAGGCACAGGAGAGATGGCTGTCTATACCAGCCAGGGAGAGAGGC/JACATTTATTGGGTAA TCCTATAAGTGCATCTTTAAAATTTGTATTACTTTAGA
WI-754	22 T C ---	---	GAAGGCACAGGAGAGATGGCTGTCTATACCAGCCAGGGAGAGAGGCACATTTATTGGGTAA TCCTATAAGTGCATCTTTAAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---	---	AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGTATGTCGTACATCC/JGJTGCGCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---	---	AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGTATGTCGTACATCC/JGJTGCGCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---	---	TAATTTAAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTAAAGGCTAAATAAGAA GAAGT/JGJCTAAAGTTATTAGTCAGAGCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---	---	TAATTTAAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTAAAGGCTAAATAAGAA GA/JGJGTATCTAAAGTTATTAGTCAGAGCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---	---	GAGCCTTTCTAAAATAGGATTGTGACTAGCAACCTCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---	---	CGGGACAGAGACAGACAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG
WIR-5f	196 C ---	---	CGGGACAGAGACAGACAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG
WIR-5e	194 C ---	---	CGGGACAGAGACAGACAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG

WIR-5d	191 A ---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGCTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAGG TTTACGTCCAG
WIR-5c	177 C ---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGCTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAGG TTTACGTCCAG
WIR-5b	159 A ---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGCTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAGG TTTACGTCCAG
WIR-5a	37 A G ---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGCTGT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACAC AGGTTTACGTCCAG
WIR-6	63 A C ---	---	TAACCTGAAACTTGTCTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[WC] CCAGCTCTGGGTTGGGCGAG
WIR-7	12 C T ---	---	TTCTGACTATTCTAAGCATCTGTAGAATATTGAATACATAGCTTGAGATTGATC
WIR-8	46 C T ---	---	GGGTCCTATGACTATCCTGGTCAATTGATTGACTAATGATTCCTGCTGCTGGCCCTTG
WIR-2	56 C G ---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAAAGAGGTATGA[CG]CTGAAG AAAGAAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGGAAACCATGGCTTGATTACT GACAAC
WI-7059	93 G A ---	---	TGTCCTTGCTTATGCCTGCCTCTTTGGCTTGGCAGGATGATGCTGTCATTAGTATTTACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGTGAJTCAGATCTATCTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAAGTACATTAGCAGCATCTTTAACACAGCGGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A T ---	---	GGTCATTCCTTTTATCTGTGAGGAGCCAGCTCTGACTTATCTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTTCTTACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A G TGC	CCTATATTCA AGTTTGGAAA	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[AG]ATTTCAGCAGCAATACAAAAGTA TTTATGAAGAAATGCATAATCTCTGAAAATTATGAAAACATCCCT

WI-18517	87	C	CAGGAATCAG GTGCAACA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTGTCAACTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAC/CTTGTTCACCTTGCCAAACACAACTG/CTGC
WI-18668	76	C	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTAAC CTGCACCTTTT GC	CGATTGACAACCTTTATTTTCAACTTAGTAACAGTCCAAATCAGGTAGATTGGCGAAAACT AGGCAAAAAAC/AGCAAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCTACT
WI-18680	75	T	AGCATCTGGA TCAACGGAGC	CCTCCTGAATA TCAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGATCCCTGAGTCTAGTGAAGGCTGTCACTCTAGC ATCTGGAAT/CTGCTCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	GGGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTTGTGGAGACACACACCAAGAGGAGTTGGGCTTGAAGGAGCC CTTGAGGAACACAGGGTCTCCAGGGGTAC/CTCCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A	---	---	TGTGGCAAACTTGTATTTAATTGCAAAAC/AGTCTTAAATTAACGACATTCAATAATGAACCAAC AGGAGATTGCTGACTTTGTAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGATACAAGGAAG
WI-18640	121	T	GTGCTGGGTG GTGCTGGGTG A	GCAATACCAC TGAAGAGGAC A	ACCAGTCAATGTTTATTTGAGGGTAAATTCCTATTAGGATATGAAGGATTACGAACGATTGAGATT GTGCTCTCAGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGCAGAGT/CTGTGCTCTTC AGTGTATTGCGGACC
WI-18533b	91	T	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAAACTCCCGAGATTTCCTCTTTATT TATATTTCATTTTCATCTTAAT/CTTAC/CTGAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAAACTCCCGAGATTTC/CTTGA TTTATATTTCATTTTCATCTTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	TCATCTGATAC CTTGTTCAGAT ATTT	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCAAGAGGACCTTCTATCTTACATTATGGCTGGGAATCTTACTCTTCTGATA CCTTGTTCAGATTCT/CTAAATAGTTGTAGCCTTATCTCTGTTTACAGATGTGAACCTTT
D49493	159	A	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGEACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCGAGTGCATCATTAGGGGTCTTTTCACTGTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT/AT/CTGGCTGGCCTGAAAGTGGCCCATCATCATCCCACTGTT
EST10030	7	C	CAATTTGTTC TCTCAAGTCCC	GCAGTGTGGT ATGGATGA	CT TATTTTCATAGAGGAGACCTAGGAGGAGGTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCCT/CTCATCCATACCACCACTGCTGATTG
EST10052	2	G	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTCTGAGGCTG/AG/AAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCACTATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGGAA

EST10605 2	118 C G	CTCTCAAGTAG ATAAGAGGCA TAATCT	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	CTTGGTAAATCACAGTTCTGTATTATACAAAAACITTTGTTTTCTCTGACAAAACGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	ATAAGAGGCA TAATCT	ATAAGAGGCA TAATCT	AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTTT/GJAA ACAAATTTCTTCTGAAATTTAGCTTATGAACCTACACTGCAACACCAGAGAGGAGCAC
EST11260 8	101 G T	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T	---	---	---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACAGTAGATTCTTTGGAGGAGGAAATCCT TCTGTGGATTACGCTTTACCGCCTTTCTCTCATCTGCTGGT[G/C]TTTCTCAGAGCTTTAATGTCCGT CCCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	CCAACCTACTT TGGAGCCT	CCAACCTACTT TGGAGCCT	TCCAGCTTCT CTAAAACTCC T	GAATCTGGGTATTAAATAGGGGTGCCAGGAGCACATAGGAAGAGCATCCAACCTACTTTTGGAG CCCTIAGJAGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGGA
EST11772 6	74 A G	---	---	---	CCAGGAATAAAAGAAAAAGTACAGAGGAACAGCTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCAJAGJGACTATTTCTTCTGACTAAGTGAATAAATACATTTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A	---	---	---	CTTGCCATTATTTTGTGCATGTTCTTTAAAGGCTTGTGAAAGATACTTGAATGTGGGAAC ACATAGATCCCAGAGJATATTAAAGGGCTGGAAAAAGTACGCTTAAGAC
WI-16644	42 G A	CAATAAGCAG CTCATTTTGAT TAC	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGATCTCAATAAGCAGCTATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAAGGCTCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAAGTAACAGTGGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT	GCCTAGTAATCCAAAGGAACATGTTTGTATATAACACTCACTACAAAAGTCTGT[G/A]ATCCAGG AAGTGACCAGCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C	---	---	---	GTGGAAAAATTTTTATCTGTACGCTTTCC[T/C]ATTATATTATCTTTGTCCTTGATTTCAGCACCC CACCCGATTTGCAGGCAGTCTTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G	---	---	---	CCCTAGGAAATGACTTGGAGTTGTGTCCTCAATACCAGTTACATCTGTTGCCAAAATTAAGCTCTC TTCCCAGAGGCATTAACTGAGATTAT[G/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTA
EST12492 4	25 A G	---	---	---	ATCTTGAGGTTTCTGGGCCCTGTCAG[G/G]AAGTGACATCTTTTACTTACACAGGTGAGGAACCCCTAT AAAGAAACTGTGTAGAAAAAGATATCAGGTGACAGCTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAACCAAACTGGAGGAAGTCCACAGGTACACTTGTCAC/GCAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGAAATGACCAATTTTAAAGGGCCATGTG GTCGTCGAGGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCAAATGACAGTGTCCCTGAGATTC/GATGATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCTTATTCATTGTTCAAAACACTGTGTAGTACCAACATTGTCACCCGGGCA /GTTGAGAAATACAATATTGAAGAAGAGTCACTGCCCTGCCCTCTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTTCTCCAGGATTCAG/CAC/CTGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTGGGAGTGACCGGATGGGAATCCATGTTGCTTGGCTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA/A/CAACAGGCCAGTTATTTACCAGAAATTTGTTGGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC/A/GTCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCCTAAATCAGTCTTCTAGGGCCACA/C/GGAGCAGAAGCAGCTTCCCACCCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAAATTGACACCAATAAATGCAC/A /G/TATTTAAAGTTTACAATTTGAGAAAGCTGACACGTTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCCTCATAGCTGCTTAGGTTTGTCTTCC/C/AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCTCATGAATAGCC AGCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT/G/GACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAACAAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GAT/CTCTGTACAGGAGCGGCTACTGTCTTCAATCTTTCATGTCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT G	AACAGATTT TGACAAAAGA	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACAACCTCCCATCAGTAGCAATACAAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCCT/C/TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGATATAACCA

EST13278 2a	51 A G G	CATTACCGAA CAATATTTAG G	CATATCTGG GTGGTGAGAA	TTGCGAAGACGTTTACAAGCTCCAAACCTTTCCACGAACAATATTTTAGG[A/G]ATTTGAAATATAT TTCTGTAGTTCTACCAACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGTGTAATTACTAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAG[A/T]AACCTTCCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G CTT	CAATTTTAGA AGTTGGGTTT G	AAATCACTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTCTGTGCTTAACCTTCAGTTACTTAAGACCTAAAGACAAAGTGGTATCATCATCATATTTTGT ATGTGGGGCTTTTGG
EST13518 2	45 C G	---	---	GAACATCCTCCAGTAGATTGAGGTAAATGATTTCAGCATTTA[C/G]ACTTTAAAAATTTACCTCA ATGTTCCCTCGGAGTCGTCATAGTTTAAATGACTTCGACCTTCCTTTATAACCTTTGATTG
EST13522 8a	66 A G	---	---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCACCGGAGTGTCTGGAGAC[A/ G]GTTTGAATTGTCACAACCTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAT[C/G]CACACAAAGGAATAAGGAGAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101 C G	---	---	AAGATTACGGACCATAGAAGCTGCCCCCGACCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAAACAA[A/C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G	---	---	CCCTAACCATCTGTAAACCCGAGCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G	---	---	CAATGGTGTCCTCATGTGAACATAT[A/G]ACCTATTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGAOCGAAACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTTGGCATGCTAGACAGAGGCAATAT[C/G]TTTTGAAGATCTTTTAAAAAT ATTTGACTTGTTCCCTTCACACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TAATGACT	TTACACTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATA[A/G]AGTACATAATGGG AATTAAGTAAATCTTTAGAAGTCCCGAGTTTGCCCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCAAC ATACTGGTT	CGGGAACA GTACCGGAA	TTTGCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCACTGAACCAAGTAAT TCACAGACAATGGCGCAACCACTTAAATAAACTTGCCCGTCATCACCCACCATCTGGTT[A/T]TTC GGTACTGTTTTCCCGTA

EST15420 6	109 C A ...	...	GGATAGCTGA	TTTAAACCCCAAGACTGTAGATGTCAGGACCTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTCATCATAATCATATAGCCAAGGACTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	...	AGACAACAGAA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAGACGTGAAAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	...	GGTTTGCCAT TTCATTATCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T CACTGTAAGG	...	GGTGGAGTCT CTGTTCTCTCA TC	CTCTTCTCTCCTAGACGTGGAATACACACGAGATACAGTATCTGGAGATGTAGCAGTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG[C/T]GATGGAGGAACAGAAAGATAGAAGATTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	...	TCCTGAGATGT CCTTTACCTGA AATCCTTATTA G	AAAAATGTAACCTTAGAGTTGCCCTCTTTGTGTCACCTTTTCTGAGATGTCTTTTACCTGAG[G/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C ...	...	...	CAGGACTTAAGGTCAATTTTGGCTGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGAT[C/T]GTGA CAGCACCACTCGGACCAGGAGTCTGAAATCGTCACACTAGCGTGCCCGAGCCCTTTTCTCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C ...	...	...	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATTCATTTTGAAGCTGTTTGTGACGCC TTTTCCAGAAAAGCCGCTC[G/C]GGGTTTCTGAACCCCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ...	...	...	CGTCTGAAGTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[T/AAAGAGCCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ...	...	...	ATCCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTCACATTCCCA GGGGTCCAAATAATGCAACATTTTTCACCTGCTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGTTGGCTC
EST16104 9a	83 A G ...	...	...	TTCTTTTAAATAACCCACAGACACCCCATGACACTTCCAATTTACAGAGCAAAAAGTATTTGCAG CTGGTTCTCCAGGGA[G/T]TGGCCCCGAGCTGGCTCAGTTACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ...	...	...	ATGGTATAACAAAATCAGTCCAGGTTTTTTT[C/G]TGAAACAAATGATCCTTTGGCTTTCCCGTGGC CTCCTAAACAACATAAACACCCCTCTACGTTCTAATCAGTCAACCTAAGATATCGAGTGGCAAGT CITTCACA
EST16118 0a	32 C G ...	...	...	ATGGTATAACAAAATCAGTCCAGGTTTTTTT[C/G]TGAAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTAAACAACATAAACACCCCTCTACGTTCTAATCAGTCAACCTAAGATATCGAGTGGCAAGT CITTCACA

[illegible]

WI-16879	79 C T	GATACAGGCC T A T A T T C C C A	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACTCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
WI-16882	99 A G	GAATATGCCA G C G T C T C T G A C	GACACATGTC GGTAAATCGC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAATCTCCCCCTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAATGAATGCCACGCTCTGAC/N/G/GCGATTACCTGACATGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG G C A G G T T C	AATGTTCTGAA TTGACCAAAT TAA	GTAGTAAATGTTTCATCACTACCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/GA/TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTGGCCTGT G T T G T T C A	GTCTATCTCT TCTAGGCAGTG GG	TTTGTGTTGTTATTTGCCCTCCCAACATCAGACATAGTTCCATGAAACAGGAACCTTTGGCCTGTG TTGTTCA/C/TCCCACTGCCCTAGAGAGTATAGACA
WI-16910	74 G A A	AAGAGTAAAG A T G G C G T A G	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGA/GA/GTATCTGTTATAGAAACGATACCTTCACTTTGGGCCCTGAACCCAGTGAAGGT
WI-16918	93 C T	CAGGCATTAA C A C C A G C A C	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATACCACCATCTCTCTGCTACCACAGAGCAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACCGTGACAACC ATGAAAGGTCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA G C C T G G G	ATGTGATTGCC C G T G G	TGAGTCAAAACGATCTTGACGGGAAAGCTTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGAGACACTGGGG[AVC/JCA CGGGCAATCAGATGAGATG
WI-16947a	58 C G	CATGGAATA G G C C T G G A G	GCCTCAGCCAA A T C C T G T	TGAGTCAAAACGATCTTGACGGGAAAGCTTTAGAGGTCTCATGGAATAGGCCTGGAG[C/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGAGACACTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43 T C	AAATGCACAC T A C A T A A C A A	TGCAAGTTATC A G T A T A A A A	CATTGTTTACITTTAAATGCACACTACATAACAACCTAATAT/CJCTTAACTTGGTCCAACATATTT AGTAACTAATAATGAGITTTTATCTACTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA G A C T G A G G T A	CATGTTGATT C C A G C C G T	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/CJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	AATAGTATT ---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGAG/JG/GTG TAGGACTGAAGGGAATGTTTGGGGGTTAGGAA
WI-16992a	46 G A T C	MGCACCCAG A A G T A C A C T G	CACATTCCTT A C A G T C C T A C A	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGAG/JC/CCCTCATCTGAGATGTG TAGGACTGAAGGGAATGTTTGGGGGTTAGGAA

WI-17010	23 T C			ATAATACGGT GTTTGAATGT CA	ATGTTTCACAGGAAAGCCATGT/CJATGACATTCAAAACACCCGTATTATTAGAAGCTCATTTAAT
EST17127 9b	74 C T			CACTCGGCAC AGACAGAGT GGTG	TGTTTAATGCAGACAAAAAATCAAGGCTAACTAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA GGTCCACG
WI-17040	94 T C A			GGGAGGCGAGG GGTG	ATTCGGTCTCCAAACAGCATCCAGGCGGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGT/CJTJGGGAGCCATGGGACCCCTGCCCTCCCGAGGCTCCTAAGTAACAAC
WI-17044	47 G T G			GGACTATGGCT TATTCAGTGAT G	CACGCGTTCAATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATCGAGTTTCC GAGAAATCTCTTATCATCTCAAGCCAGT/CJCATCACTAGTAATAGCCATAGTCCAGTCTCGTTTTTCC AAATCTTTCTCATATTGT
WI-17044	47 G T G			GCCAAGGAT TAACGTATAG TGTTAAGA	TTGTTTGTGTTTTTCTCTCTGCCAAGGATTAACGTATAGG/GTJCTTAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCAGTACTCTCTGCAGAAATGGCAGGGAATCGAAT CAAAAGAAAAGCAAGTG
WI-17021	62 T A ACTC			TGGACTTGTCA GCCTATAACT TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACAGCTATAACTACTCT/AJG CAGCTGCCACTAACTCTACAGGCACAGTAACACTACTTTATACAGGAGCACATGCCAAAAGTGCCTGG GAGGTGCCAATAAATCA
WI-17065	90 T C T T			CCAGAAAGGA AAGCATAAA AATGAATCCT	TGTAAMAAATGTAGACATGGGGGAAAAACAATCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAGGAAMAGCATAAACTTT/CJAGGATTTCAATGTCTCTGGGT
WI-17066	32 A C T			GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAAACATCACTGTTT/CJATCCAGAACATTTTCAACATCTCAAAAAGA AACTCGACCCATTAGCAGTATCCCTGTAGCTTCCCTCATAGGCAATGGCACTGCTGATC
WI-17074	86 T G ---			---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCTACACAGGCCTT/GJCTACATAGGAGTATATTTGGCCAAGACTCACCACTAGAAAGTGAAT
WI-17104b	108 T C ---			---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGGAGCTTTCCCATTCATCCCA AATCAGAAAGCAGTCAGTGGCCCCGTGTTCCAGAGCGGCTT/CJCTCTTTGTTAAGAAATTA
WI-17114a	37 T C			TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAAACAGATGTTTCCATCAAGGACTTTGTTT/CJGTCCTTCACTCTGCTATTATAATAC AAGCTACCTCCCAGGCCAGATGCTCTAAGTCTAAAGAAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G C T C T			TTCTCAGAATC AGATAGTCTTC G	CGTGGCTGGACTAAGTGTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTTT/GJCATATCTCCAGGATTTCTGAGAAGGGCCCTCTTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT			CATTTCTTTGT AAAAATAACAA TTTTGCCTT	GAAATCGAATACGTCCATTCTTTGTAAATAACAATAACGTTT/GJAAAGGCAAGCAAGATTCTGT TAAACCAACATTGAAAAGGGACACAGGGAGGGGAGAGGAAAGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAA

WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCTCCCTCCAAATTCATTAGCTATGATGGAGTTATCAGTTTACAGTTTACAGAGCGAAATTA
WI-17180b	81 C G	CTGAGGAGC	CAACTGCTTC	GGCAGGGGGTTTAAATATCTGATGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	TGCA	---	GCAGTTGAAATTTGAGGG
WI-17156	54 G C	TCCCA	TGTCTCTAAA	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTTC/CJCCCCAAGTCTCGTCGCA
WI-17149b	79 T C	CTTGTCTAAA	CAAGAAATAT	CAGGCTTCAACAATTACCAACATCTTGCCCATTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17149a	48 C G	AGGAGGACACA	ATATTGATTC	GGAGTC
WI-17197	67 G A	CTGGGCTAC	TGTGGAA	TGAGGTAGCAGGGCATTCTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTC/CJTTCACAGA
WI-17198	38 A C	CTAGTTT	CCACGACGTG	ATCAATATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
EST18753	27 C T	GGTCTCAT	CATGA	TAATATCTTG
WI-17108b	74 C T	CA	GGTGGTGGT	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGGAA
EST19067	41 A G	---	GCATACC	ACCCAATTTGTCAT/CJGTGTATGAACACTACAAAGGATGGGGAAAAGACACATTTTCTCACA
EST19067	40 A C	TTC	GCATACC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACAT/CJGTTCATGCACGTGCGTG
EST19125	28 A G	---	GCATACC	GAAACCCAAATTTGTCATGTGTATGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAAATGCACATCC
WI-17108b	74 C T	CA	GGTGGTGGT	ATTTTGTATGTTGCCCTGGGCTGAGCTCCAGCAATCCCTCTGCCTCAGCAGAAAGTAGTGGGGCTAC/C
EST19067	41 A G	---	GCATACC	A/JGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAATAGAATATTTGAC.TTTTAGATGCGCA
EST19067	40 A C	TTC	GCATACC	TGTAATTCAGTACTTTTCTCCCTCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC
EST19125	28 A G	---	GCATACC	ACCATCTCTGTTTGAATTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAAATGCACATCC
WI-17108b	74 C T	CA	GGTGGTGGT	TTC
EST19067	41 A G	---	GCATACC	TCCCTATGCTACCCAGGCTGGTCTCAT/CJTTCAGGCTCATGGATCCCTCCTGCTCCCTGCTCCCTGCTCCCTGCTCC
EST19067	40 A C	TTC	GCATACC	GATAAGACAACTGOCACAGGCCCTGCCCTAGGAGTAGTCTTAAATGCCTGATGGTGGG
EST19125	28 A G	---	GCATACC	TTATTTTAAACATAAACAGATGCACCTTGGTTTAACTTCTGCTGTTTACATTCCTGCTGTTGCCATTGCTCAAAGT
WI-17108b	74 C T	CA	GGTGGTGGT	AAACAC/CJTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT
EST19067	41 A G	---	GCATACC	ACACAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/GJGTGGCATTAAAGTACATTCAACT
EST19067	40 A C	TTC	GCATACC	TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
EST19125	28 A G	---	GCATACC	ACACAAAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JAGTGGCATTAAAGTACATTCAACT
WI-17108b	74 C T	CA	GGTGGTGGT	TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
EST19067	41 A G	---	GCATACC	CTGTTTCTCAGAGATGACACTGCCAACAA/JGJTCACAGTTTGCATACAAATACAGTTATGATTGGC
EST19067	40 A C	TTC	GCATACC	TATTCACAAATTTACAGTAGTGTGTTTTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT TGGACCGA	AAGATTTTATC TGGACCGA	GTGTGGAAGCCGGAGTTTATTATTAAATCAGTCTCTGTAAGAACTCAGGGATTGAGGTTTTTA AGGATAACTTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTCTGATTGTCGGGGTCCAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCTCAGAACTTCTCAGCCCTGAGCTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGAGTGGGACCA
EST21904 b	128 G A	TTCAATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGGCTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCAATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTTTCGGGGCTGTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCAGTCAACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTCTGCCATTCACCGCATCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAATCCACCACCTGTAACACAG TAGCATTCAATGGTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAATCCAGTAAATCCAGTAA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT	TGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATTCACATAAAATCCACCACCTGTA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGCAGCACCACCAAGGACGTGTGTCAGGGGCAACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCTTCT TAAGCCCTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGGTTACAGT TAACTGACAGA	GATGTTAATGACTTCTTTGAGATATGATGGAATAATTCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCAAGGTTTACCAGTGTCTGAGTTAAGCTGAAGCTGAAAT CTGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TATCTGCACA	AGTTTCAGTT GCATGAATTTT	TATCCATTTCAAGAAAAAATGACTTAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACAGTCCATTTGAAGAAAAAATTCATGCAAACTGAACTATGCTTT



WI-17623	46 T C ...	...	TGTGGTTTTAATTTCCCATATAATTAATGTTGGGCACATT/CJGCAATGTCCTACTGGGTC ATTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTGCCCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46 T C ...	...	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT/CJGGCAGTCCAACTTCT TGGGAGGAAGTAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG/CJAJACAATCTGATGGGCAGTCCAACTTCT TGGGAGGAAGTAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ...	...	TCAGCTTTAATTTAAGGGACATGTAAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTAGACCAGTAACAACAACCAAGAAAGCAAAAGTCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ...	...	TACTTCAGTTTAAGGCAATTCACACAGAGACTGTCTC/JGJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCAACATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ...	...	CAAGGATTTTATTTGTTCCCTAAAGTAATAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/JTTCACATGGGTGACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTGGCACTTTGCAACAATTAATAATTTATC/JAJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTTACACATTTCTGTTAACAAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC C	ATCTTAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTG/CJTAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTAGGAATGTTT
EST27788 3	100 A G ...	...	ATTTATTAGGCGGTACAATTCGAAGTGGTAAGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACCTTTACATTCAAGGAG/CJGJGCTTCCAGACAGCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAATTTT C	GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAACTTTCCTTCTGTTGGATCCCGAGTGCAGTGGGAAGTCATCAGAACCCAC/CJAJGTACTT GGAGTACCTCTCTGCACCAAGATAGTGGCTGATTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A AC/ATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTGAGATACATTCCCAATGTAAACAATAAATTTCAATCTGTACACACAATC/JAJAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/CJAJAAAAGAAATGATCAATCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGCCAGGGACACACCACCGCGTCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG
EST28036 4	37 T C ...	...	

EST28483 7	31 T A	GGAGTAAAG GTGTTCTCT	TTTCTGCGATT TATTTTATAC CA	CAATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACAGACATGAGTTGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCGCTCC TGTC	TGGGTGGCAG TGTC	AGAAATGGTCTAGTATCGTTCAGGATTCGGTGATGGGCCCTCCCTGTC/T/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG AGC	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATT/A/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTANGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACATTAAGCATCATTTGTCACCT/G/AJGCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTGTTGGGCTTAGGGCTACCCCTATTCAGCAGGTGCC/A/GJTTATTT TCACITGGTTACGTCGTGAAGGACCGTTCCAAATGAGGTTACAGTACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	CTGCCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTTATAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAVAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGAAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTTGATGCTTAGGGAAGATTCTGATTTAGAGATATTAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/G/CJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTAATAATCC/A/GJGGATTAAATTCCTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGAA GTTTCAATAATAGGTAGC/G/AJATAACAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGAA AGAGTTTCAATAATAGGTAGGAGTAAACCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATAATTGTGCTTCTG/AJGCGCTGTTTCTTATACCCCAATATCATAGAATT GTTGTGCTTCTATAATGTTTCAGCTTCAAAATCTTTTGTCTTAAICAAATCCAAATGAATTACCTGAATT TTCTCCTCTGTTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACTCTTTTAGCAATGACA TCGGTTGTCCAGCCACAAC/TGGAGGTGATTTGGTGGGAATCTTATCACAATTATCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCT/GJAACGTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST31968 8a	75 T C T	GGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/GJAATATGGGATTTTCTGCTTAACGTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTTCCCTCCGACCAGATGCTGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTGTAGT/C/GTTCAGGCCCATTTGAAATAGCAAAAGGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACTTGGGTGTGCTTAAGTTTCTGGTCACTGCAGCCCCC[AVG TTCTGATTAGGGAGCACCCCAAGCCCACTACAATATGGTCTTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GAAGACTGGGATTAATTGTAGGAAATATTTACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATCCTAAAGTCTGGGATGACTTTCCT/GJATTCATCATCAAGTAGAACCTTAAGCCAAT TCAGAATCAGAACTCCTTTTGTCCATCAAAATCCAGCTAACTCCAGCTGAATTTAAATGTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAATA/T/AJCCGACTGAC TGCCTCTTAGTCTGTGATC
WI-17860	121 T A	TTTGGCAGCA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATGTT/AJTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCAGATCAGAGTAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	GAAAAAAAAGTCAAAATGTGTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATCGCCACGAGAG/GJA/ACTGGATGCCAAAGAGATGG
EST33301 4c	80 G A	---	---	GAAAAAAAAGTCAAAATGTGTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT[GJA] ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A	---	---	CTATCCAAAAGATATTATTGCAGCGTGGTTTCAATACTAAACA[GJA]GTAAACAATGCAAAATATT TAACAATAAATACAGTGATTAAATAAGCCCATGGCATATCCAGTTGATGTAATACITTTGCAA
EST33460 1	44 G A C A	ACGGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATT GCATTGTT	

WI-17904	50	A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAMGCGATGACAATAAAATGAACACIAGTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCGAGTTAAACAACAACACAAAATGA GTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGIGATTTTATTAGTTGTCTCGTAGTAGTTTGGTATTTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34149 5	69	A G A T	TGCCAAATAC TCAAGTGTGA	AAGTAAATC ATAAAATC	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC[A]TACAAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95	C A ...	GGACCATATG ATATATAACT	---	GGTACACAAATTTTAAATGGAAGGAACCAACAGGTATGTTGAAGAACAATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTTAAAGC[C]TGGAAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17982	98	C T C C T A A A A G C	CCTAACAGC	CCTTCC	CTCAGTAACCTCGGTGTATAATCTGCCATTTTATTGATTTATTTATGATAAAACAACCTCTCATTTGTA AAACAGCTAAGGTGACATCTCCAGACCCCACTGCTCCCTGTAATGTA/CJCTGCTGAGAGTCC ACAATTTGGAAATCCAAT
WI-17993	118	A C ...	GTAGAGGCGA AGGAAACAG	---	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAACATCTCCCAGGCTCGCAGT AGAGCGAAGGGAACAG[A]GJGCTGCCCATGTGCCTGCTCTCTAAAGAGCCACCCCTCAGGTTGATGT CACTGTGGGAGACGGGT
WI-17136	33	C G ...	---	---	ATTCTTTATAAAACACCCTGCTCCCTAAAATGTC[G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24	A C ...	---	---	GCCACTGAAAAAAGGTGCTCTCC[C]C/CJGTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGATTTTAAAGGAGTGTGATGCTCCAGGAT TCAAATACCTTAATCA
EST35164 8a	57	A G C C C C	CACAGCCCTGC	CCCTCTGGATT CTGAATCTCAA	TTGAAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCAGACAGCCCTGCCCC[C]GJCTTGA GATTCAGATCCAGAGGGTCTCAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCTCTTTG
WI-18052b	67	A G ...	---	---	AGGGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTATGTACGAATCTTGGTTACACATCTTAC A/GJACAGCAGAGTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T C A T C	CTCAGGCAGCT CTGCTGT	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTATGTACGAATCTTCTGTTTACACATCTT AGAACAAGCAGAGTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G A G A T A A A A	GGGAGTGGG	CGTCAACCTGC TTCCA	CTGTTGTGCTGAGAACAGAAAGGGGTCAAGGGAGTGGGGAGTAAAA[G]ATGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTCAGGTTTGTAGCAACAGAGGTAATG

WI-18064	54	GA	AGTGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGCCAAATCATCTCTCAAAACCCTGTGGTAGCTGCTAAGCTGTATTTCAGAG(A)GAATGTCAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTCTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	TCAA	GCATAAAATT TTCCAGTTGGT	COCTCGGCAOC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT(C)AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	AC	GTGTAT	AACTCACTAG TTACTCAGAGT GGTTTTT	AAACCCACTACTTACTCAGAGTGTGTAT(C)ATATTAAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTCTGTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	CT	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTTGTAAATTAATACTACTATGCCGIG TTTGACITTTAT(C)TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	GA	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTTGTAAATTAATACTACTATGCC(G) AJTGTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T	CACTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTCTTGTAAATTAATACTACTATGCG CGTGTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT GTGGCCTCTATAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTTCTG(A) TGGCTTTGTACACGGGTTTCTTCAAGAGGAAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63	GA	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGACCTTTGGTATTCCTC TTCTCTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115b	71	CT	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGACCTTTGGTATTCCTC TTCTCTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70	CT	TT	A	TTTTGAGAAGCCTCTGTAAGGCAAGGATGCATTCAAAATGGCTTTGAGGATTATCTCTCTTTA GGTAAATTTG(A)GTAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC(A)GTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18136	78	AG	---	---	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC(A)GTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18169	115	A	GGAAGCTC	CCATCTTCCG GAGTCTGCTT GTGCTCCA	TGAAAGAAGTCGACACAGCGGACACT(GA)TCAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAATCTCTGCCGA
WI-18190b	26	GA	---	---	

WI-18190	62	G A	...	...	CGTTTACCAT	TGAAAGAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGACAGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A C	CAGATC	...	TTG	GACAGTGAACAACATTGAAACACAAATACACAAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAATATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAAC
WI-18215	78	G A	CTGCOCTC	...	CCTCCCTCTCT	ATTACATAAGCATTCTCCTGAGTACAAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCT[G/A]GTGTGGGGGGGAGAGAGGGGATTCAGCAATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T A	AA	C	TTTCAAGGGT	CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGTATACACTTAAGT[A/G]AA CCCCGAAAACCTTTATTTGNAATTGAAGTTTTGCTCAGAAACTGGGCGAGAACTTTTCACATTCTG AC
WI-17892	76	T C	ACA	...	GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C/T]CTGCTCAGTAGTCTATTACCTTCTGTGGCATTTCCGGCAGAAAGTGGC
WI-18242	30	G A	AATCGTAACA	...	CITTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGMATGTTCTTGGCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C T	...	...	...	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	...	...	...	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	TTCAAA	...	TTTGCA	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	...	...	GGAGAAAAGG	CTGAGCCTCTGGATATGTGGTTAGTGTATCAATTAATTTGGAAAGCTGCAGCTATTGTTATTC AAAT[A/G]TATCTTCTGCTCCCTTTTCTCCTTTTCTGGGATTCATCTGCATGTGTATA
WI-18330b	66	A G	...	...	GAGCAGAAGA	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGG[G] A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAAACCATAAATAAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGA[G]A[CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C A G A	AAATTCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAAATTC AAGCCATCTACAAAAGATT[C]TCTCATTTAGGGCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTATTACCTACAACAAGTAAGGAGACAGCTGGGCAGTTTCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G]A[IGCTGAGCCATTGTATGGGAGGCAGA GT
EST37624 6b	102	G A ---	---	---	GTGGCAAGCAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	C T ---	---	---	GTGGCAAGCAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCAC[CTGCTGA TGGCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	C G C A T C A A	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGTGAGGTGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C]G[TCATCTCAGTCTTGAGTCTTCCAGCCAGGTCCAAGCTT GTGGACACAGAGACAAGCC
WI-180129	117	A G ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-180121	113	G A ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTC CCCTT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAAATAA	GCTAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCACAGATAATTCCTCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG[A]G[A]TAAGTTATTATATCAGCTGACTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T	GAATAC	TTCCG	CACTGCACTCT GGGAGC	TAATAAAACGTGACCCAAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATCTCGT/GGCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C	TT		TCTGTTAGGAC TTGGGGA	CCTGACCTCCTAAAGATCTTTTC/TTCCCCCAAGTCTCAAGAAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATGTGCTGCTCTGCTTTCAGCTTTGATTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T	CA	AA	AGGAAGGTA GTATAACACAT	AGTGGTCAAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/C/TCTCTTATGTGTTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA
EST38616 9	101 C	G	CTTC	GAGGAATGGAT GGTGGC	OCATCTAGGCAAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGCCTCAGCCCGGGGGGCGGCTGG AGTCTCGGGGGGGGGGGCTGCTCGGCCCTTC/C/GGCCACCATCCATTCTCTCCAGGGG
EST38652 8	59 T	C	CAATTC	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTTCTGTCAGCAGGAATATTACGTCTGAACCTGGGCAATTCATTC/CJGCGTG GTATTTTTTCTTCTTCAATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T	C	GTATTA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTAATATATCAGTTTTTACATAT/CJAGATAGAAGATTAAAGACCAT CACTGAGTCAATAGTCAAGGAGGAGATTAAAGATTGGACCCAGGAGGTTGGTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAAGGAGATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCG/AGAGGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTCTTCTGGAAA
EST38707 9	75 A	---		---	GAOCTTGTTATCTTCACTAGAGGGGAGAAGATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATGG/AG/CCTTAAGTCCAGCATGGTGACCTAAACTCAGTTTAAATCTTGGCC TAGCAGCACC
EST38759 2	86 A	G	GGTATATG	TCACCATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCAAGCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38775 1	40 T	A	C	GGCTTTGCTCT GAATCAAA	
EST38815 4	91 C	A	CA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTTCATTTCAACAAG TGTTTATGAGAACCATTAACA/C/A/AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C	T	TGAC	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTCTTACAACCTTCTCTCCAAAGTTTGGGGTGTTCATATTTGTTATTTGTTATTATTA TTCAACACGAGTAAAGAAACTCATGA/C/TTTCTCTTGGACTCGCTCCTCTCCCAATCTCGAT ACCGACTGCACGTGTG
EST38865 2	72 T	C	TGTCGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC/TCTGTGTCCTCGTCTTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTCAATAAA TCTCATGTCT CA	CCATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAATTCCTGAGGACATGAGATTT ATTGAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTTCCC TTATCAATGTCACTCACACATTTCTTTATTTTATTTTATTTTCTCAAAATATCGGATTGTTC TCATGAGAAATAGGCTGAGGAGCTGGCAGCGAGCTCTCTCAAGCCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 GC	...	...	TTATCAATGTCACTCACACATTTCTTTATTTTATTTTATTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGACGCGAGCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TTT	CAA	TA
EST38909 5	47 A G	GCTAAACG	GGTATTGTG ATTCCCATCT T	GCACTAACTAACITTCATTTG'GGATTGCACAGCATGGCTAAACCG[A/G]TAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAACACACTACACATCAAACTTAAAGGAAATGTGTTAGTGTGACGTTGAG GGAACTTATAACCTCAC[AG]CGCTTGTTCACAAACACAGCAGACAAACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	CAC	GAACAAGCG	TAAACATCCCATTTGAATTCCTTGTGGG[G/C]GGGGGGGGTGGAGATTGCAGTGTCTCAAGATAAA TATCAGAAATATATCAAAACITTCAAATTTGTCTATGCATTACACACTGACATGAGCCACAAACAATT CCTTTCACAGGACTGTAC
EST38955 5	30 G C	GGTGG	CACTGCAATCT CAOXXX	CCTGCTATGATGCTGGGAGATCCCGGACCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGCTGG CCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATAGGCTGACATCCGCAACCT C
EST39002 0	42 G A	TGACC	CTGGCAGGGAG CCTG	CACGTGGCCCTAAGTTCCGGGTCTTCTCAGTCTGGATGGCTGTGGGAAAAAGCTTGGTGAAG GCCTAAGGAATTTGAGGGGAGGGGGCGATGCCGCCAGGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	CCTAAGGAAT	ATCTCGGCTGG OAGC	AAAGATAATGTCAATCACAAACGCAACATATAGAAACATAAAGAAATAAGTATCCACCCCTAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCA	GAATGGTTGT GAAAAATATA TTGATAT	GGTGTCTTTCATGATTTTCTCATTTCTCTATCAGGTTTCTGGTCTTTGTCTCAATTTTAACTT T/CCTTTTATATAGGGAATTAGCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCCAGTT
WI-16403	69 T C	ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GCITTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGATTTAGAGCAATAGGTGCCCTGAA
WI-16406	24 C T	AGG	CCAGAACCAG ATGTGTTTAAA AA	

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCCTTTTATTCATGATTTGTTTCATCTGAGAAATAAATCTCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTCTC TTT
EST39294 4	63 G T	CCTGAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAATTGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACAGGCC AGCTCTGCTTGCTGTCAT
EST39366 2	72 T C		---	AGAAACACATTCGTCTGATCAGAGGAAGATGTATGTAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAAATGGAAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCTAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAAATTCCTCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAATGCTTCTTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177 23 A G			---	ACAAGTGACATATCCAACCAACCI[A/G]TCCATCCCCACCTGTGCCCTATCTTCTTGTTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCCCTCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTTTGATT	GGTCCCTTAG AAGCCACC	AGGTTCTCTGGTTGCTCCCAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTTCTGCATT TTCTGGGTGGGCCCTAGGTAATTCGTGTTGCCCTTGGTCCACAGACACAATTAAGAAGATCAGGTCT GGCTGTGTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTCCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/J]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAACC	AAAGCCCTGTAACTGAAGCTAGACAACGTCACACTTTGGAAGAAAATAACAGGAACCTATTTATAT ACGTAATCACITTTATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTTCCAGGATTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGCC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAA TGCAGGAGGGTGG[C/J]AGAGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGAAGACCCAG
EST39501 0	81 A G	AAAGATTCCCT GTAGACATCT AACATTAG	CAC TTGCAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTTCAGACATCTTGACCAAGCCATAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGCAAGTTCAAGTCAACCAATTC
WI-18387b	84 A C		---	CACAAATGGGACTGCTGAAGAGTGAGAGTTGGACCTTACTTTTGGTGACCCCATACATTTGTGGTCA CATGCTTAGCCATAG[C/J]CATGGTAACATTGACTATGGAGTCTTTGTGAAGGTGTAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCCTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	GTACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTAAGAGTGTAAATGTGGCATG
EST40601	78 A G	GCGTGGAAOCT GAAACAC	TTCTTGGGA AAGCGTC	GCTATGTAGACATAAAGA TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGTGACTCGCGTGGA ACCTGAAACACIA/GIACGCCCTTCTCCAAAGAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTCAGGAT	GCACACCCCTC ACACTGTTA	TCCATTCAAGTGATCACATCTTCAGGATAGGT/AGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGG	AAAAC TGATTT GTTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/C/TGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTGAACATCAAAAGAAATACAAATATATTTTCAAAATTTCTCATCAGTGTAAATTTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC	AAATCTCAGC ATTGCTATAAG	AGAGAGACAAACAGAAAGATAAGGGAAMTGGGAAGAACAGAGTGAATTAAGCAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCNAAAAAATCAA/T/C/GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG	CCAAGATTTC TTTAAATTCAC	AGAGAGACAAACAGAAAGATAAGGGAAMTGGGAAGAACAGAGTGAATTAAGCAATCTTGGA GGATTCAAGATTCCATTAAACAGGAAGTTTCTCAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATTTC	---	AGCTGATCAGCTGTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA/AC/TGCACACAAACAGGAGGTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CACCTGTCT AGACAGATTTC	CCTCCTGTGT TGTGTGA	AGCTGATCAGCTGTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA/AC/TGCACACAAACAGGAGGTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGMACTATAAAAAGGAAAGGAAGAGAAAGTAATCAAGGGAGGCCAAAGTG GGAAAGCTGTATTGCTGATTAACGTGCTTCCAGTCTCTTTGGCTCTAAGTGGGACTA/C/TTC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGTGCCCCCAAGACATTATTTTATCTT AAATGTCCAAATATCTGCCCTGATGCTGTGTGTGTGCACATTTGGGGCCACAGT/C/AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTGTACACCACAAATGGCAGAGGTGA/AG/TAGAACCCTATCTCAAAGCCTAAVA TATTTACCATAACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGAAC	TGAGGAGGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG/C/TGGT CACTCCCATCGTGGCCCTGGCCGTCCCTCCACTCACCCACACTGGCCAGTCCACGTTGAGGT

WI-18491	109	GA	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCTTGTATCC	CATAAGATGAATACATGAAGGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAAATGAC(G/A)GGATTACAAGAAATGACACA GGT
EST50757 b	79	CT	GAGCTGAGG CTCTCTCT	ACCCTTCAACC GGCC	AGCCCCCTCCACTCCACTCTGCTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGACGGCC(C/T)GGCGGGTGAAGGTCAGAGA
WI-17875	103	TC	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTACCAGGTGCTGAAGAAAGTGTCTTCGTTTAAAT TGCCAAAGCAGGAGTGGACATTTGGATGGTGACTT(C/C)CCTGGTGGTTCCTCCATAGATTCAACCAT TGCTCTAATGGTGCTA
WI-16543	67	GT	AGATAAACTA CATTTGGGTT	GATTCATCAT ACAGGGACTT	GATCCATTACCTAGGGTAAATCTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTGGT G/TAAAGTCCCTGTAAATGATGAATCAAGATCCTCAAGTCTGCTTGCACCCCATTTAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	CG	GCCAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCAAAACCATCTCCCTGACCCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCTGCTGTCGCAAAAAGGTTGGGAA(C/G)TCTGGTGGTACAAAAAGTAATT G
WI-17690b	79	AG	AGGCAATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATT GGCTCCCTATGAGATTACAGACCCATAACTCTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	GA	AGGCAATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTT(G/A) TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCACACTCTGCTATGCTGCTG
EST51717 b	128	CT	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCTCCAGATTATTTCTGAAGTGAACCCACCTCCGACCCCA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGCGGAAGACAGTGAGCTGT(C/T)GAG CTGGATTATTGCCCTCAA
EST51717 a	39	CT	...	...	GATCCAATCTCAGTGTCTAACTCATCTCCAGATTATTTCTGAAGTGAACCCACCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGCGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAA
EST53012	97	CT	TGGTCACTTTG GGCC	GGCTCTGCCCA GGCC	TTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGCGAGGAGGACAG GTGTCTGGAGTGTGTCACCTTGGGGCC(C/T)GGGTGGGCGAGAGCCACTGGGTTTACATTTCTCTGT GGGAGGTTGGGACAC
EST53349	96	AG	TGTTGAAAGC AGTCACAATG AGTAC	CATCTGGATAT CTTGTACAT TT	AAACTGCAATAACAAAACAAACAGAAAGTCCAAAGGCTAAAGCTAAGCTAATAATACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC(A/G)AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	AG	GGAGACCTGC AGAACTTAAA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC(A/G)GAGCATTTATGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAGGGGAGATGGCC

[illegible]

EST98276	61 A C ...				GAGTCTTGCTATGTTCCAGGATGGTCTTGAGCTCGTGGTTTCAAACAATCCTCCTCCTACGAGC
b		...			CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276	22 A C TTCCAGG	GTC TTGCTATG	AACCAGGAGCT		GAGTCTTGCTATGTTCCAGGAG/CJTGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTCCTAAGC
a			CAAGACCA		CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53 A T ...		...		GCCTCCAGCTGCATGACTCCTAAGCCATCATTTTCCGAAGATTTTGGCTAATTTG/AJTJAGTCTTACAA
					AGGCGAGTCTAGTTTACCAGGCAAGAGGGGGTTGTGTTGGGAAGCGCTGCTATCTTTGTTTCAAAAC
					TGTAAAGCAAGTTCCCTC
J02931	138 G A GTAA	CAGCATTAGTC	TTGGAATTGGT		AGAGGATAGAATACATGGAACGCAATGAGTATTTCCGAGCATGAAGACCCCTGGAGTTTCAAAAAA
		ACTTTGAAAT	TG TAGTACCAT		CTCTTGATATGACCTGTTATTACCATTAGCATCTGGTTTGACATCAGCATTAGTCACATTTGAAATG
			T		TAAC/G/AJAATGGTACTACAACCAATCCAAAGTTTTAATTTTAAACACCATGGCACCTTTTGCACAT
					AACATGCTTTAG
L41680	88 G A A	GAGAAATCGA	TTTAGAGCACT		GGATCCAAAAACACGGCTGGGTTTCAGCATCCACCAATGAACCTGAAGGGTGAATAAAGGACGTTCAIG
		CTACCAGCTG	TTGCAGGTATT		AGAAATCGACTACCAGCTGATG/AJAATACCTGCAAAAGTGCCTCTAAAAATTAATATTTTGACTTT
			T		AAGGGTCTTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGTATATAATCAGTAGTGTTTACAA
					GATCCAAACAGTGCACCTCA
M15795a	84 C G ATATGTAGA	CAAAATTGTGTA	TTGGACTTTAT		CTTTCTGTCCACCAAAATTTGACCTCTAAGTACATATGTAAGATATTGTTTTCTGTAAATAACCTATT
		CCTCTAAGTAC	TC TTTAAACAA		TTTTCTCTATTCTCTC/GICAAATTTGTTTAAAGAAATAAGTCCAAAGTCGATCTGGTCTAGTTAAC
			ATTG		CTAGAAGTATTTTTTGCTCTTAGAAAATCTTGTGATTTTTATAATACAAAGGGTCTTGACTCTAAAT
					GCAGTTT
M20472	103 C T C	GTTGAGTTCCT	ACAAATGAACA		AGAGCCACCCCTGTGGAACACATACATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTC
		TTGGACCAAA	ACTCTAAAGAC		ATTGGATTAAATTATGTTGAGTTCCTTTGGACCAAAAC/CJTTTTTTGCTTTAGAGTTGTTCAATGTTTG
			AAAAA		TGATGTCATGTTTCCCTTCCCTCAACTGTGTTCCCTCGCATTCAGAGAGGAGGAGGAGGAGGA
					CCCTCTGACCTGCAGGCCAAGACAGCAGGACGAGTTGGGGAAGCCCTCTGCTGCCATGGT/CJGT
			GCCTTCGAGA		GTCCCTCTCGGAAGGCTGGCTGGGCATGGACGTTGGGGCATGCTGGGGCAAGTCCCTGACTCTCTGT
M32315b	129 T C CATGG	GCCTCTGCTGC	GGGACAC		G
					TTCCAGGAGCAGCAAAAGGGCCCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATATACA
			ACCTTTGTTAA		CACACACACGTGTATACACATATATATGTTATGTATATATATATATATATATATATATATATATATATAT
			AATTTAGGTGG		AATAACCCACCTAAATTTTAAACAAAGGTTCCCTTAAGTGGTAGAACCTTGGGGTGGTATTTTACCTTC
M33875a	131 C T GAGGTGTGT	GGTTACAGCTG	TTAT		CTTCT
TIGR-		TTTTTGTAGAG			
A003M18	29 A G C T	ATGAGGTTTTTC	GGCAGACGGAT		TGCTCTTTTTGTAGAGATGAGGTTTTTCTT/JAGTGTGGCCAGGATGGTCTCGAACTCCTGACTTCAA
a			CACCTTGA		GTGATCCGCTCGCTGGCTTGGCTCCCAAAAGTGTGGGATTATAG

TIGR- A003P30	117 C G ---	---	---	ACAAAGTCAAAGGAGAACCTTCCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCCTGTGATTTCTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA(C/G)ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	TTAAA	TTAAA	GCTTGCTTTTATGTTTAGTTCGGGGGAAAGGAGGGGCTGACAAAGGAGAGATCTGGACACCCAGC AAGGTCAGGGGAGGTTTGCAGAACTTTTGTCTTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATCTCCCTATAAA(C/T)CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---	---	---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT(C/G)AAATAGAAAACTTATAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCTTTATCA	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGA(G/A)TATGATAAAGAAATTTGCATGGCGATTAAAAATAGAAAACTTATAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT	CAGGAAACA GGCATCTCTT	TCCTTCCCACA AAAGGC	CCTACAATCCTATAATTTGCAAGGGTTGGGAGGATGCAGGAAACAGGCAATCTCTTAT(C/G)GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGCAAAATTC AGTAGCTGTCAAATTTCAA
TIGR- A004V26	125 A G ---	---	---	TCTAGCTATAAGACCAGATTTTAAATATTCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAAATGTTAACAGCTGGATAAACCGGTAAATATATGCATTATCTTCACATGA(A/G)AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	TGTTGGGGTG CGATCTC	CGGAGGTGCA GTGAGC	CCAGGCTATAATGTTGGGGTGGATCT(C/G)GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCGCTCAGCCCTCTTGAGTAGCCGGGACTACAGGCAACCCGCCACCGCACCCTAACTAATTTTG TATTTTATAGTAGACATTTGATTTTTTAGTAGACACAGG
TIGR- A004X20	25 T C GA	AAGTTTCCCTT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCCCTCTCTCTGTAGGAT(C/G)CTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACCTGGGCTTCGCTTCAGAGGAGTTTGATATTTGGAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTCTCTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TIGR- A004X30	26 T C CCAC	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC(T/C)ACTCTAGTAATACCTTGTAAATAAAATTAATAGTTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTCAATTTGGGT GATGCAAAACT	CTTATAATTAG AAATTTTCATGA AAGCAA	CACGGTATATGCCTTATATAGGTATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT(T/G)TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTTCATATTCATTTGAGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGCTGCCG GTCC	GTCITAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGCGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGGACGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C		---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTATAGACTGAGAGGGG AAACCCAGCAAGGCTGCTGTAGATCTCTTGGCCTCTCTGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGCCAA GAAGATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTATAGACTGAGAGGGG AAACCCAGCAAGGCTGCTGTAGATCTCTTGGCCTCTCTGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTAAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTAAAACTGTACACTGTTTGTGGCTTAAATATAGACAATGATTTTGT TCTATTACTTAGTGATAGACAAGTACTTTGTGTAGACAAAGTACTTTGTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATACCAAGGCTCTGAGCTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCCTGCCATGGGATAGTACTCTTGGCTGTCTTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC AGAG	---	CTCAGTGTAAAACTTTGTTAGGGAAAAAATAAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGATGACCCCTTGGGCTCCTTATTTTCTTCAACAGGACC CCACAGATAATTGGCGTATGTCATGAGGACTGGGGATGCTCTCTATTG/CJGGATGCTCTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTAGGA AGCGATGCTAATGGGTATTCATAGGTAAAGTATAAAATGTTGTATTTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGTAATGT	ATGACAAATGATAGTATTAGCTTACCTACCGTTTGTAGCACCTACTCGGTATCAGGCACTGACTCGG TGCTTTAC/GJATACATTACCTCACAGCCAGGGTTGGCAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCACACAGCAGACATCTGAACCG ACTCAATTCCTGTGTAAAGAGCAGCTTTGTCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGATATTGTAAAAATTTCCCCAAGAGCCGCATATGAATCTGCC

X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTACCTATCTCGAAAAAATAATAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTG/CJATGCCTCATTTTATCTGTCAAT GAAAAGCGGGGTTCAATGCTACAAAATGTGTCTGGAAAAATGTTCTGACAGCATTTGAGCTGTGAG CTTTC
X74070b	72	T G TGGATC	CTTTTAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC	TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TG/GATAAAATCTAGATCTCTAATATTTTAAAGCCAAAGCCCCCTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATTTCTTGACGCTAATTAAGCCGAAGAAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T ...			---	ACTGCCGAAGTGTAGCGGGCCCCCAACCTTGTCTCATCACAG/C/TJAGAGCTTCTTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACAGGTGTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAG TCCA
D28513b	133	A C ...			---	ATGACCAAAAGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCAGAGCTGGATCTCTCAGCTCC CGCCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAAGCAGTTTGTGACTGCATGAATGCIW GJTGCGGTGAAGCATGAACCTTTGTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ...			---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA/VGJTTCTCCAAGTATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ...			---	CCACTCCATCCTGATGCCCA/VGJTTATCCACAGCCTCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAAGTATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A ...			---	CTCCCTGCCTCCTCCTCCTGCTGCTGATGCTCGCTCTCAACAGCGGAACCTGTCTTGGAAATGGGG GAGGGGGCGTTTQ/GA/CJTTTCTTCTTGGCTTCTCTTATCTTCCACAAACCAATCTCAATAAA GCCAAAATCTTCTCTTCTTCTCCCTCAGGCCACCTCCTGTCTCCTACCTCCTGTCTGCTGGCTTTT CTGGA
D37931	64	T C ...			---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTCTGTCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATAACTCATTCTATAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAAGCTTCC TTT

D63807	101	C T	---			CAGGCAGGACTTCAGTGCAGTATCCCTGCCCTCAGTCTCTTTAGAAATCACAATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTTCTGTGCCA[C]/GGAAGAGGACTTTTTGTTCCAATTTGGATCAG AATGCAGAGGAGTCTGTTCTCCCTCCCGCTGCTCGGTCTGGAGGGTGACCTGTCCCAGATGAC
D90145	21	T C	---			TGGGAACATGGGTGAGACCTC[C]/CJACAGCTACCCTCTCTATGGACTGGTATTGCCAACAAGCCACA CTGTGGGACTCTCTTAACCTTAAATTTAATTTATTTATCTACTATTTAGTTTTTATAATTTATTTTTGAT TTCACAGTGTGTTTGATTTGCTCTGAGAGTCCCTCTGCTCCCTGCTCCCTCACCCTCCCTCACAGTGTG TCTGGTG
EST14035	59	T C	---			ATTACTCTCAAAAATTTTGGTGCTGTTTAAGTACTTTCTATTATGAGCCCC[C]/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16668	71	C T	---			GCATTTAAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG[C]/JGTAGATTTTCAGATGTAGGTCGTCATCTAGCAGCACTTATCT
EST16904	57	C T	---			ACAGACTATCGCCAACTTAAATGCTTAACTTTATGATCAATAGTAATMAATTACA[C]/JGAGATA TTCACACTTTATTAAAAATAGGGTTGTGAAGATGATTTTTCCCAACTGTAGGTTAACAT
EST21863	49	A G	---			TTTTTAAGTACCAGGGCACCTGCTGGAAACAGGATGAAACTGATACACC[A]/GJGTTACTACTTACTC TTCACCTCTTCAAACCTGATCCCTAAAGACTTCTACTTAGCMAA
EST21885	80	G A	---			GGGTGAAGTAGAATCAAGGTTAAGAACATTTTATGACACTTATCCACAACAATTTACTGAGCATA CTAGGTGCTGGG[A]/JGTGACAGTGAGCAAAAACACAA
EST22623	26	A G	---			ATTTAGTGCNAATGACAAAGCCCA[A]/GJAGAACAGAGGATCAAAATGAATGAAATGTATTACC TTCTATAAGTATACGAAGTTTAACACAAGTATGGGAGT
EST22644	98	A G	---			AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTTAAATGATTATCCATTTATTACAG[A]/GJAAATGTGGAAGATGGCTTTTAAACCCC
EST23587	31	T A	---			CCTCATTTATTTAAAAAGACGGACATAAAA[A]/TATACAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246	106	T C	---			AAAGATCTGGCATTTATCACATCATCTCTAAATATTTGTAATTAATCTTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT[C]/GAAATAACCCATAGTTACAGAAATTGG GTCGTGTAACCTCAATT
EST24308	45	A G	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT[A]/GJATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAATATATAAACCTCGTTTC
EST24435	73	G A	---			CTTGAACCTTCGGTCTCAAGTGGTACGTCGCTCAACCTCCAAAAATGATCGGATTACAGGCATAAG CAGCC[G]/JGCCTGACCCACATTTCTTTATCCGATCTGTGTGATGGACATTCAGGTTGTTTC
EST25089	25	T C	---			TATTGTTGCATTATCAAAATGGTTA[C]/JAGTTTTCAATTAACAACTGAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGGTTAGTTAATGCTACATTT

[illegible]

EST33508 1a	36 A G ---	---	---	AAAAATGCTATTGAACAAACTTTTTTATAAGA[A/G]TAAGTTGACTGAAAGGAGGCTTTTAAAT AACATCAACTACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	---	ACAACATAGGACTGGTTATCTTGTTTGAATAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAA[C/T]CTTTGAACACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	---	GAAATATCCTCCAGTGGCAGGAACAGACTCCAGATCAACAGGTTGACCTTTTCGTTGATGA GCTGATAGCTCTAGGCTGTTGGGAACCT[C/T]/AGGTGCCTTACAACCTCACTGCGAGAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---	---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/T]GCTTTCTGGTGGCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST35230 0	93 G T ---	---	---	CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[C/G]GGCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	---	TCCTTTCAAATTTTGTATGATGAGGCATTTAATG[C/T]TATAAATTCCTGCTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTGTTCCATTTTACTTAGTTTCAAGACTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	---	CTGCCCCAAATTAACTTTAGGCAATGGAAC[C/T]TAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCCCTGTTGTG ATGTGCAAAGTGTGGCT
EST35747 9	51 C G ---	---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGTTGAGATT G
EST35751 9	89 C A ---	---	---	TGTTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCCTCCCATGAACCAAGA[C/A]CTTGTCTCATATAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGCCTGTGA
EST36301 4	93 C T ---	---	---	CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCAAGCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAAATTAGCCCCCAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	---	GCCATCAGCCCCACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATATACTGGCTGGCCTCTCTCTGT CACAGGGGTCTTAGTGT

EST36620 6	50 GA ---			GACTTATTAGATAAGGGTTTCGGCTACCTCAAAGCTCTCAGGACTGG[G]AGCTAGGGTTTAAGG AAGGCTATTATTAATATGGAATAAATAACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 CG ---			CCGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTACAGGA AAGGAAGTCTGGGATTCTT[C]G/JAGGGGACATATCACACATATTTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 CT ---			GAGACAGAACCCATCAGTTAAATGAGGTTAGGCCCTCTCCCTCTAATATACTGATTGACAAT[C]T/A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 AT ---			ACTGCTGGCCGATGATTGGAGCTTGAAATAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A]/TJCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 CG ---			ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C]G/JTTA GGGAATTAAGACAATGCAG
EST37054 3	88 TC ---			GGTCTCACTCTCTGCCAGGACGGTTTGAACCTCCTGAGCTCAAGTGACCTCCACCTGGCTTCC GAAAGTCTAGGATTACAGGTT[C]GTGAGCCACCCACACCTGTGCTTGGTTTAAAGTAACCACCTGAA C
EST37269 3b	105 TG ---			AATAGTCTATGGCTACGGGCGCGTGGGATGTTAAAAATTGGGATTTTAAATTAAAGATTGTGAACATG CAACCCAGCAAAATTTCTCAGCTTATATTTTGAAAGT[C]G/JCAGGAGAAAAAATGGGGTCC
EST37284 2	93 GT ---			AAAAGACCTTTCTCAGCAGTAACCTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGAA GCTCTGGATAATGTCACTCTAGGA[A]G/JAGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 AG ---			AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCTGCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATC[T]G/JCCCTGCCCTGCTAGAACCTCAAGTTTGATGGGCAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 CT ---			CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C]T/AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCAAACACATTTTTCAGGGCACTCTAGCTACTACA GGA
EST37376 8b	101 GC ---			GTGACATCATGCTCTCAATGCCCTTTCAATTAAATAGTAGTTGAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTCAAATCACAGTGTGTCTCTGCA[G]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T/C ---			GTGACATCATGCTCTCAATGCCCTTTCAATTAAATAGTAGT[T]G/JGAGGGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAATCAGTTATGAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGCTGGAAGCTAGCCTATCGCAITTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTACC[G/G]GTGATGAATTCATTAATAAACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGCCAGAACTAAGCTTTACATGTTTATATACATTAT[G/J]TATCTCA ACAATCTTGAAGGGTGTATTATTTCCCGTCTTAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAAGTCCACAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/T]CGCATGG AAGMCGCTCTCTTTAATTCCTTAACCTCTCTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCCTCTTTCATTACCAAAACAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTATCTGACTGAC[T/G]TCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCGGT[G/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTCTG CTGAAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAGCTT ACAAACAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTTGTACTCTGTAGCCAGTCATTAACTGAAGGTTTAAATATATATATTTTATTTGGGATGAGATCA TAGCTTTTACACAAATGCTATG[T/C]AAACAAAGTTACTGAATATTTTACCCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCCTCTGCTCTCTAGCAGTCAGACCACCAAGAAAGCCCTGGAAGACCCATGGAAGGAAAGTA TGC[G/C]GTGTTTAGGGAGAGCTGGCACCTGCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCACCAATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCAC TAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCCGTGTGACAGGGAACCTAAGCTC[T/C]TCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTATACACTACGATGCACA[G/J]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCATTGTAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGAGTTTACAGAAATTTTATCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCAATATCTATGTTTAAAGCT

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EST51340	51 G A ---				GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---				CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTITTCCTTGGTCTCCAGTGGGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63 T C ---				CTGAVCTCCAGTGGCCCTACAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACCTAQT/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAGGCAGTCAATCCT TAGTAAAGTTTCCAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---				TGAGTCTGACACGAGTTGCAGCCAGGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC CT/CJATCCATTAGTTTCCACTGCCCTGCTGTGACATGAGGCCCATCTTCACCTCTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---				GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTTTCTCTGACCCCTGTAGGGTGCCA TTTGAGTTTCACAGCCTAGAAAGAAAGAGGCTTTGGCCCTGTGTGGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAGGAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---				GGGTCCAGAACCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACACCGTCCCCCAG CC[G/C]CGTGGTGTAGTATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTTGAG
L39059	123 T G ---				ACTTGAGAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTATTTCTTTGTATTTGTATATTTGJGSCCTGA AGATCATCCCGAAGGAGGCTGGAGGTGCCGGTGGCCCTGTGTCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---				CAAAGTTGTCTCTGCCCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCAAATGTACCAGCAGCTGGAATCTGAAGGCCGTGAGTCTGCAT CTTAGGGCATGGCTCTTCTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCTCCCTTGCTTACAAATGTCT AAGGT

L48728b	111	T C	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTGCTCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAAT/C/GAAGAAGCTTATTCAGAAAG CAGAAATAATCANTGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52	G A	---	---	GCGACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGACAGAAGTGA/JTTTATTTCACC CCATCAAGTATAAGGTTACTGATTGTTGGTCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAGTAAAGCTAA
M19169	113	T C	---	---	TAGGGATCTGTGCCAGGCCATTGCGACAGCCACCCACTCCACCCCTGTAGTGTCCACCC TGACTGTGGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCCTGTC/GCCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTTGTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114	T G	---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTCTCATCAAAAGCCATCCAGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCGCCCATGATGATCCCGACAGCAAAAT/G/GTTTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCAAGTGTACCTACTAG/GATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCAAGTGTACCTACTAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC TCTGATTTTCTTTTCTCAAGTGTACCTACTAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C	---	---	TAAGGCAGCTGTGAGGGAGGCCAGTCACAGTCCAGCAATTCACACCCCTTGAC/GCJAATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAAAATAAGCAATCAATC
M81695	34	G A	---	---	ACTTACTTACCCTCAGCTGTAGGCTGACGGGA/GA/GAACCCACTGCACCACCGAGAGGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTGTGCTGGGAGGGGCTTTGCTTGTCAAGGTTG CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	CT	---			CTCCTCCTTTATTTACGATGGAGGGTTTAAATGGAGGATCTCCTTTCTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTCACAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATATTCTATGTCAATGATTTTAAAGCTA TGAATACAAATGGGGGA
U09607	39	T	C	---	---	GAGGCTTATGAGGGTCTCTACTTCAGGAACACCCCAAT/CAGACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTCGAATTTGTAAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTTGGCCCAAGAAAGCAAGCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T	C	---	---	GAGCAAGGCAAGAGCGGAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGAAAGTCTGGTCT/CACATCTGCCGCCCTTCCAGCCCTTCCCCAGCCCTCCTCTTGTTCCTTC ATTCAATCAACAAAATTTGGC
U10694	20	G	---	---	---	GTGACATGAGGCCCATCTT/C/GJCTCTGTGTTTGAAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCACTCTGGGTTCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTGGAAITGTTCAAAATGTTCTTTAATGGTCAGTTTAATGAACCTTCAACATCGAAGTTAA TGAATGACAGTA
U13877b	162	TC	---	---	---	AAAAGGACTCTGGTTCAATCCAGTTCATTTTGTCTATCTTTGTACCTTGACAAAGTTGTTTAAAC CTCTTTGTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCMAGAGAT/C/TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	TC	---	---	---	TTCTGTCCACTTTACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTGTAGATATCCGTACAGAGAGT TCCAGTAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG/C/TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	TC	---	---	---	TCCAATTATTGGTCCCAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCACATCTCTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAAAACAACATGCTCTTGG AATTA
U18543	58	TC	---	---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTGATTCAGCTGGGTAGTCTAGAACTT/CJAGAAG CTCCATCTTTAATGTTTATTGTTATGTCCCCCTCCCGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTAGTAGAGAGGCC

U25975b	164 C A ...	...	...	<p>TCACTGCTGTGGCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT  ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAAGCAAAATGACTATTCTCTG  AAGACAACCAAGAGAAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTCTTTAGG  GTCCAGAAGGAATTGTGGACTGA</p>
U25975a	143 C G ...	...	...	<p>TCACTGCTGTGGCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT  ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAAGCAAAATGACTATTCTCTG  AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTCTTTAGG  GTCCAGAAGGAATTGTGGACTGA</p>
U25997	61 A G ...	...	...	<p>CAGGAGAGGTTATTACAAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT  TTGAGTGTACTGTGCTGGTTTGATTTTAAAGTAGTCCATTTTCTATCCCTTAAAGAAAAATT  GCATGAACTAGGCTTCTGTAAATCAATATCCCAACATCTGCAATGGCAGCATCCCAACCAACAAAA  TOC</p>
U28413	29 C T ...	...	...	<p>ATTCTGACAGCTAAATTAGCCCTAAATG[C/Π]GGGTAATATTTTCTCATGTTTAAATGAGGTT  AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCTTGATCC  CAGATGTTGTGGCCTGGAAAGCCCTCATTTGCTACAGTACAAAGTACACAAGTCGTTGTACCTCAGTT  G</p>
U30884c	89 A G ...	...	...	<p>TAGGGGTAGCATTTAAGATTACAGGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATATCTGTT  CTTCTATCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT  TGACGGAAGTCATTAGAATGGCTTTGTGATATCTGTATGGCTTGAACCTTGCCACAGTTGAACACAAGT  GCTGTCA</p>
U30884a	34 A G ...	...	...	<p>TAGGGGTAGCATTTAAGATTACAGGAGTCATTAGC[A/G]GTGATGATTTTGGACCTGCCGTATAATCT  GTTCTTCTATTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT  TGACGGAAGTCATTAGAATGGCTTTGTGATATCTGTATGGCTTGAACCTTGCCACAGTTGAACACAAGT  GCTGTCA</p>
U31216b	78 A G ...	...	...	<p>GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATTGAGACGGCTGCAACCAACA  GCCGTATCAA[A/G]CCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA  CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC  TGGTAGCCCTTCCAT</p>
U31216a	70 G A ...	...	...	<p>GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATTGAGACGGCTGCAACCAACA  GCC[G/A]TCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA  CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC  TGGTAGCCCTTCCAT</p>

U31416c	76 G A	---			AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGAGAGTCTCATCTTAGGGCATCGCTC CTCCTCAQ[G]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCTCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCATTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T	---			AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGAGAGTCTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCTCCACTGCCTGCTG GAAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCATTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T	---			ACGGTCAACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCAACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTACATGACTGCATCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGACGCTGCTGAGAGAGGCCGAGAGGCCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G	---			GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGCCCTGAGCGTCTAGJCCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGGCTATGCCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C	---			TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTATACCCACCGCATGATTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGAAACATCATGTTTACCTGTGCAGGCACCTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T	---			TCAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAAATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCATCTCTGTTTTTTCATGTCTCTCTT GTAACCTTGAGATCATCAG
X52011b	148 C T	---			AGGAAGATCCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCMAATGAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A C	---			AGGAAGATCCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAATTCGAAATTT GCGAAATCTGTTGTGACGCTCAAAATGAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	---	CAGGCCACCTGCTCTCCACACAGTGCACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCGAGGCTCCAGGCTGCGGCTTGCAGGCTTGTCAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTTGGCTTGTCCAGGCCACGCTGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	---	AAGCATTTCGTTTACAGTGCATCAGATACATTTTATTTCTAAATAGAAATATTTATGATTGCAT AAATCTGAAATGAATTTATTTTGTCTTATGATACAAATTTCTAAATCAATTTATGAAATAG GATGCACAAATTTACTAAATACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA GCCGTCTCTGACACCTCCAGAACGAGGTGCTGGGCGCTTCTGCTGGGACCCCGGGAACCTCTC CTGCCGAAGCCGACGCGGATGGGCCCCAACTTCGCCCTGCCACTTGACTTACCAAAATCCCT TCCTGGAGACTTGAACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGATGTGACAAAGCCTTTAAGCGGTGTACACTTGATTGATATATAAGATAATTTGTT CATACTGGAGAAACTCCAGAGGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTTATCTTGAGAAAAATTTGTATAAAGATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	---	CTCAACCCATAACCTCAACACATCTTCTATCTCCACCCACATCCACACATCCACCTCCATCC CCAGCCATCTCATCCCCAAGTACAGCCCAACCCAGCCGACACTATCCACAGCCATCCCCAA CTCATCTCATCCCCAAGTACAGCCCAACCCCAACCCAGGGCCATCCCCAACCCATCCCCAAGCC AACTCAACACCATCC
X78932	62 T G ---	---	---	ACCCCAACTCAAGTCCAGGCCCGGCGATCTTCTGCGCTGCTTGTGGCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTGCTAGCTACTTCTCTGCTGACATTTGAAAGACCCCTCCACTCTGGCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGCCACCTAGAAAG ACCCCAACTCAAGTCCAGGCCCGGCGATCTTCTGCGCTGCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGTGCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGCCACCTAGAAAG GGCACCCAGAGTGAACACAAAGTCCAGCAGGAGGGCGGCGCTGCGCTGCTGCTTTCTTTT CAGCCCGGAGAGGTCTGACCTGGGGCTTCTCCAGGCTCACTGGGCCACGCTCCCGCCGCTCT CTTTCTCCCAAGC[G/A]AAACCAATGGGCCCCCTTCACTCGCGTGGCGGTGGAGGGGGGCTT CTTTCAGAGC
X80026	25 T C ---	---	---	ACCCAGCCATGGTCTMGGACATGGATCGGGTCCCCCAGACGTTGCACAGGGGACCCCTGCCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTTGGGGC ATGGCAGGAGGAGCCATCGGGTACTACGAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X80197b	99 G C ---	---	---	
X80197a	28 A G ---	---	---	
X85106	150 G A ---	---	---	
X87160	128 T G ---	---	---	

[illegible]

1282	130 C T	---	GTGGGATCACCACACTACAGTCTAAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGTACCCATTAGCAATATTCTCTATTCCTGCCCTACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCC[C]/ACTTGACATATCATACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTTCTTCACTGAGAATAATGTTTTCAAGGT
6810	68 C T	---	AGTATCACACATACCTTAATATATTAGATATACACATAATAAATCACTCCCTACCTTGAAACCTTTA/C/TAAGAAGCATTTTTTAATTTACAACACAAAGCTCAACGAACTTCAATAAAGTCTAGTCTGTGTTACGTGGCAAGGATAAGGCTGAACATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAAATTTCTTTTTGAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC
6817	118 A C	---	CCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTATTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGGTAAC/A/C/TTGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACACCTTGTGTTCAAAATC TTGTTGAGGTGCGGCCTGTGCAGATCGGCTTTTGGTTGGTCTTAG
6819b	212 C	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTGCTCTCAACAGTTTGTGCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATACTTTTGTCTCTATATGACACCTAATATCCA
6819a	166 G T	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTGCTCTCAACAGTTTGTGCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[AG]TTATACTATGGCACCAATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATGC CACAATTCAGAG[GT/CT]GTTATTGGTCTATTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT
6972a	122 A G	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[GT/CT]ATTGATTAT TGGCCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGCAG[AC]
7598j	208 A T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGC[AT]GA
7598i	192 G T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[CT]ATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGAT[CT]CCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTATTTCTTG[AG]GGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGC[CT]GGCTAACCGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAA/GJAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACA/C/GJCCAAGCCAAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTTCAAGGTCCTCCCAATAATJCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTTCAAGGTCCTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTTCAAGGTCCTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCTGTCAAGAAAAGACCAGGTGG AAAATGGGTTCCCAATAAATGGAAATTTTAGGGCAACAAAGCTTAAAGGCCA/GJCAAAAAGAGA AATAGCACCACTGTCATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGTAATCCACACAGAGCATGCACACACAATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TJGGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAAGGAAAAATTAAGT
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/A/GJCGCAAAATCCACTTTGCTGTAACTGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAAGGAAAAATTAAGT
8498	84 C T ---	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAAATCTTCATTAAATCGAAAAAGAAAAATTCCTTTAAGGAAAAAA AATCCAGTTTAAAGACAATTAACATTAGTCITTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAAGTCAAG

WI-18562	29	GA	---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	AC	---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAAGTGAGGCCGAGCTAAGAAC[A/C]GCGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAACACACAGTGTGCGACAGATTC AC
WI-18683	22	CT	---			TAAGTGTTCAGGACTGGACTC[G/T]GGTCCCTTTATTAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCAAAGCCTGCCCTGCAGT
WI-18520	75	GA	---			GACTTTGGTGATTTAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAAACAAACACGGGCATCCACTCTGCTCTCA TGCTCTCTCCGTGAGAC
WI-18563	94	AG	---			AAATAAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	TA	---			GTCCTATTCAATTTAGCTAGACCCATTTCATTCTGTTAATGGCTACATTTGTTTTCATTGTGAGAC T[A/GTCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94	GA	---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723g	71	TC	---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	AG	---			TTTATTACAATATTTAGGTGGCACATAAATAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18619	44	GA	---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCAACCCCC
WI-18535	107	GA	---			GTAAATAAAGTTTTATTGGCACAGCCAGCTCGTTTCATTATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCCGGTG
D17525	107	CT	---			AGAGTGGTCAGAACACACAGGCCGAATCCAGGCTCTATCACTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTCAGTTCTTCATATAGATGGAAC[A/C]TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGATGATAGCACTTAAACAGAGTGATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAAGGTGCTGATGTCTACCGGCAGACGAAG

DWU-133c	313	A G	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC ITCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T	---	---	ATGAGATCCTTTAAATCCTTCATGAACGTTTGTGGTGGCCACTCTACGICAAACATGAAGTG TGTTCCCTTCAGTGATCTGGGAAGATTCTACCCCTTGACCAACAGTTCCTTCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCAGCCACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAGGATTCTGTGGAAATATAAAGAT
DWU-387	169	G T	---	---	GTGTATAAATGCAACTGTTGATTCTCTCAACATGGCTCACAATTTCTATCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAGTTCACCTCATATATAAAGCATTTATTTTA CTCTTTGAGGTGAATATAATTTATTTACAAATGCTG/AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTACCACAGTATCAAGTAATAACACAAATGAAGTGTCAATTATCAA
DWU-447b	172	---	---	---	ATTTTAGTGCTTTTGGGTTAAAATCAATTCGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CCATTATTTTCAATTTGTTTCTAAGAGGATTGANAATCAGTTTAAATGTTCTTTCTGTTAG GCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G	---	---	ATTTTAGTGCTTTTGGGTTAAAATCAATTCGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA/AGATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CAACCATTTTCTCAATTTGTTTCTAAGAGGATTGANAATCAGTTTAAATGTTCTTTCTGTTAG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G	---	---	GTAAATTCAGTTTCTTCCAGTCTCTTTTGTGCTGCTTCTCAATTAAGCGTTTAAAGTGAGTC/GAT AAATCAACTGTCATCAGGTGAGGTGCTGCTCCATACCAGCGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ...	---	TCATACTAGGGCAGTATCTCTAGCTAGTGCCCATACAGAAAATTCCTATCACCATACAAAAATTA A/TJGCAGTATTTATGTTTTAAGCACAGGTGTACCGAAAAGTGTGAAAAGTCTGAATTTATGGGTT CTATGCAATGCAITTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACITTTGAGCTTTAAACITTTAA
DWU-512	131 A G ...	---	AAATCCAGGCATTCGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACCTTATTA AGAGCTCCACAGTGAAGATGGAGAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTC[AG] TGCGTATGGCAGTGAGCAGGTATGTTTGGCTTTGCTTGCACTGAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ...	---	AACTGCATATAGATAATTTATCCAGGATGTGGCTCATTCTTTTCAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTGTAAACCATATGATTGA[C/A]AAGAAGAAAGTCTATGCTTAGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTATCTCTAAATCTAGTCTGATTG
DWU-59	94 C T ...	---	CATTCTTTGTGAAGGTAAATGGACTCACAAAGGGGAAGAACATGCTGAGAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTCACATTTGGC[C/J]GAGCCGTGTTCAAGTCCCAGGTGGCAGACTCGTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ...	---	CTTGATCATGGGTGGAATTTTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ...	---	CACACTGGCATCTAGGCCCTCGCCCTGCATTGCAGAAAGGAGAGCCAGGTCCCTCTGGAGAA[C/J]G CTGGTTCCCCAGCCCCACACCGGCTTTGCACACACACAGGCTGTTGAGGCAGGAGTGGGTAAAGCGT AGCTGTAGACCCCAAGCAACCAACAGCCCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ...	---	TCCATTTACATTTGGTGGCATTTTGTGAATAGCTACAGAA[G/J]GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ...	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAACTTCTTCATAA[T/A]CTGACAGGTCAAGTAAGTAAAGGAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ...	---	TTCCAATGTAAGAGTCAAGTACCAAGTT[C/J]AACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAACTTCTTCATAATCTGACAGGTCAAGTAAGTAAAGGAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ...	---	TGTAAGGTGACTTCTATAAGCTTCCTAACCTGTCAAACTTTCATTACTAGATATTTTCAGGCCAAT GTGTC[TT]GTTGGTCTGAGATTTGATTATCAGCTGGGTAAAGTTAACCTGTTCCCTGTTTCA

WI-18063	105	GA ---			AGGCTTTAAACTGATACAAATTTGCCCTTAAATACATACATAAAAACTCTGCACCTTCATTCTCCTTC
				---	CCATGTTTCTGATTTGATGTAAACTTAAAAATTTGTG[A]TCTTTAACAAATATACTGTAGCTGCA
WI-18078	86	AT ---			AGTGAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAAGCTCAGATTCAAACTGGTCCAGTG
				---	TTGTTTTCAGCATCAG[A]TGTCCTAGCCCAAGTTGATCTCGAGTATCTACATGTGGT
WI-18091	90	TC ---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCCTTTGTTAATCCATCAGACACTGTGGT
				---	TTTCATCTCTAGAAGTTTGACTTTC/GGGGCTTTTTTATACCTCCATATCTCAACTTGTTAAGC
WI-18119	38	TC ---			GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGATTC/TGTGTAATGGATTGGAGTACTTAC
				---	CACATTTTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAAACAGTTTAAATTTGGTCTT
WI-18142	66	TG ---			TTCAAGATAAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATACTATATACT
				---	T/GCCCAATAAATCACTACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	TC ---			GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCACTCCATGCTGGAGGTAGTCTGGGGG
				---	GTTC/GCGGCGGGATGGACACAGACACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	GT ---			TCAACTGAAACCTGCTGTAGGCCAGCATGGGT[G]TGGGAGGTGATTATGGCTGGGGAAGATG
				---	GGCACTCAGCCGACAGCAGCATCTAGCACACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	GA ---			ACAGATGTCAGTTGTTGAATTGGCCCATTAAGATATGGGGCTTTCTGTTAAAAAGTCATCCAAA
				---	AGGCTTGGCAAGATTTGCTATACACGGAGGGACAGAGAAACATGA[G]A]CTGGGGAGTAGGCTCT
WI-18261	26	GA ---			GACAGAAGGTGGGCTGTC
				---	GATTTGAAGGGATTGCTTTATTAACTG[A]TGMAAGCGTGATAGAGGAACTGTTTAAGATAAACAA
WI-18268	88	CT ---			CTTATAAATACTCCCAATTTGTAGAAGTGAAAGATTG
				---	TAGGAGGGAAGGAGGTGGCTGCTGGGCGCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAAGC
				---	TTCTTACTTCCCCCATAGATCTTCCTGACAATGTGCTGAGAGGCTCCCAACCTGGAAC
					TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCCAATTTTT
WI-18299f	107	CA ---			ATCTATTTGGGTCTGAGAAATCCCAATTTTG[A]G]GAATCTTTTGCCCAATTTATGACATATCTG
				---	CAG
WI-18299e	101	AG ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCCAATTTTT
				---	ATCTATTTGGGTCTGAGAAATCCCAATTTTG[A]G]GAATCTTTTGCCCAATTTATGACATATCTG
				---	CAG
WI-18299d	77	GA ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCCAATTTTT
				---	T/G]ATCTATTTGGGTCTGAGAAATCCCAATTTTG[A]G]GAATCTTTTGCCCAATTTATGACATATCTG
				---	CAG
WI-18299c	67	TG ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCCAATTTTT
				---	T/G]ATCTATTTGGGTCTGAGAAATCCCAATTTTG[A]G]GAATCTTTTGCCCAATTTATGACATATCTG
				---	CAG

WI-18299b	52	GA	---			TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCAITTAACITG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18299a	48	CT	---			TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCAITTAACITG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18307	76	GA	---			TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCGGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTTGACTCTGCAATCTGCTGGTCAC TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGGTGGGTACTGATT TATC[G/T]TAGATCCAAATAAAGCATGCAGAAGTG
WI-18324	72	CT	---			ATGAAAGTCACCTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGAT[G/C]TAAATCTATGAATA GGTGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18350	48	TC	---			TCCTGACATGATCTGAAATAAGGTGATTGGTTGAATTTCTCGAAATTTGAAGAATAAATTG ATTATCAAG[G/C]TGTCATTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18395	77	GC	---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGGTT[G/T] GATAACATTGCCAGTAAACATAATTCAAAACAGCAGAGAAATTTGGAGGATAATTTGTT
WI-18398	62	GT	---			CTCGTTGGTATCTCTCATCC[G/A]TTCTCTTTCGCTCTTTCTAAATTAAGAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAATCACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21	CA	---			AAGATGGGAAAGAGGAAATC[G/A]TTTCTTACTAGAGATTTTTCCTTTAATCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGGCCCAAGAGCCCCCAAGTGCTA
WI-18409a	20	CA	---			AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAAAATAGTTTCTGG[G/C] TTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGGAAACACAAGAGAAAAAAGG TTTATAGGTGGAGAGAGGA
WI-18442	62	CT	---			TTGATGTTAATCTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAACCA
WI-18452	38	GA	---			ATATAAGCTGGAGACTGTGGAGGTGAGAGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAGACTGCAAGGATTCAACAA[G/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	AC	---			CTGGTGGGAGGAAACAAATTTGGTATATTACATCAATGAAAACTTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACAACAACATGGACAAATCTCAAAATCATTTATGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT
EST5b	93	A	---			

EST5	93 A	---	---	---	CTGTGGGAGGAAACAAATTTGGTATATTACAAATGGAAACTCTTCAGAAATAAGAGGAA CAAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACCTTTCTAAAGCTCT GAACAAAGCTTTTCTTCCCTTTGCAACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A	---	---	---	GGACAGGACCTCTATTCOCGCCCTGGTGCAGCAGCGGCTGATGGACTGAGGCCAGGGGATACTGGGOC CTCTCTCAGGGCGCTCCAGGACCCAGAGCTGTTCTGCTTTCCTGCTTTCCTAGAGCTGTGGCGGCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 G	T	---	---	TCCTCATTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTATTACCATCATGTATC[G]GAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---	---	CCAAAGTCTCCTGTGCTCATAAAGAAAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGACAAC[G]TTGATTCACAACAAACCCCTTCCOC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAOCCATTGTGTGTTTCCCTCTT TGAAGCAATGACAAGCACCTTACTTTCACGGTGGTTTGTGTTTCTTAT
WI- 18985a	105 C	T	---	---	GCCAGAGCTGAAGCTCTTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTGTGTAAGCTGACCGTTTTTATATTACTTTTGAAATATCTT[G]ATCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-18746	114 G	A	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCCTGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAACACAAAGAAACCGAGACAAA TCTTTTGGAGATTTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACCGGTATATCTTTGAG GGTGACAAGGG[G]ATCTCTTCAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19112	212 G	A	---	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGCTATCTTAGATCATGT CTCAATGGAACACACTCTTCTTCTTAGCCCTTACTTGAATCTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCCCTGAAATTTTCATCTTGAATGTCTTTGATTAACTGAATTTTC TTTTAAGCTAACAAAGATCAATAATTTT[C]A/C]ATGATTAGCCGTGTAAC
WI-19092	232 A	C	---	---	CCCAATTTATTAGGOCAGTGATGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCCAGCGGACGCACTG TCTTCATGAGGAACACACAGTGCAGATCCCAAGCTC[G]ATCTCTTCTATCTTGGTTTGGCCACA
WI-19057i	175 G	A	---	---	

WI-20103	168 C T ...	---		TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACTGGGATGGCT AGGATGGACAGGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCACTTCTTCAATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ...	---		GCCTTACCCATTTGCACATATACATATGCACCCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAAAGACAAGAAATGGA/GA/JTTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ...	---		TGGTTACAAAACCTAAGCCCATATACAAAATTTAGGAACACATTTAGATGCCTCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATACAAATGCAATTTTTA/GJACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ...	---		GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATAGTAGTACATCTGTAGTATTAATGCGATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA/GA/JAAAGGGAGTTTCCAGCGAGCCAGTGGTGAGC TGC
WI-20613b	156 A C ...	---		GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATAGTAGTACATCTGTAGTATTAATGCGATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA/GCJAGTTGGA AAAAAGGGAGTTTCCAGCGAGCCAGTGGTGAGC TGC
WI-19984	47 A G ...	---		CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/GJTATAACATTAGAAAA GCAAAATCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAAATACAGG TAGGCAAGAGTTTTCACACTGGAAAATGAAGGCAGTTTCCAAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ...	---		GCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCAATCAGGCAATA ATTGTTCTTGGAACTTCGACCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAGT T/CJTGAAAACCAACTGGAGCTGCTTTTCCAAGATGTTCTGTGCTTCAAAATAGGAATTCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTCAATGACCTAAGCTGA
WI-18845a	49 G A ...	---		GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGGTGCTTG/AJAAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCCCTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ...	---		AGCAGTGGCCTTATTCATCCCAAAACACGCTCTTGACCAGGCTGCTCCCTTGTGGCAGCAAGGGC ACAGCTAATTCCTACTACAGTGTCTTTAAGTGAAAATGGTCGAGAAAAGAGGCACCTG/AJGGAAAGCCG TCCTGGGCGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTTCTCAAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTTCTTTTGCCCTTTTGCAACC

WI-20146	31 T C ---			---	TGAGCTCTCTGTAATTCATTGAGCAGTTAGCTTC/CATTTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAAATCCCATCATCTACTGGTAAAGCCCTCATTTGAATGTGTAATTCATATACAGGC
WI-18922	74 G A ---			---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTACCTGGACTTAAGC/GA/JTCTGGCTCTAATTCACAGTGTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACCCAGTCTC
WI-18763b	53 A G ---			---	TTTCTGTGTGGGGTCAACCGTACATGGTGTGGGAATGACGATGATGGA/JG/JATTTTGAATGTACCATATTTTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCATGTGTTTTGCCAA
WI-18763a	38 A G ---			---	TTTCTGTGTGGGGTCAACCGTACATGGTGTGGGA/JG/JTGAACGATGATGGAATATTTAGAATGTACCATATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCATGTGTTTTGCCAA
WI-18771b	75 G A ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCCTGCTCTCGGAGGATGCCCTAGAAAGATGTTGGGAACAGAA/G/AJAATAAAGTGA/TTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCCTGCTCTCGGAGGATGCCCTAG/JG/JAGATGTTGGGAACAGAGAATAAAGTGA/TTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---			---	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTTGGTGTGTTGATGAAATTTCTGAGGCCT/C/JTGATTTAAATCTTTTCAATTTGATTTGATTTCCCTTTTAGGTATATTGCGCTAAGTGAACCTTGTCA
WI-18742b	51 C T ---			---	ACAAAGTCCCTGAGCCCCCTCACCTTTCCCTGTTTTCACATTTTGCCAAATGA/C/JATCGGGTTTGGTTTCTGTGATATTAAACGGTTGTGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTACC
WI-18882	94 C T ---			---	GTGTGTCACAAAATGGGGTCTGCTCTGCTACCTTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCATCAATCCCAACAACATCCTCTGCCA/C/JACACAAACAACGTAAGTTTTCATTTGGGCAAAAATTGAAC
WI-19970b	167 G A ---			---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGGTGCCTGTGGAGCCTGCCACCGGGCCCCGGCAGTGCAGTCAGCGGGGAGGAGGTGCCGTTCTGCCAGTTCTCACTGCGGGGACAGCAAGGCCCTTCTCACTGGTTGGTCAAAG/JATGACACTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACAGAAATCTTTTAAACGACTGACCTTCCCTTAAACAGAGA
WI-19970a	126 T C ---			---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGGTGCCTGTGGAGCCTGCCACCGGGCCCCGGCAGTGCAGTCAGCGGGGAGGAGGTGCCGTTCTGCCAGTTCTCACTGCGGGGACAGCAAGGCCCTTCTCACTGGTTGGTCAAAGGTAGTACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACAGAAATCTTTTAAACGACTGACCTTCCCTTAAACAGAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCCTGCTCCCAAGAGACTGCCTCCGCAATCCACAGATGATGGATCTTCAGTGGGTTCTCTGGGCTAGAGTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAIAGTGTTCATAAAAGAAAT/GJACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCCTGCTCCCAAGAGACTGCCTCCGCAATCCACAGATGATGGATCTTCAGTGGGTTCTCTGGGCTAGAGTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAIAGTGTTCATAAAAGAAATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCCTGCTCCCAAGAGACTGCCTCCGCAATCCACAGATGATGGATCTTCAGTGGGTTCTCTGGGCTAGAGTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAIAGTGTTCATAAAAGAAATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCCTGCTCCCAAGAGACTGCCTCCGCAATCCACAGATGATGGATCTTCAGTGGGTTCTCTGGGCTAGAGTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAIAGTGTTCATAAAAGAAATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATATC
WI-19106	247 T C ---	---	TTAATCCAGGCTACCTTGTAGTATTTTAGGAGACAGTCAAGCACTAAAAAGTGGCTGAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCCTCCACGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCTCTATTTAA/TCTGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTAACTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC(A/G)TGTAAATTAATTCACAATATAAAGTCTACAGTTAATTATGTGCATA TTAACAATAGGCTGGTTCAATTTCTTCTTCTTAAATAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTATAGATTTATTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAAATAAACCTTTGGGAAAGGTGTAA(G/A)ACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAACCTGGAATAGCCTTCGAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAATGTTGCTGATTTGACCTGATTCAAGTTAACTGTTCCC CTGGTATTTGTTAATACCTGTACATATCTTTGAGTTCAA(C/T)CTTTAGTACGTGTGGCTTGGTCA CTTGTGGCTGAGGTGAAGAACGTGCTGTGTGAAGACAAGTCTGTGGCTTG

WI-19042	193 A C ---			TTTGTGAGTTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAAGGTGAACCTTTGTGCTCAAGGACATTTGGTGAAGTCCCAACAG ACACAATTTATCTACTCGACAGAACTTCAGCATTGTAAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCCTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTTGCATTATATAAATTCATTAAAACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGACAGACTATTTCGCACGTATTAAAT GTAACCTATTAAATGAATCAGAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAATGCTAAATGTCAATTTATCACTGGCATGTTTGAAT
WI-18851	90 T A ---			GCTTCAATTGGCGATTGATTGAGTGCCCAACAATGTAAACAGGTTGGTAGTTGTTACTCATTTGAAT ATACCTTTTCTTATTGTATTCTT[A/G]ATAATAGGATCCTGGAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---			TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTGCCAT[C/G]ACTGTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATAACATCTGAAATCGGGAAACAAAGGTTTATCTAATAAGTGCTCTCTCCATCAGCTTG CTAOCCTAACCACTTCCCTCTGATTTCGCTGAGGAGCTGGCATCTACTACGTACGTGGCATAAC ACATCGTGTAGGCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---			TGGAATTCCTTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG[G/C]TTAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATTCCTCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTCTCTGCATGTTACCAGAGGCTTCTGGTCTAGCCAGCCCTGTATGACCCGGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---			CACGGTCTCTGCATGTTACCAGAGGCTTCTGGTCTAGCCAGC[A/C]CTGTATGACCCGCAAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---			TTAGGAGGTGGGTGAATGCTCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTTCCTT/ CJCGGCTCTTCTGGACCTTGACCCGTGGATACAGGCCATGTGCCATGTTTGGGTCTCTGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCTGTGGCTTATGTACCCACAGAGGGTCTGAGAAGTCTGGCTGGGATGGCCCTGOC CCCTCCTGGAAGGCTCGCAGAGATGACTGGGCTGGGGAAGCAG/AGTCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCCTGTGGCCACCACGGCACTACGGCTTCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTTGGCCA
WI-19016b	184 C A ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTCTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTATGTATTAACGAAGTTCAAGATTAGAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/TTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTCTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTATGTATTAACGAAGTTCAAGATTAGAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/TTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTTATTTTGT/CTGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCTGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACCAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCCC CTTAGGGTGGGAGCTCTCCG/CACTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACCAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGATATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTCTTACACGG
WI-20310	125 G A ---			TCCTCAGCTCTGTCATCCTTGTCTTGAGGGTTCTGTGTACGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAGGCAAAAGACATACAGCCAGCTCTCTAGAGGCTCCA/GATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGATGAATTTTGTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAGTGCACACTCAGGCAATCTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTTAAGAGCCTTGGCTTGCAGCCCATTCAGAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAGCCCTTAGTATTGTGACATCTGCCCTTTATCCTGCTCTCT CCCCAGTGTCTACACTTGGGCAAGCAGAGTGGTGGCAGCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGGGCTATTG/AGGTGATGGCTCTGCTGCTCTCTGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTAAATGAATACCTTTTGTGT/CTCATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTAATGAAGACACTCAAAAGCCATGTTTCCAACCTTAGGTTAATAATA GGCTATTGTCCACCCACTCTTCGGGCATTGCTGCAATATTCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTCTCT

WI-19766b	93	A G	---			TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTC[G]GACAAACAGAAAGGCACACCAAGCCTGAACCCCTC
WI-19766a	31	G A	---			CGGACACAGCAGAGTTACACAGCTAGGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTCACCCCTCCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126	C G	---			TGGCCTCAATGACTGGTACATTGGAGAAGCT[G]ATGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC
WI-20512c	59	T G	---			CGGACAACAGCAGAGTTACACAGCTAGGGATGTCCTGGAGGTTCTGACCATGAGAGGCCCCCTCACCTCCTTACCCCTCCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19599	230	C G	---			CTTCTCTGTTGGCTTGGCATTGTGCGATTGGAAAAACCATTTGGAAGAGGGACTTTCTCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGA
WI-19909a	29	T C	---			TTAGAAAGGAAGTGAATTCCTTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGCAGCTGGGGAGGGCCCAACGGGGTGGGATCACCTGA
WI-20341	221	G C	---			GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTACAGCAAGGATCGACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCAGCACACCTTGATACAGAAATGGCTCCGTGAAGTCTTTTAAACG
						GACAAAGGTAATCAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAGGGCA[C]GJTCCAAAGATAACACTGCTA
						TGTTGAAATAAAAAATTTCCATGGTCTTAAATTGAACCTGTATGTTACTTTCTTTTAGAATATCCTTTTTCATTAAATAAT[C]TCTAAACCACTCTATGTGTCAACCTCTCTGTTTAACTAAGATATGGGT
						TTTTGAAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGGGCAATTTGGTCTTGTGTTGGAAAGCTCTCCAGGGTGTTCOCAGAA
						CCAGAAATAAGCCCTGAATATCTCTT[C]TAAATAATAATTTTCTCTCTTTGCTCTTCCAA
						GTAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATATAACACTACCTAGGCGGGTTTTTCTTTATACCTTGTTCTGTACTGTGGAATCAACTAA
						TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGGATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTAGCAGGA
						GGCAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGGTAAATTTGGGTGACGTCATGCATCCCCATGCATTGGTTT[G]ATGTCCTCCAGTGAGCTGTGGCAAGTCT

WI-20113	60 TC	---	---	TTCTGGTACATGGTAAGTCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAGCAAAATTACACACAATTAAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAAATCTATCCATAAACACAGGTAGATAATGTGACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 GC	---	---	TGATGGCAAAGTACAAAGGCTCTGAAGAACACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTCCACAGCAGGAGAACACTTGACTTCATTAAAGGCAAG/CJCTTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCAATCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72 TC	---	---	CCTGCAATCACAAAAGTGAACCTAGTTGATATTTTGAATCATACTTGAATTAACCAOCTTCAGAAA TTCAT/CJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 AG	---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTCGAAGATCCCTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 CT	---	---	GCCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACAGTGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGCGGTGA/CJGCTCTCTCAGGCTCATATGGATGTCCT CGAGGTGCACAGGGAACCTGCTCTGCTGTAGAAAGCTTCCTC
WI-19348b	98 GA	---	---	GCCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACAGTGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGC/GJA/GTGACGCTCTCTCCAGGCTCATATGGATGTCCT CGAGGTGCACAGGGAACCTGCTCTGCTGTAGAAAGCTTCCTC
WI-19635	98 AT	---	---	ATTAGTTCGTGTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAGGTACAGTAAATAACAGTATTATJATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGCTGACTGCATGCAGATATGTGTGTAAGAACTTTGCGCTT T
WI-19641a	46 AG	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJATATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATGAATGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 CA	---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTC/JAGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180 CT	---	---	TCTGCCATGATCAGATTGATGAAGAACATGATGGTCACTAGTAGGTAACTTTCTGTGCTATTGCGCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTGGCATCACCACCTGTAATCTAATAGT GAAAGGCAATGATGTCTCAGTATCAGTGTGAAACATTTTCTGCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAAACACAGCCC

WI-19673a	35	GA	---				TCTGCCATGATCACATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAATAATCTAAAT AGTGAAGGCAAAATGATGCTCAGTATCACTGTGAACAATTTTCCCTTGGACCAGCTGAAGAA TCTTGAGGAGCCTGAAGGCTCAAGGCTCCACACGCTCAAAAAACACAGCCC
WI-19724	35	AG	---				TTTATTTGGAAACAAAGGATTGTAATTTGGGTAA[A]G[CTGAGTCAACGGTGGCCCTGAGTAGTGTC CTAGAAGCAACACGAGAGTTTGGTTTTCTCT
WI-19307	196	TC	---				TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTCTTGGATTGGCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGGCTGT GGTGAACATGCAAAAGGAAACACAGGCAATGTATTCATAGAGGCCCTTTAAAGAGACCCG[T/C]TGG AAATGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGGCTG
WI-19269	85	AT	---				CTTTCCTCATCCCTCTTCCACCACACCATCCCGGAACAAGTGTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGCC[A]TJTTGGTAGCAATGTGGAACACACAGGCCCTTGTGGAGAAAATGG AGGGGTGAGGAGTCCACAGAGGGGCTTATTTAGGGGCTTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122	CT	---				CAATGGACTGAATGAGTGGTGGTGGTGGGACACACACCTTCAATACACGTCGAAGGTG CTTCCAGTTTGA AAAACAGAAATCTGCATCTCAGCCTGAGACGACAGAGAGGT[C/T]CTTCCCTG ACCAGACGCACTCAGGAGGCTGCTGTTTCAAACTGCATTTAACTGGCCAGAGAGTTCA CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	GA	---				CACAGCATGGTGAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCAATAAATAATTATA ATAAATATACATCAAGTAACCTTTACAGCACACATTTTATGGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAACGACCCAGTTAGCAGAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCAAACAGAAAGCTTCTGAACCTCTCTCGGGAGGTAGCTGACAAG
WI-19076	40	GA	---				TTGGTTGGATACCTTCTGGAAAAA AAAAAGACAGTTTAAAT[G/A]GTATTCAAAATACCTTTTAAAA GTATCTAGCACAGAATTTTCTGTAACTAGATTATGTGTAAACTTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTTATCCAAATCATCTTGCCTCTCGAAAAACTGCAGA AAGGCACTGAAAAGCTTCTTTAAGATATGGGATTTCTTTTTATTCTT
WI-20218	26	TC	---				CCACACACTCTGGTTTTATAAGCTAT[T/C]AGGACAGACAGAGATGGAATGAAAAACAGGGGTAG AAAAAATACATAAAATTGGAGGGGAACAGTGGGATGCAGAAAAGAAATGACAACAGCCACATGTGCCCA GTCAAAATCTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	TG	---				CAACCTTTTGTACAAGGGGACGTGAATTTCTGATGAAAGTTATCTACCAAGTTTAAATTCATTAATG GGAATTCCTCTTTTAAATATCTCAGGCTTGATTGGGAGGGGCTGGGCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT[G/C]CCAGAGAAAGCGGGGAAGCCCAAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTACCTCTGTGCAC[CTCTCATGCTGGGACTTGTCTTTCGGGG

WI-20361a	192 GA ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAIGG CITTATGCAAGATGACAGAAATATGTAAATCTGATTGTCAGAGAGTTACACTCTGCAGCTCCAAAGCTA CAACAGTGCACAGCTGAGAGTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G]ATCCTTC AAATGGGAAATTCCTAACTACAGAGACAAATGGTCTCTACAGTAGGCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAAT[G]TCATAAAACATCATCTTTTACACATGGAGAGCGAGGTAGGCCATAATTGTTC AATTCATCTTTCTCAAATTTTAAATTTTAAATCCCAAAGGTGCTATTTGAATCTCTCAAAAATA AACTGCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTGATTAT
WI-20588	133 GA ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACCTTTTAAAGAAATGTGAGATCCTTTTGTGGTTTTTATTTCTTAAAGTACAAATGCTAAAC GAGAGCGGAGCTCTCCGCAATCAGG
WI-20593	79 A G ---	---	TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTG CTGTACTTCAG[G]TTTAAATCTGGGAATGAGCATGCAATGCTCCACAGATGAGGAAGAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCTTCAACCAGACTAT CCAGAGCCATTCCATGGGGTATTTGGCTGTCATCTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTGCCAAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCA[T]CJATGTATCT TGTCCTGCTGCTTTTGGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAATTTGCCATGGAACTGAGC AAAAGGCCACGTGGGATAAAATCACTACCATCGACGCCACCACTATT
WI-19066i	239 A G ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTCATTCGAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCTTCACT[G]GTTCTTTTA
WI-19066g	184 C T ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTCATTCGAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACTAGTTCTTTTA
WI-19066f	148 T C ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTCATTCGAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACTAGTTCTTTTA

WI-19066e	147 GC ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACCTGG CATATGTTCTTGC[G/C]TTGGTCACCCCTGAGCTGAATACCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100 GA ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGC[TTGGTCACCCCTGAGCTGAATACCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87 CT ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGA[C/T]CTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGC[TTGGTCACCCCTGAGCTGAATACCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19086a	72 CT ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGC[TTGGTCACCCCTGAGCTGAATACCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105 GC ---	---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTG[G/C]TTAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTATTCCATTCTGTTCTGTACAAGATAGAACAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGTCTCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCCTGCATGCATGTCACCCCTTGGT[C/T]TTCGCTCCATCGOC TTGAAGCTCTGAA
WI-18768	120 CT ---	---	---	TTCCCAAGGTTCTGTATTGCAGCTAAGCTCAATGTATGTTAATCTTAGTTCAGTTCGCTTTTG GTCCTTCTCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAGGTGTGC AGTGCCCATCCAGCATGTGTGCTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 A G ---	---	---	GAAAGCCAGAGATTAGCCCGGATTCGGCATCTGTCAACAGGACAGAAATGTCATGGACAAGGGA TGAGCTTTACAAGATGATGCACCTTGGAGATCAGAAAATTCATATTAAGCAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 AT ---	---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCT[C/G]GTGGCCAAAGCCAGACACTACCCACCTT CCCCAGTGGCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAAGAACACCCAGGCTGCACA GAAAGCCAGATGGACCTGAGTGTGGTCCAGCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA
WI-18987	35 GA ---	---	---	

WI-18919	26 C T ---	---	---	TGGATGAAACCACAGGGATTCCGGAC/TJGCCAGACCCCAATTTTATACITTCACITTTTCTCTACAGTG TTGTTTTGTTGTTGTTGTTTTTATTTTATACITTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---	---	---	CTTCTGTCAGAGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---	---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA/GCJACAGAGTATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---	---	---	CTTCTGGTCAAGGCTTTGGACAT/GJCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---	---	---	TCAGAAGCAGACATGGCATCTGTTCCCTGCTTGGTTGTTGGTTGTACCTTTCCAGAGACCTGAATT TTAGAAATGCCAGTGTGCGCAGAGTGAGTGAGTGAATTTCTCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAACATATCAACCA[G/A]TAGCATTAAACCATTTTATTTCTGCTGCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	48 T A ---	---	---	CCAAGTTGCATCCATGTTGATTCTCTGATGAGACTAGAGTGACAG/T[A]GTTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGACATCTCTATGAGATGGGATATGCAGATGGCCTATGGAAATGCAGCTGC ATAATTACACATTATCAAGTCTCTTACAAATTTATTTCCGAGCATGTACAGCTAAGTAGACCCA ATGGGAGAGAAAATGCCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---	---	---	CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAGCCCTAGACAGGTAAAGACACACATTTGGATG GCAGCATGGGTTCTTCCCATTTATGGGCATGAAATATGGTTTAGAATAAGGAACAAGCATTATT CCTTGCCAACAGCTCACTAAGAGGCTTTTGTGCTGAGTCAAGCAACACATTTGCCCTGCTGCTCC CTTGGAG[G/C]TGCAITTGACCTGCTCTCACTGGTAAAGTGACTTGGTGGC
WI-20014b	214 T C ---	---	---	TTGAAATCCAGTCTCTGGCCCCCAGGAGGTCTGTCAACCATAGATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTCTTGTATTCTGAAACTGGAACCTGAACAGTTTGGCTTTCTCTCTAGTCACC AAGCATACTT/CJCTCGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---	---	---	GTCTCCACAGAGTGCTTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTCCAGGGGGTGGCTTAGTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCATCTCTCTCAATACAGCC/T[C/G] CCCTTGCAAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20 G A ---	---	---	CAGTTACCTGCTTGGCTC[G/A]AAAGTGTCACTCAATTTGTAAATTTTAGTATTAACTCTGTAAAGT GTCTGTAGGTAGCTTTTATATATATAGGACAGACCAAAAATCAACCTATCAAAAGCTTCAAAAAC TTGGAAAGGGTGGATTAAGTACAGCACATTTGGCTTACAGTAAAGTAACTGATTTTATTAACT GCTTTTGGCCATATAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGGTGGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGAAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTACAGCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCTCTTTTCATAGGGGAAGAGTGCACACTCTGGCTATCTCAGGGGGAATGGGGAAGAAG AATCTTTCAAGGGCAAGAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCAGCCTTTCTAAGG CTCAGCCCAACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATATTAATTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAGC[CA/AT]TTTACCGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGACGATGTGGGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAGCATTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGACGATGTGGGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAAGTGAGGAAGAACCTAAACATGAAGGAAAGGGTGCCCT CATCCAGCAACCTGTCTGTGGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTGCACGGTTTAGG
WI-19235	173	A G ---	---	TCAGGAGGTGGAGTTCGTGCTCAGCTCCTCTGTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGCTCTGTAGTTCCTCTCAGTCCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTCTCTGAAAGTGTGACAGTGTCCAGCCGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCAGTTTAGTTTGGGATGATTTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTCTGTAGGTGAGTGTGTGGGTTTTCCTCCACCAGGAAGT GGCAGCATCCCTCCTCTCCCTAAAGGAGCTCTGCGGAAC[C/T]TTTACACACCTCTTTCTCAGGGAC GGGCGAGGTGTGTGTGTGACACTGACGTGTCCAGAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGAGGAGGAGAAAAGAAATGCACTAAGACAAGAACTCTCTCATAGAACATTG ATCTGTTTACAGGAAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAATTTTCAAGTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG



WI-18017	87	C A	---		ACAAAAGAAATGGAATAGTTTGGAAACCTTATCTGCATGTACAAAGTAATCCCGGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---		TTATTGGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTAGAAACNTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---		TATACGGATCATGTAATTTGTGTGACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAG[T/C ]GCCAAATCCCTCTTCTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117	C A	---		CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCTTCTGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGTAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGIGGTTCTTCAG
WI-18295	40	C T	---		ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAGGTTGATTACT TCCTCTCCAAAGGATGATGTTAATGAATCCCTTNCCTTAGCTTCATTCATAATGCCAAA
WI-18459b	64	T C	---		GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT[T/ C]GAGTAATTACAAACATAATTTTANATGACAGTGAATTAATTAACGTCTCGGTAAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56	A G	---		TTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---		GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC[A/G]TCTGTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---		GCCTTGTCTTTGCTCCTCAGAGGCTCAGATGGATACGCAAGCTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCAAGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98	C T	---		GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTATTTTCCACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCAATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---		TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTCAGCACCTAAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TJTGTCACACAGTACAGTGCACAAATCCAGAGGGCAACACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---		TCAGAAATGCTTTCACCTGCCCCCAACCAAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTGGAGGTTCATGACAGGATTAGTCTCTCTGT[T/C]CTTGGT GCAAGTTGAACCAAGTATTATGTACCAATTGCATCAGAGCATCTGTTCCCTGTGAGATCCCCACTAG

WI-20561b	94 T C ---			CGTTGCTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/GGGAATCAATGTCCTTTTAAATTTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---			CGTTGCTATTTAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTAA TTGTACTTCAGATGAAAAATCCTTACATGTCGGAATCAATGTCCTTTTAAATTTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---			GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTAGAACAT A/T/AATAATCTATATCATATATTTATACACACAAACACATTTACCAGCACGTGTAAGACACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---			GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTAAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTACCAGCACGTGTAAGACACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---			GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTACCAGCACGTGTAAGACACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---			AAAGATTGTCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGACATATTACAACACAG NTCCCAAAATGGTGAACCTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTAATAAACGC G/A/TGTGAACATAATGTTTAAAGATTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAAGATAATAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAAGTTTCGATT
WI-21444	39 A G ---			CTGGCAGCAAGTAACCAATTTAAGAAATACTCTCAAC/A/GIAGTCTTTTTTATGGGGTATTTCA GTTGTTAACAAGTTAAATACTTATTGGAACATAATCTTTGTAATTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTACTTATGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTTGTAACATGCTTATCTAGCTAACCTAACTGTTTCTGTAGAAATTACTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---			GGCGTGATTTGATGCAATGTCCAACCAAGTCAAGCTATCATTAATGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCATGTAACATACAGCATATACCTCCCTTAAAGTACTCATATTTTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAGATGTAGCATTAAGTGGTATTACTTGGAGGCA ACA/G/AJAATTACGGCTTAAACACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45	A T ---	---	CAACTGCTCTGAGGCTTCTACTAGCTGATTATATATCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAAGTCTGTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTGAAGGCTGTTTTGTTAATTGCTG
WI- 21778b	155	T C ---	---	AAAAATCCATAAATATTGAACCCCAAGTTACAGAGAAAGTTGCTAACTTTTTTTATTGAATTATTGAC TCTGCCCGCGTGTGTTGCTGGCTTCAACTCCAGTCTGTCAATGCCCTGTGTAGTGGGTGCCAG GTCTGGGCTTCTGAGGTCCTGJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241	A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGGGGTACATGAGGGGCAGTTGTTTCTAGTACCCATTAGCCG ATGGCTCTTCAAGCCAATTCACACTGGGAAACACACCCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI- 21449b	222	C T ---	---	AACAGCAGCAGTCACITCCAAAATGCAAAAAAATTACAATTTTAGAATAAAAATTATAATGTTTA TAATGGGGTCAGAAGANTTGAAGGTACAACAGAAATCAATACGCAGCACTGGAGGCGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGCTCCACACCC AAATCATACCCCTCAGCTTCCCA/C/TJTGACAGAGCCAGTCTCTGGGTTAG
WI- 21558a	157	G A ---	---	GCCTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACGACTCCAGCTGGAAACCTGCCCCTC CCATCCCCCTTAGCGCCTCTTGGCTTCCGGCTGATTTCTTGACAGCAGTCTTGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCCTAGGGCTGCAA AAGGCCCCCGTGAAGAGAGATGTGGTCAAGGCTTATGGGTCTCTCCACC
WI- 22187b	178	G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTCATGAAAAATTTCC CCTAAACCATAACAAAACTGCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 22187a	110	C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/C/AJAAAAACAAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTCATGAAAAATTTCC CCTAAACCATAACAAAACTGCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 21609b	146	G A ---	---	TCATGAATATGCAGCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTACAAGCTGTAAA AACAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTCAAAG/GAJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAAC/CTGTGCAGTCCGTTTCAACAGCTGT AAAAAAGCCCAACCCAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAGGAGGAGCCTGT AAGGATGTTCAAGAGGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGT TTTTCCATATTGCTCCACTGCTAAATCCCTTGTGGCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGTGACCTCAACCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGAC/ATGTGACAG TTTC/AGJTGCACTGGTACAGAACACACAGGGAGTTTCAAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGAC/ATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCAAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATACTTATGTGTACTTCTTG[AGJTTTCA TCATACAAGACAAGCACAAAAAGCACCACCATGCCTCTGAGGAACATTTGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGTTAAATAACTTATGTGTACTTCTTGATTTC TCATACAAGACAAGCACAAAAAGCACCACCATGCCTCTGAGGAACATTTGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAAAT[AG]ACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAGGAAC AGATGTTAACAAAACAATTAAGGCTGCTGGGGAACTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAAGGGCCGTGAAGGCGATGATTGGTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGAATAATTAACAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTTGAAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCTGACAC CAGCAAGGGGGAGGCACCATCACCAGCCCTGCCCATCATGATGCCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGGCTTGCT[CTGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

WI-21661	117 GC ---	---	---	GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGATAAATAAGAAATGACATTTTAAATAAAATAG/CJTJTAGTCACAGTC ACACAAAACACTACCTTCTAAGGAAAACGTGCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC ---	---	---	TCAGTTTAAACACACATTCAACAAGGAT/CJAGATTAAATTAATGTACAGGTAGCATAAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---	---	---	TGCTTGATTAATGTGGTGTACATTATCCTATTTACAGATGGAACAGAAAATACCAGCTTTTTT AAA/AGJTAGCAATATCTATTATATAATAATTTGAATAACACCATAATAATATCACTAAGGA AGTAATCTAATGTGTTGATTTTCAGAGGGAGAAAACATTACCTCIAGAGCTAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 GA ---	---	---	TTGCTATAATTTCCITTAATAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAACAGATAACATACCTGGACACGGTTTCAGGCATGAAGGATACA/GA/CAGTTAAATTAACATAAG GAACAGAGTCCCTGCAATTCCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAAATACCTGGGCC AAAACCCACTGAACCTACCCAGCTGAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 CT ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCGTATGACGACCTTCGCGTCATCTAT AATGGTTAATAACAGCATTCTCTACCC/C/JTAGATGCTCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCGTATGACGACCTTCGCGTCATCT TATAATGGTTAATAACAGCATTCTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---	---	---	TTACCTTCCAAACACAGGCCACTTTGGAGAAAG/G/JAAGAGAAATGCTATTAAATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 AG ---	---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCGAGGGCTC TGCATCCCTTTCTCAGCAGCAGCACCATCTTCACCTCTCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGCTCTTTCTCACCAGGGTAAGAAATGCAGGTTATTGCAGAGGGGAGTGAGTCTGGGAA/AGJG TGGGACAGACAGACTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI- 22703c	134	A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCTCAGCACAGCACCATTCTTACCCTCTCTGGAAAGCAGCATTTGGAGCCTACACQ AGCTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG
WI- 22663c	139	G A ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTACAG GC[G/A]GAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAAATCCGTTTGAATGTGGGT
WI- 22663b	55	C T ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTAC AGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAAATCCGTTTGAATGTGGGT
WI- 22663a	38	C T ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTAC AGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAAATCCGTTTGAATGTGGGT
WI- 22668	99	A G ---	---	TCTTTTATCTGCTGCTGCTGAGTATTCTGGGAATCTACAAGGATTGAGGGAGCCCTTGGGATT CCAACCTAACAAATAGTTTCTGTAATATTA/GITTCAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAAGAACTTTTATT
WI- 22631a	52	T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTCTGATTCAGCACCATT CAAGTTTAGGCAAGGATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI- 20258	157	G T ---	---	AATCCACACTTTCAGGAGGGGACCAAGCTGCCATGTCTCCAGGCTCAGCAGCGCGGCTAC TCTGCTGTTGTTGGTGCAAGGTGGAGATGGTGACGGCGCATTTGAAACCCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCAAGTTCAGTTCAGTTCAGCAGGTGATGGCTGGCAGCGGCGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI- 22714	212	C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTGCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCTCTGTAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TTGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44	G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCTT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCGCAGCTCGTGAAGCCATAGTTGGATGGCGAGACTTTCCGGCAGAGGAAAT AGCAAGTGCAAGGGGCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---			TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACGTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48 G A ---			TGTACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[A/G]GCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTCAGCATTTGACCATTTCTGACTGTGCT
WI-22775a	60 A G ---			TGCTGTTCTTTAGTTGATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143 C T ---			CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAG[A/C]TAGCAAACTGATTAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---			TCTCTGCTGCTTGAGCCCTCATCCGACCCCTCCAAAGCCCTATGCCACACACCCGTGCCACATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCAATTCGAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31 C T ---			TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGCTCCAAAGGTTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122 A T ---			CCATATCCAGTCTTCTTGAAGCTTCTATTGACCTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTATTTGTTTCTCCATTTCTGTCAAACTTTTC[A/T]TTTGTATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTNCTGTAGTTCCCTGAACCTCTTTTAGAGG
WI-21186	95 G A ---			AGCGAGCATCAGAAATCAGCTAGAGGTTGACTAAAGAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCTTAAGTGTGCAG ATGCTGTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTCTTTTAA GGAGAGACAGGAATTCAGAGAACTGCTAATTTAAGCATATGTTATGAAT
WI-21187a	94 A G ---			CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTCATCAGTGGGGAATTCGTAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAGCAACCTGT

WI-21190	39 TC ---			TTTTCCACATACCAATGCACCTGTTTGATATAAACTATT/CJGTGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTATAACAAATAATTATTAAATCTGTACTATTACTGC TTTAGTTACTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTATTTCCATGTATAAAAGCTT AACACA
WI-19937d	186 GA ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCNTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCACCTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 CT ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCNTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCACCTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTTCCTCAGCAAGTC[C/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 CT ---			TCACCTTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA/CJTTAACAGGAACTCTGTTTTC TTATTCAAATGTACAAAGCTGACGGTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAAATACTGGAAATTCACATTACAGACAGACAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCTATTGTGGGTTGCT
WI-2122a	42 CT ---			CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACATTCCACAGGAG[AG]CAAGGAGAAG CTGTTCTCTGG
WI-21254	53 AG ---			AAGGAACTGCATGGGTACAAATG/TTCCAATTCATACTTAACAAGGTGGGGAACGGGTCACTCT TGGCCTGCTCCAGAACAAGGGCGAGTCTATGCACCTCTG
WI-21054	23 GT ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGTTGCAITTTCCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCAGTGAAGTCATTCTCTATTCT/CJAATTGAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCCTTGCCTAAT
WI-21058b	181 TC ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCAITTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCAGTGAAGTCATTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCCTTGCCTAAT
WI-21059a	63 CT ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCAITTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCAGTGAAGTCATTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCCTTGCCTAAT

[illegible]

WI-21627b	153	A G ---	---	---	GCATGAAAGAACTCCAATCAGACGCTTTATTCATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTACATAATAAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106	A G ---	---	---	GCATGAAAGAACTCCAATCAGACGCTTTATTCATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTACATAATAAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75	CT ---	---	---	GGATTTGAGTCCCAACTGATCTCAAAATTCACCTTCTTGATGTAACAGCTCATTCCTCTAAAGTT TCAGTTTC/JTTTACCAGTAAGGAAAAGGTTGGACCAGACATGTTGGCCGTAATTCCTTGGTAA CTGCCTTCGCAATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68	GA ---	---	---	CGATGCTGCTAAGATAGGAGGTTAATTCCTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT C/GAJCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGCTGCTTTAAAACAGTAACCAATCAAAAAGAAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATCCACAGAGCCCTTGAAGGGAAAGGCCCTCACT
WI-21249	155	TC ---	---	---	TTCTGGCATTCAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCATCACAATTTGATCTAAGTTTCACTTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTACTTAT/CJATGGAACAGTATTTATTCNATTTAACTACTGTTTCAATGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATATAAACATTGAGA
WI-21504	147	CT ---	---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGACGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT/CJTGCGGTTCTGGCTTCTCCACTGGTGGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115	GA ---	---	---	CTGCACCAGGGAGACAGCTGCTGGCAGGGACTAATAAACCCCTTCCACCTGGCCATGGTGGTGTT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGCAGAGAA/CJ/CACTAGCTTGGGGGTG GGCAACAGCTTCAGACCCCTT
WI-21475c	181	A G ---	---	---	TAGCCCTTCTGCCAATCTGGCAATNTGAGGCTGGGTGGAGCTGGCCGTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAAGTGCCTTTGGAGAAGGCA/GJAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGTTCTCCACCCTATTTCCTCCCTGAAG

WI-21475b	117 A T ---				TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTQ/AT/CTTGTCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGCTCTTTGGAGAAGGCAAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCCCGTTCTCCACCCCTATTCTCTCCCTGAAAG
WI-20893d	207 A G ---				TGTTGTGTTCCAGCCACATCTTCTCAAGGAACCCACCCAGCCGCTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTACTAGGAATACAAATCATTTGACGTAAGTTTCACCCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/AG/JACATAACATTTGGTAGAGTAAACAAACCAACCAAGCCTAAATG
WI-20893c	179 T C ---				TGTTGTGTTCCAGCCACATCTTCTCAAGGAACCCACCCAGCCGCTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTACTAGGAATACAAATCATTTGACGTAAGTTTCACCCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAAACAAACCAACCAAGCCTAAATG
WI-18941c	71 C G ---				GAGCTCAAGGGAAGACCTTACCAGATAGGGACTAACTGGAGGGTGGAAAGCAACAAAGGTGAAA GGTATC/GGGTCTGTGAGACAAAAGCAGGGGGCTGAGAACACAGAGCAAGGGTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGTCCTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI-21552b	166 C A ---				TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTCACCTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACTCTTGATTTTAAATGTA/C/AJAATTAATTTATTTGAATTTAGTTACCCCC ATTGTCTATCAAAATTCAAATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21552a	66 G A ---				TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCTCACCTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACTCTTGATTTTAAAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCAAATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21512	54 C G ---				TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTCTGCTGTGAGGCAACGTCCAGGTCCGGGAAGGCACTCGTGGTGTGTGATCTGTC TCAGTGTGGAGGTCTCCACTCGCCCAACAGGCAAGCTCGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCGTGTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---				CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCTTAAGGCAGGACAAAGCACTTTCATT ATTCTTAGTTAGACCAGAACTTTAAATTTATTTCTCTTTAACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGTAA/G/AJAGTAG TATCTCTACATACCACAGTATACAAATGATGCCTTCTCTGAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCCCAATCTTCAAGGAAGGAGGACACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGTAAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCCCA[AG]TCTTCAAGGAAGGAGGACACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGTAAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAACATGTTGCAGTGGCGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTTCATCGGTTCTTAATACAGTACAAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/AG]TCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGCGAGTGGGCACTTGGAAAGTGAACACATGGCAATA AGCAGCCTATCTCTTACCAACCCAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCAATGGTGGAAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCCAAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTGTATTATGAGGAACCTACTATAGGAAGCAACTTATGAGTG TGTAAATTTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGGGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCC[C/T]GTCTGTCAAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCATAANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT[A/T]TCAATCAAGATCCATGGAAATGATGCAGITTAACATGTGTCTCAGC TTGCCTACTGACCACCTTCCCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---	---	TGTCCTTTAACCTCAAAAGTCCAAATAAACATAATAGACATTTTGANTATAGCTAT[C/GA]TTTTAACA AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACCACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCAGATGACTATTTCAAGCTTATAGA GAACTTGCAAAAAAAGTACAAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTTCAGTGAGTATTAT[C/TA]GGGACACAAATCGACGGATGTAATCTATTTGANITATACCATAGGCC TATCTATATTTGGCCCAAGGGAAGGTAAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---		TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATAATCTTGAAGAAAAAATTAAGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---	---		TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGACAGATACGGTGTAAACGCGCTCTCCACTGCT TACTGTGTACCAAGAAGGCAGAAAGCAGCTACCCAAGCCTAACCTGGCC[C/T]TGCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAACCTGGGATGCGGGAAGGCCAGGGTCTGCTTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---		TGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTATCTTTGGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCCTT GTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCCAGTGGATCTOCC ACAACCT[C/T]TCCAGGGCAGGAATTTCCACCCAGGGCCCGGGTGCOCG
WI-19105a	33 T C ---	---		TGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTATCTTTGGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCOCAGTGGATCTC CCACAACTTCTCTCAGGGCAGGAATTTCCACCCAGGGCCCGGGTGCOCG
WI-21760c	81 C A ---	---		CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTCTCTCCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---		CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTCTCTCCTAGCTTTACAATAAGNGG AGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---		TCTGCCATATTGTTCCAGCACCCTACTTACTGTTATTTCTCTTTGAGGAAAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTTAAATCCTTTTCCCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTACT[C/G] AGAGACAATTCATAGTTTCATAATCTTTTCAGGGTGTGCTTTACTTTGGGGGGC
WI-20934a	72 T G ---	---		CCAAATGCAACATAGTCTTCATTCTTAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAATATTCAAATGGCCTGGCCTAGTGGTAATTCAGCAGAG AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCTCTTAAGATGGCAGATTAGAAGACCTTNTTCCCCAGGAGA
WI-21561	55 T G ---	---		TTTCCATTTTATTCAGCCGGCCCATCAGAACATAGCATCTATACCTTCGAAACQ[T/G]CCTCTTAAC CTCTCCCAGGCAAGAAAGGAAAGTATGATCATATTAATTCCTCAGAAATGGTGGATCTCAAGACTT TTTAGAAAGTCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCTCA

WI-21961c	200 T G ---	---	AGCTTTGGCTGAAATTTGGTACTTACTACCTTTGCAATTCCTTTATTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGGTACAGGAGGTATTTGGTTATAAAGTTCTTTAGTGGGATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACCGGCTTTTATCCCTCGCCCCCTT/GJC
WI-21961b	73 G A ---	---	TCCCACCTTTCCCTCAAGTCCAAAAGTCCATTGTATCATCTTATGCACTTTGGTACTTACTACCTTTGCAATTCCTTTATTATTATTATTACTTTTATTTTTCQ/GATTAAGTTATTGGGGTACAGGAGGTATTTGGTTATATAAGTTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACCTGGTCTTTTATCCCTCGCCCCCTC
WI-21956	26 T G ---	---	TCCCACCTTTCCCTCAAGTCCAAAAGTCCATTGTATCATCTTATGCACTTTGGTCTCTTTCAAGTGAATTT/GJTTCCTTCGTTCTAAAGCCCTTTTAAAAATGAACCTCCCACCTTTGGGTCTCTTTCAAGTGAATTT/GJTTCCTTCGTTCTAAAGCCCTTTTAAAAATGAACCTTCCATTCTGTTCTGAACTTGCCTTAGTCTGTTTCTGCTTCATGCCCCCTCAGTCGAATCTTTCTTCTAGGGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCCGTTAACTCAGGGTAACTCCTATCTCTCCACCGGTAAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	CAACATACATTTATGGCTGCCCTTTATTAAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTTGTTAGAAAGCATGAGTGAGTGTGTGTGTGTGTGCGCGCGCGGCAACGCGCATGGCACTGAGGGGATTGCAATGGG/GJAACAGGATAAAAAGGTATAAAAACCTTGGTCCGAAATCTTTTGCTTATTAAACCTTGGCCCTGCTCTCACAAATGTTTCTACACTTAATTCATAAGAGAGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTTGGTTACATGGATGAATTTGTTCTAATGGTGAAGCTGAGATTTTAGTGACCCATCACTGAGTAGTGATGATGTACCCAACTTGTAGGCTTTTATCCCTACCTACCTCCACCCCTCCCCATTTTGAGTCT/GC/CATAGTCCATTATATCACTCTGTATGCCCTTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTAAGTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTTCTCTGTGAATGGGTACAA
WI-20317b	217 G T ---	---	TGTGGGTCAGCAGTAAAGGAACATAACAT/GGTACAGCACTTCAGCACAAGCCCTGGGCACACAGCACTGCATGGAATACACAGGTAACATTTTAAACAGTGGGGACAAAATTTTAAAGTACGTGGCCAGCTGTGGTTGCTTGTGGTCATTAAGACAAATGTTAAGANTCAGGAGTACTTAAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	AATTTTGTCTCTTCAGTTTTTTCATTAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAAG/GTTTATTAATTAATTCATATTTTGAAGGCTACTCTCAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCCTTTTGTGTGAGTTATGGTTGTGTGGGTTTTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGGGGTACACGGGGGCTCGGCTCAGTCCCGCGGAAGGACGATTC/GA/CTGAACCTGGGACGAGTCTACTCTCCCCCACAGAGAGCCACCGATTTCAAATCCTCTTTTGTGTGAACCTCT

WI- 22082b	67	C T	---			CAGGAC TTG GTT GCT GTCCCACTGCACATAAATGTCCCTTTTGTGTTGAGTTATGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTTCGGCCGAGGAGGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAACTCTCTTGTCTGCAACCTCT
WI- 20993	139	A G	---			AACACAACTCCATGCTTTCAAGATCCCACACCCAGATACTAAGACATAATTAATAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATAGGGGAAAAAACCCCTGG GCTTCTAGTTAAACAAGTGAGTATACATTAAAGACAGTATTCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGCTCTCCTAGCTCATCCACACATCACC
WI- 21723b	125	A G	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI- 21723a	82	G A	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[GA]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI- 22132	99	T G	---			CAACAGATGCTTGAGCCAAAAAGCAAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCCTTAATCTGACITGCTTTACTATCCTTT[GC]CCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTTAAATGGGACAGTGGG
WI- 21006a	106	A G	---			TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[AG]AGAGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAAGTGCAAAWAGGCTTCATTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCCT
WI- 21761b	138	C G	---			CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCCTGGCTTGGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATCAAAATATTTTCACATCTTCTTCTGCCAGTTAAACGTGCCGTGG CT[CG]CAATACACACCAAGCAAGCGTAACCTTGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI- 21079c	166	G A	---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[GA]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTATAGGATGGCAAT

WI- 21079a	50 G A ...	...	AATGAAATGCGACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGGAAATCAAGT TGTTTAAATACCAGTGTGAGCTTTGATTCCTCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAATTTACAACCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCGCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 T G ...	...	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTGTCAATAGTGTAGCTTAACAGTTAACTTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ...	...	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGACIAGJGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCCTCACCCAGAGAGCCTCACTGCATTGAOCCACACACCCACCTCAACC CAGCACACAGGCACAGCGGGGACACGCACACACGNTGCACCTACCAOAGC
WI- 18916b	42 C T ...	...	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCAACC AATGCCACCTTCATA
WI- 18916a	35 G C ...	...	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAG/CJCTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCAACC AATGCCACCTTCATA
WI- 19828c	200 A G ...	...	TTCCCTTCTCCCCAAGAAGTGGGCAAGAAAGCTTTGTTAACCTCTTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTCCAGGNCCTTCTGCCCCAATTCGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCCAAAAT[AG ]CTTTTAACTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTTGACCT
WI- 21863b	47 C T ...	...	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTG/CJTAGCTGCATGCCACCCCTC ATATCCACCCCATCCAGCCTCTGCCCCCAGACACCCCAAGGCTGCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTTGATCCAAACACAGCATCT
WI-19860	51 C G ...	...	TTGACCTAAAGCCTAGCATAAATTTAGCTAAGTAGAATGTTTCCAAAAGATG/CJGJCTGCATCAGTAT CTCCATCCCACATAATTTCTGTTGATTTTGCCATTCACCCATAAATGGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGGNCTCTGATCCTGCTGAAGGATCTGAAGCC
WI- 19889b	80 C T ...	...	ACCCAGCTCCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAAGGGCAAG AGGAGTGAGGGG/CJTAGACGCAATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTCG

[illegible]

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTTAATAAGGTCATTATGAATCTGAATTTCTTA/GJTAAAT ACTCTGGTGCAATTCATTTCATCTGCAAAAGCAACTGGCAACCACTCTTGGCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTTNCATTTATGTAATAGAAATGGCAGTGAAGTGTCTATG AA/CTTGAGGCGAGGAATGGCATGGCGTGGGTACCGCTGGACCTGGACGTTGTGCTTCCAAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAAGTTAGGACATTTGTGATTTCTCAGCCACTAACGA GCTGTATGACCTTGGTCAC TAGGCTCTGCAGGCTCTGGTG[CTG]TCATTTGCAAAATAAACCCCA GACCGGTGTCATCTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGTGAGAACCTTGCTTTT [CT]TTCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGGCCCTTTNATTTCTTCTTCCCTCTATTCC CCTCTTTCCCAATGTGCTAAGGTCCCAATTTCCAGAGCCCTCCACG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCTCATGCTCAGTACCAGA[AG]GTTTGAGTAC GGTCGTTAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGTGGACATCTATACCCTCTGGCTCTGAAAG GCTTGCAACCAAAATGGGCAGCTGGGCTAGGCAATTTAAACAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCTCTCTCAGCAAGGCAAGGATGTGGT[CT]CTCTTGTTTCTG AACAGGCCCGAGGGCAGCCCAAGGCATGCCATCACTGCGACACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAAATTTTGTGTTTAAATTTCTATACAGAAATGGTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGGCAACTCTTTAAT[AG]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTCAACCCAGCTACACTTTACCTTGTATCTATAAAGTGAATTTAGAGT AAATACATTGGCTGAAGTGG[AG]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTCGACAGTTTGTCTTATGTGTTTCAGACAATCAAGGNTGCGCTTCCAGGCAGGCCAGTGCT [CT]CTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	---	ATTTCCCTTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT[CT]TGGAA ATCTGCATGATTAATAACATTAACAGTTTCAATAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCCGAATGCAAAATAGGTATCCCTCAAAATGCACATTTCTCCTCTAGTT T

WI- 21763b	154 A G ---	---	CATACCCTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[GA]GACAGACATTGCCTGTGCTTCTACCCAGCAGCTGCTAGTGCACIT GA
WI- 21763a	135 T C ---	---	CATACCCTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGCTAGTGCACIT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTGGGGTGCACTTCTTCTTATCTTGAAGCCACTTGGGTA[AC] TCCATTTCCAGCTCTGCACCTTCTCCAGITTTTCTCATGTCAAGTCCCTGGAGGGAGGAGGCTTCTTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTTT/C/GAAAAAATACACAATGGGAAGTACACA
WI- 21965a	112 A G ---	---	CAGGTTCCACAGAGGCTTTTATTTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCC[AG]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTTCAGGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI- 21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAAOCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG[C/G]TGTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGAGGAGGAGCTGCTGGAG AG
WI- 22374a	149 T C ---	---	AGCTTTTACAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAATTTTCAACTATTGACTATACAGAG TCTTCAATTTCCAAAACAGTTAATAGTAACTTGGTGGCACATACACATGCAATTGAATACTCTGTAT TATTCAAGTAACTAAAT/C/JAGGNTCCTGCATCTCTTCACA
WI- 22250b	132 C T ---	---	ACTTGTCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTACTGTAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI- 22250a	89 G A ---	---	ACTTGTCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCT[GA]TAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR- 04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAAACCTCCAGGCCACCTGGGGCCAGAGCACTCTATGCCAGCAGCAC CTAGTGGCCCCAGTACGGACCGCCCTGGCCCCAGGTTCTGGGCTCTCAGGACGTCGCCAGCAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG[C/G]AGTGTCTC TTTACGGGGGCCCGCTGCTAGCTGCTCCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149 C T ...	...	GCAGCATCTCTCTCAACACCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTAGGTGGCCGAGTACGAGCCCGCTGGCCCGAGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCCAGAGGTTTG(CA)TTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGACCTGGAGTCTTC TTTGAGGGGGCGCGTCTCAGCTCTCTGGAGGTGAGGAAGAGGT
siFIBBb	412 G C ...	...	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBBa	341 T C ...	...	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siILV2	61 T C ...	...	GTCACAGAGGAGCGCTCTCGGAGGTCTCCACCATGGCTGGCTCTGCTCCTCAGT(C)CTC CTACTCAGGACACAGGTGACGCCCTCAGGGAGGGGTCTGGGACCTCTGGGCTGATCCTTGGTC TCCTGCTCCTCAGGCTCAGCGGGGCCAGCACTGACTCAGTGGCATGT
siSG1001 7c	70 T C ...	...	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TAT(C)AGGCATGAGCCCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
siSG1001 7a	33 G A ...	...	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCG(CA)ATCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
siSG1002 3	63 A T ...	...	TAATGATAATTAGGCACTTCTCCACACGAGGATGACACAATTGACCCAATATCATTTGAGGC(A/T) AACAGTTTGGGCTGTTTTCAGTAGTATGACAGTGA
siSG1009 6	36 G C ...	...	GTGGAGAAAGATCGTCTTCTCCCTCCCATGACC(C)GGCTCCCGGGGACCTGTGCGTTTCC ACCCGAGACGGCCTTTGTAGGACCCACTGCCCACCTCGCTGTGGCTGGGTTCCGCTCTCTAG GGCTCGAGTGTAAAG
siSG1011 8	107 C A ...	...	TAGGCTTAAACCTGGAACTTACAAAGCCAAAGTCCCTCCCTGAGGGCAGTACCTCCATTGGGC ACAGTCCAGACCAAGTCAAAGATGCCCATTCCTTGG(CA)CTCAGCCCTCAGTTCCTTCTATCC ACGAGCCGCTGGCTGTTGAGTTTCTCCCTCCAGTGAG
siSG1012 0	89 T C ...	...	TAGTAGTAAGAAAGCAAGGAGGATTGCTTATGGCAGTCTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACTTAATA(T/C)GTTGTTGTAATCTGATTTTATCCTCGTCTTACAAATG
siSG1017 8	42 C T ...	...	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG(C/T)GGGAGGAGAAAGTGAACAGGAA TCGATTCTTGTCTTAACTGCCCCCTAGTTAGGAGATGTTAAATACTTGGC

stSG1019	3	136	GA	---				GGACAATACTACCTAAGGACAAATACTATTATAAAAAAAGTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACITTTTAC T(G/A)JTTGAAAACTGAGATTTAAGTTGCAAAC
stSG1020	2c	143	GT	---				AAAGCTAACTTAGGTGAATGGTCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCCTGGCTTGCAGAG AGTCAGCCTTGGTCACCTCATACGGGGCTCCAAGCTAAGGCTCAAGGGAAGCAGTCCCACCTGCTTCT CGGTGTCAGTCAAGACCAAGGCAGATGCCACTGCTGCTCTTTCTTGTCTACTTTCT
stSG1020	9b	75	AG	---				TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCCTCTTAAGATCCCACTTAT TTTTA/G/GCTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1020	9a	34	CT	---				TCCTTTCTCTTTTCACTCTCAGTCACCATGATTTC/TAATAAACTAATTCCTCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1021	8	29	TC	---				TACTAGACATGCAAAATGAGAAGATTACNIT/GJGTGAATATTTAAAGAAGTTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAGTTAAAGCCAGTTATTTCTGA
stSG1025	2	108	AC	---				ATAGGTTTCAGGAACAAATCATTAAATGGAAAAATGAGAAGATCTTTATTTTGGACCAATTTT AGGCACCTTAAGAGTTTCTTTCTCTCTTCCCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915	0	123	AC	---				CTGTATTAAATGAAGGGCACTATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAATTCGTGAC TTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/CJATTTTAA GAACTGAGTTATTGGAC
EST11023	1	166	TA	---				TTTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAATAAAAAATAGTACATGTTA/TJ/GTGTAAATAAAATTTAAATTTACAAAAGGCTTT TCCACTCGTGGAATTGATTCCTTTTGGAGGAGGGAGTAATCCTGG
EST14096	8	71	GC	---				GGGATGTATATTACAGATAACACAACCTCACAATATACCATCAGACATTTGAAAACCTAAGGCCATTCT GTG/GC/JTTATTTTAAACCTTGGTTTGCACATAATGATCTTAAAAAATAAATGAATACCAAA ACCAAGATCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113	6c	125	CA	---				TGCAAAATGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAATGTGAGGTG CAGGGATGCTTAAGTCTTCCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCCTCTCA/CJ/CCCTTC TCTCAGGGTCTGGAG
EST22555	7	60	GA	---				TCAAGCATGTGTAAGGCACCTGCCCGGCCAGACCCCTCTAACTTCTGCACACTGGAAGGTG/AJAAA CCTGGAGAGAGAGACACTCCCTCTCTAGCTTCTAAGTGGCACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	---	GTAAACCTTGCAAGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/CTTGACATGGGCCAAAGACTTCCAGACAAAGCACCGGAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGCTCTACTCA/ A GTTGGTTGCTAGCCTCACTGCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACTCTCCA
EST36745 3	56 A G ---	---	---	GAGGGGGAACCTCAAGAGGATTCCACAGTGAAGCAGATCATGGGGCAAAAGTC/AG/CTATGG GGCCAGACTGAGGTGGACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGGC ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTGATCTCTGAGACACATTTATAACATTCTGGTATG T/A/TTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATG/TTGTTTGAATAAATAACAAATGTGTGATCTCTGAGACACATTTATAACATTCTGGT ATGTATTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCA/CT/TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAATAACAAATGTGTGATCTCTGAGACACATTTATAACATTCTGGT ATGTATTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	---	TATCGTGGGAAGTTCCAACTCATACCTATGCTGCTTTTCTACTTGTAAATTTGGATGCTCTTGCCA GGCTC/CT/TTAAATTTGCTGTAACTGGAAGAAACCTTCTACTCTCCACAAACCTGAA CAATCTGAAGAGATGCATAGCGGATGGTGGCTTTCAGCAGCTGCGGAGGTGGAGTGGAGGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAATAATTTCCGGACCTAGATA/CT/GTGACGA AGGTAGCACGACACTGTGAGTGCATAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAACTGCAAGCAAAATCACTGTTAATAAGAAATGTTCTTCTGTT/CT/GACAGTTG AAGTGGGTGAGATGGCATAGCAATGAACAGTGGGAGCCATGAGGCTCAGATGCGGGGCAAA CTCCTCTGTGAAATGTAT
siSG1026 6	55 T C ---	---	---	GTATAATTACGATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAATCTTTTACA AGAT/GAAGCACAGTAGTACAATAATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---	---	---	CACITTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCAGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTGATATGCAATAACAGCAAAATAATTTTTCAC/CT/CTTG TCAATGCCAATGCATTGAAGGCCAGAAAAATGAGAAAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 C A ---	---	---	

siSG1033 1b	116 TC ---	---	TTTAAAGCTACATGTCGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAACCTGCTCCTAGGAAGGCTAGACCTCAAAACACCAACACCTCCATTCGCAATTCCTCTTTGG CTACTATGCTCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGACCTCC
siSG1033 1a	107 AT ---	---	TTTAAAGCTACATGTCGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAACCTGCTCCTAGGAAGGCTAGACCTCAAAACACCAATTCACCTCCATTCCTCTTTGG CTACTATGCTCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGACCTCC
siSG1243 b	225 GA ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATGCTTTAGGCCAGGATTCGACACCGCTGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCCTGTTCTGAAAGTATTTTCAGACCAAAAGGAGGT
siSG1345 b	60 GA ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAAGTGTGCTTCTTACGAGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1345 a	54 TG ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAAGTGTGCTTCTTACGAGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1385 b	117 TG ---	---	TTAATGTCATCCAGGGAGGGGCCAGGGATGAGGGGAGGGTTGAGGAGCGAGGCGAGTTATTT TGGTGGGATTACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTGTTCAATCATTAAGAA GACAAAGGTTTGTGAACCTTGACCTCGGGGGGATGACATGGGTATGGCCTCTAAACATGGCC CCAGCAGCTCAGTCCCTTTCTGTCG
siSG139	69 TC ---	---	TCGTCTCCTTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTACCGCACAGCACTTTGTGCT TTCGCTTTGAGCACTTGCACCTGGCTGGCTGGCTGCCACTGATTGTGTAATGTTGCTGCTGCC
siSG1427	103 TC ---	---	GATCTGTTCCAGACAAGGCTGATTTCAGAGACTCCACGTGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTCTGTCCTCATTCAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCAAGTCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
siSG1471	50 AG ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCAGTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
siSG1483	44 TC ---	---	CANAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCCTTTAATCAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTCTTCTTAGTTCTGCAGATGGGTA
siSG1896	67 TC G ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCCAAACCAAGTGTGCA TCGTAATGTGGAGGATGCTGTTGCAGCTGTAGTACTAATGCAGGAAACCCCAATGCAGGAGGAA AATGCCTGA

siSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGTTAAATAAAACAAGTGAGAGACG[G/ATTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGCT TCAACACAACCTG
siSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGC TTCNAACACAACCTG
siSG1897 a	83 AG ---	---	CTTAATGCCCTTCTCTCTCTGACAGGAGACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[G/GCCCAACCACTTCTCTCCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---	---	TGCTTGAGGTTTCAAACTCGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATATACAT[C/ATTTCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTTGTTCAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGGCATTTT
siSG2108 c	71 AG ---	---	TTGAGCAACAATGATTTCGCAATTGGGCAGCTCCAACCAAAATGATT[C/G]AGGGCTCCACAGAGA GAGC[G/AT]AAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2108 a	49 TC ---	---	TTGAGCAACAATGATTTCGCGAATTGGGCAGCTCCAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2141 b	173 AG ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATATCTCAGAAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G/AG]AGTTCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCAATCTTGTGCTCTG
siSG2141 a	113 CT ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATATCTCAGAAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTAAAGGC AGTTTCAGAGCACTGGCAATCTTGTGCTCTG

stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTAGTGCATATTTTAGACCGTGAATTCAGAAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGAGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATGACCCAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGCGTACTCAGCTAATGCTACCGGGTTGGCGCACACCGAGCCCGAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGAGTGAAGGACCA
stSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGTAACTTTGAGCACCTAGTGTCTGAGTACTTCTGATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGTTCTGTATGATG[C/T]TTATATTATGTAT AATGTCTTACCTGATGATACCCAAACATATTACTAGCCTTAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCCTGCTCCTGCTCCCACTACTACCCCGTCCAGCAACTGCTCTCGTATAAATAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTCAAGAACTCTGCCAAGCACTGGCTGCTCCTCAGGAGAATTTCTCCT
stSG2306	67 A G ---	---	GTCAACAGCGTAGAGGTCACCTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCCAAACTGATACACCATGAGGTGAACACTTTCAGTGTTCACAG TTCCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT/GTTGCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAATTTGCTTGAAGTGAAGTAACTGCTGTCACT[C/ G]TCTCAGAGTCAACATTACGGTGAAGTGTCTATTTCTGGCTGTGCTTCTTCTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGTATTCACAAATAACAAGTCATGTATAGAGAATGTAAATGATACTTGAAACCAA GATATATAAAATATTGAAGTCATTTATGCCTTTTGTAGTACTGGGTTAAATATGCAAAGCAGCTAAAG GAATAT[C/T]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAATTCAGAGGATTTTAGACCAACTTTGCCCTGTGCTATCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCAT/G]GAACAATC CCGGCCCAAGATTAAITAT
b			

siSG2577						AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCGCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[G/T]ATGAACAATC CCGGCCAGATTATAT
a	121	CT	---		---	
siSG2700						ATCTCTGAGTCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTCTCCGGCCCC[G/A]AGTCAC TCAGGTTTCGGGAAATAAACCACTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGACACCA
siSG2724	58	GA	---		---	
b	101	TG	---		---	AAACAAGCTTTGTCATTTCCACTACATTTTGTGCTTTTATTAATATTTGCAAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTTTAACTCTGGGGTGTGAAAGAAC GTGGCCGATCTTTACTTTCCAGAAAGGGGTAATAAAACCTGTAGAAAGTCTCGAATATGC[G/
siSG2776						AJTATGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAAACCACAAA ATATCCACTAATCCCGAATATAGTAACTGCTTGTCCGAATG
a	65	GA	---		---	
siSG2791						AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTTAGCAATTTTAAATAATTT[G/T]GGGCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
b	109	GT	---		---	
siSG2791						AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTTAGCAATTTTAAATAATTT[G/T]GGGCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
a	100	AG	---		---	
						CCGCAATTTTCAACACACATTTCTATGAAACTAAGGTGGATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAA[G/T]GAACAAAAATAAGAAAGAAACCCATGAAATGCCCAGGTTTA ATTTTTTTTC
siSG2826	85	CT	---		---	
						ATGGTGCATTGTAAAGGCAATTAATACTTTTTAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
siSG2850	88	GA	---		---	
						ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGCAATTTCTGTGGTGTGAGC AA[T/C]GCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
siSG3031	71	TC	---		---	
						GTCCCAACTCTCTCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAAGAAAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
siSG3058	81	GA	---		---	
						CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCATATTGAAAAACAAGCCAAAGTTC CAATCCAAAATAATAAATGAACGTG[T/G]GATAAACATTCTTCTATGGTCCAGCCCCCTACTTT AGTT
siSG3092	94	TG	---		---	
						AAGAAGTACTTTGTAGCTATTTAAATAAGAGGGGGTGGGAATGATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTTGTCAGTGGAGTC[AG]GTGGGGTGTGAAGTGTCTGAAGTAG
siSG3230	95	AG	---		---	
						ACATCTCATOCCAGTAAGATGCAAGAAAGGAATATCTGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCACCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGT[G/C]GTACTTGGCTTAAGTACTCATGCTTTAT
siSG3245	160	GC	---		---	

siSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/GC/GCATTGTGAATAGTTTCTCAG TTTTATTATGGAAGATGATGATTTTACAGCCACATTCAGTGTATGTTCTTAATAACACAATCGAC AGGACTGTCTGTTGAGTACAAATGGAGGACAGCTTTTTCAGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTGTGACGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 C T ---	---	TGTAATTACTGTGTCATCCTATCCATTCCTTCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJGTAGATCCCCAAGTCCCTGACACATTTTCTTCAAGAAACT
siSG3269 a	24 A G ---	---	TGTAATTACTGTGTCATCCTATCCATTCCTTCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTCAAGAAACT
siSG3284	130 C T ---	---	TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATTACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACTTTTGTAAATTGCTGTAAATGGGACATTTGTTGTTTGTATACCC
siSG3292	99 A T ---	---	GTCTCAAGTAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/A/TJTAACAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGTCTCACT/C/AJCCAGTGTATCCATTTTCCCAGCCGTAGAGCTTTCTG TTTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGCACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTTCATTCCTTTTAA GATCCCCAGTATTATTTCTAANTGAATGTTGTTGGAATATAAATACTGAGGACCACTCAGAG GG/C/TJATAAGGGAACCCCTCTTTGCTTATAGTTTCAAGGACTTTCT
siSG3369	69 C T ---	---	CAAGACTGTAAAGACGTAGGCCCTTTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACATCCCGAGGAAGGAATGACATTTCCAACTGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
siSG3398	125 G T ---	---	TCTTACTCTGTTAACTAGTCTGGAGTAAAGGATGCAATCACG/A/GJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCACCTCAGCCAACTGAGTAGCTGGCTGCAGGACAAAGTCAACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43 A G ---	---	GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGCGACTTTTAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGGTAACACTGAT/AJCAAGTTGCTTAACTTTGTGAAACAC TTTCTTATCTGTAACAAATGGACAAACAGAACTTTTCTTCCCTCTC
siSG3424	173 T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTCAAGGTGATGGAGGCCTCACAGA ATGAGTGGCAGAGAGGGCCCCCT/AJGAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88 T A ---	---	

siSG3463	103	C T ---	---	GATACAGAAGATAGTGTGATGGATGATGATGAAGGACAAATAATACAAATATATTTATTTG AAATAAACAAATAATGCATACACAGCTCAATGGGTACAC[CT]TGGAAACAAACCTGCTTGACTATATTA CTGA
siSG3491 b	71	G A ---	---	CAAGATACTTCATTGTCTAAGTAGTGCAGTGTGGCAATATTTCTACGAAACAGGACGATTG AAGA[GA]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCAITTAATACTATTTCTGTGATG ACAGAAATAAGTTAAC
siSG3523	33	C T ---	---	TAGCCATCTTACTCTAGTCTCTTTTGGGTTTAC[CT]GCATATATGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTGGCAATAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G ---	---	AGTACAAACACAGATTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATCTGGCCTTGTCTGAAACGCATCTCACTGTCACTTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAG[AG]TCTCTGCTGGGTGTTCTCAGTCTTGCATGAAGTATG
siSG3583	112	G A ---	---	GAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTACGAACTCTGGCATGATCCA CATCGTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[GA]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586 a	60	G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTTAAATTTAAAAATCAGGTGTGGTGG[GC]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101	T C ---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAGCAATCTGGCCATATCAAAGGCCAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGA[TC]CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAAACAAAAGCTATATACAC
siSG3590 a	70	A T ---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AAA[AT]TTTCTCTGATGTC[CT]TGACCTGTAGGAAACACATTCAGTTTCTACACT
siSG3619	78	A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCTTTA[GA]ACAAACTCCAGAGAAACTGGGCTCTATATTTAAG
siSG3644	40	T C ---	---	ACATATGTAAGTCCCATTTAGTAGCCATATTTAGGATGAGAT[GC]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCAITATGAATAATAAGTTATCTGGGAAACCGCCATTGTCCCAACATTTACTAA GTGCTCTACTA
siSG3646 c	70	G A ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAATATATGATGAACAATAATATGCTTACT GGT[GA]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAATA[A/G]TATGCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATG[A/T]TATGATAACAATAATATGCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTCTCCCTCTGAAAGCGGATGACCATCCAAACCCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTCTC[C/Q]/TTCGAAAGCCGATGACCATCCAAACCCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 G A ---	---	TCCTGCCCTTTGTTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]GAATAACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCCTGCCCTTTGTTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTATTGGGAGATAACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGOCATCCTGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTCT
stSG3725	104 G A ---	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGGAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATTACAGCCAAACAGCAACAGCCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTATAGAAAGATGATTTTG AGGGCTTCAGTATTAAAGGGGAAAGCAGGCTGGAGGGAAAGAGAGAGGATATGGTCCQ[G/A]TT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAATCCACATCATTTTGGTAGCAGAGGATCTTTA[T/A]AAAGTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAAATAAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115 G C ---	---	GACAAGAGGGGAAGAGATGCCAGAGACAGGGCTGGGGAGCTGGGGTCCCTGAGTGCAGGGCGC CACCACACGTCTGTGGGTCAAGGCCCTCCTCTGGGGAGAGGTTCTAG[C/G]GGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

siSG3880 a	36	G C ---	---	GACAAAGGGAAGAGATGCGCCAGAGACCAGGGCTGCGCGCAGCTGGGGTCCCTGAGTGCAGG CGCCACACACAGTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTCTCGCCCT
siSG3895	44	A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTGTA/GJTTTTCCTTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAT
siSG3902	104	T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCCGACTCTGGTGGAACTCCGCTTCCTGATAACA TCATCTATTTACACCTAAATGTGAACCTCTTTCTTTCTG/CJTCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
siSG3935	50	G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTCAACAAGCAATTTGTCCG/CJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACTTCCTGGACGT
siSG40	25	A G ---	---	GAGGAAGAGGTTGAAGAAGTGTCTGA/GJAAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCAA
siSG4009	32	A G ---	---	GTGTGGGCTGCTGATGAATGGCGGCTC/CJGTACTCTTTACGGCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
siSG4033	123	T C ---	---	AGAAAGCTTGGGACAATGGCAGTGCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT/CJGTGTAAC AGGTGGCAACAC
siSG4038 a	29	G A ---	---	GCTGAGACGCTGTACAGCCACGCCCTGTG/CJCGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGAGAGCACCCTGAGGGTTCCATCACT
siSG406	53	T C ---	---	ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAAT/CJGGTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTCTCTAACAGAGATTATTAACITTTTATCAGGTGT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGTACTATTGTCTGCTAGATGTATTAG/CJATAAAAA GTTTGCTCTGTAATACITTTAAAGTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27	A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGT/CJGATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTCTGTAATACITTTAAAGTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65	G A ---	---	TGCATGTTCCACATCTTTCATACAGGAAATGTATAATAAATACCTACGTACTTATGGATAATCAC/G A/CITTTTCCCTCAGAGAGCCCCACAGTTAAACAGGTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54	A G ---				CTTGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGTGTACATTCT[AG]TATATTTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTAAGTCACTCTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGG
siSG4209						CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCCTTGACAGGCGGCACTCCCTC[GA]GC AGGGGACCAACGAGGCGACAGTGTCTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
siSG4209	128	GA ---				CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGGCTCACAAACATCCACATGGCACAA[AG /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCCTTGACAGGCGGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGTGTCTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
siSG4254	65	GA ---				CATTACCCAGAACCCCATGGAGGACAGAGC[GA]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGCTGCTCTCCCCAGGGGCGAGCGTGAC TGGGGGACCATGGCCGAAGAGGATGACCCGGTCATG
siSG4301	81	T G ---				TGCAACAGCTCTGAGAGGAATCCTTGGCAGATCAAAAGAGAGGTAGTGGCTCCACACATTCCAT TTAAGCAATAAATTT[GA]GCTTCTGAGTAGTGTGCCAGTTTACCCCAACATTTTG
siSG4331	71	T G ---				CTCACAAAGGCCAACACAGAAAAAGATACAAATACATTATCCAGCTAATATTAGTTTTATGACAC AGAGT/GTTTTCAACAAGTTTAAGTGTCACTGACGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTTCTGGCCTCGCCCTTGATTTCTGTTGAGGGGTGTC
siSG4340	76	GA ---				TTTTGCAACAACATGGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAACC ACATGTTCTC[GA]TAAAGTGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361	109	A C ---				TTCCCAACCATAGTGCAGAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTTGC[AG]CCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
siSG4361	24	T C ---				TTCCCAACCATAGTGCAGAGAGCT[AG]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTGCACCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
siSG4376	73	A G ---				TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTCGAAGTCTTCTCCAAAGGGAG AACAG[AG]CTGGAACTGGGCTCTGCAAGAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50	T C ---				GAAGGCCACAAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTT[AG]TCAGTCTTGTAGT ATCCACAGTAGTGTGTGTCCATGTACAAAGTGTCTGCCAGAACACCCATTAAATTCATGCC
siSG4410	79	A/G ---				ACCAATGGTTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACACCGC[AG]GTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT



[illegible]

stSG8362	88 G C ---	---	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T ---	---	---	CACATCTGTGTTCTGGAGCAAGGGAACACACAGAGGCCAGGAGTTTGGGTGTGCACTGG[G/T] GTCITTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAGAAGATAGA TGCTT
stSG8022	53 G A ---	---	---	AGCTCCTGACTCCCTGTTCAAGTGACGTGATGTTGGTAGCCTGAAATGGAACAC[G/A]GTGGGAGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATCGCTTATTCTTTTTCAGAGGGCAGGTT TATCAGCACACGCTGATCTCC
stSG8032	67 G C ---	---	---	TGATTGTTAGGATAAGTGGGCATTGTGTTACAAATTACTCCAAAGAAATTCAGAAAATTGTGTGTT G/C]TGGAGGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46 C A ---	---	---	AGCTGGCTCTTCTCTGTCGTGTCGGGAGGCTTACGTCTCTG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAAATGCCAGGGAGAAATTCCTGTACATCAACACGGGAACA
stSG8064 a	23 G C ---	---	---	AGCTGGCTCTTCTCTGTCGTGTCGGGAGGCTTACGTCTCTGCGCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAAATGCCAGGGAGAAATTCCTGTACATCAACACGGGAACA
stSG8072	59 A G ---	---	---	CACCATCATACATCGAGTAGGCTAGGAGCAGGAGGGTGGGTCTGCTGTCTTAGGG[G/T]GGC AGAGGCAGAAAGGAAGTCCGAGTATTAGTGGCCGATGCAGTCAAGCCTGTGCTGTCAAAA
stSG8100	40 A G ---	---	---	ATACCCACACACCCCACTCAACCTTGTATCAAAITCCA[G/A]AAGTGTAACATAAGATATAAGAA ATCATGACTAGTTAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG
stSG8102	138 T C ---	---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCCATTTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGAT[C]TGTCAATAATCAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110 A G ---	---	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGGGAGTTCCTGTTGGAGTCTAGGCTGAGAAATATTC[G]TTCTAACAAAGTTCCAGGTGA CCCTGAGGCTCTGGACTGGGAACATGCTTTGAG
stSG8130 b	96 T C ---	---	---	GTGTGATACATTTGGGAATGGAGGAAATAAATGACTGGATGGTGGCTGCTTTTAAGTTTCAAAT GACATTCAGACAAGCGGTGCCTGAGCC[T/C]GTGCCTGTCTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G ---	---	---	GTGTGATACATTTGGGAATGGAGGAAATAAATGA[C/G]TGATGGTGGCTGCTTTTAAGTTTCA AATTGACATTCAGACAAGCGGTGCCTGAGCCGTGCTTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124 T A ---	---	---	TTGTGGACTTCAAATCTTCTCCATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTTGTGACACAAATCTAAGAAATGAATGAGATGTTT[A/C]TGAAA TCTGATTCAAACACTTATCTTAAACTGACTCTCTGTCAATCCTCTGTCTCTGTGAAGG



ESTD-AT3a	--	--	---	---	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAAGTGGAGGAAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
ESTD-B3AR	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGCGCGCCTAGCCGGGGCCCTCTCTGGCGTGGCGTGGCGTGGCCACC GTGGGAGGCAACCTGCTGGTCACTGTGGCCATCGCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCCGTGGCCGACGCGACCTGTGATGGACTCTCTGGTGTGCGCGCGGGGCCACCTT GGCGC
ESTD-BA511	--	--	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTBCAG TGAGCCAAAGTGTGCCACTGCA
ESTD-BCL2	--	--	---	---	AGCTGGATTATAACTCCTCTTCCTTCTTGGGGCCGTGGGGTGGAGCTGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGTACGACAAACCGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCCAGAGGGGCTACGAGTGGGATGCGGAGATGTGG GGCGCGCGCCCCGGGGGGCGCCCCGACCGGSCATCTTCTCTCCCA
ESTD-BCR	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTACAGAAACCATAGAGCCCCGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTTGCCCGGGAAGGAGGCGAGTGACAAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGGCACA
ESTD-BRCA1a	--	--	---	---	AAGAAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGGAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTAGGAAAGTATCTGTTACTTGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTTCAATGTACCTGAAAGAGAA ATGGGAAATGAGAACATTTCCAACTACAGTGAAGCAAAATAGCCGTAATAACATTAGAGAAAAATGTT TTAAAGAACCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTACCCTACACATTTGGCTCAGGGTTACCGAAGAGGGGGCCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCCTCCCTAAATTTGCTCCGGGAAGCACATTCATCAA CCCAGTCAAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCCTTCAACCATGCATTCATCAA GCTCTGCAAAAT

ESTD-C7	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATATGGAATGAGGAGACATCACCTGGAATGTTAG
	--	--	---	---	---	GCAGTGCCTAACTGGGGATGGACAGACAAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC
ESTD-CB23	--	--	---	---	---	AGGCAAGGAAGGGTAGAACCAATCAAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAG
	--	--	---	---	---	TAACATAATTGTCTTCATTATGCTCTTCCGGCCTTCTCTCACACAC
ESTD-CB24	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC
	--	--	---	---	---	TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACACAGAGCCCTACACAGGACCAAGACAGCT
ESTD-CB25	--	--	---	---	---	CTCAGAGCAACCTAGCCCATACCTCTCCCTTCCAGAGGAACCTGAAAAACGTGTCCCAACCGGA
	--	--	---	---	---	GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB26	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA
	--	--	---	---	---	AAACGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG
ESTD-CB27	--	--	---	---	---	GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGACACAGCTGGAGCTGGTGGGTGAATGG
	--	--	---	---	---	GAAGGAGGTGCACATGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB28	--	--	---	---	---	GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTTCGCGCTC
	--	--	---	---	---	TCTGCTCTCGAACCCAGGGCATGGAAATCCACGGACACAGGGGCTGAGGAGGCCAGAGCCACCTG
ESTD-CB29	--	--	---	---	---	TGCACAGGTACCTACATGCTCTGTTCTTGTCAACAGAGTCTTACAGCAAGGGTCTGCTGCGCACC
	--	--	---	---	---	ATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGCTG
ESTD-CB30	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT
	--	--	---	---	---	TGTGTGTTGGGCTGGTGCATTTGAGGAGTGTCTGTGGAGTCTGCTCATCATCAGACCTATCTCTGA
ESTD-CB31	--	--	---	---	---	TTTAGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCTGCT
	--	--	---	---	---	TTCTCTGTTCATCTGATGGAAGTCTCAACACCAATTTCCATACC
ESTD-COL2A1c	--	--	---	---	---	AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA
	--	--	---	---	---	GTGGTGACATACGTGTCTATTATGCTCTCTTCTCTGTCATTTTCAGGTGTTCAAGGTGGAAAAGGT
ESTD-COL2A1d	--	--	---	---	---	GAACAGGTCCTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAACTGCTGCTTTG
	--	--	---	---	---	GTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD-COL2A1e	--	--	---	---	---	TGAGAAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC
	--	--	---	---	---	AATAGACTGAGTTGCTGGGACCTGGAACACTGGACTTCTTCTACTGACGACAGCAAGACTTACCC
ESTD-COL2A1f	--	--	---	---	---	AAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAAACACTATCATGGAACAGC
	--	--	---	---	---	ATT
ESTD-CPT2	--	--	---	---	---	GCCGCAATGCCCCGGGAGTTTCTCAAATGTGGGAGAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA
	--	--	---	---	---	GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCTCATCATGAAAC
ESTD-CPT3	--	--	---	---	---	TGGGAGGCGGGCATAGTCTCATGCCCTGTAAATCCAGCATTTTGAGAGGCTGAGGCGGGGTGATCAG
	--	--	---	---	---	TTGAGGTGAGGAGTTTGAACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	---	---	---	ATGGCTGGCCTTGGAATTCAGCGGCACAAAGGCTCAGCTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTTCATCCCTGCTCTGCAAGCAATGCAGTGGCCAGCCCTGCTGTGGT ACTGGCCAGCAGCGAGGCATGCCAGCTTGTGTGTGATGTCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	---	---	---	CAGCCAGCGTGGTCGAGTGGTCACCATCCCGCAGAGAACAGTCAAGCCACCATATGCACAGGT TCTCATATTGAAGCTGCTCTCAGGGTTCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	---	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCAATAAATTCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTACTTGCATCTAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATATGCCCCATAT CTGCATGTC
ESTD- D17S33	--	--	---	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCTCTGCGGGCGGTG GGGTTGTGGCTATGTGGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	---	---	---	TTTGAGACCACCTGGCCAAACATGGCAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCCAAGATCACACCCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	---	---	---	AACTGATTAGAACCTGAAATACATAATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTAATAAGAAATTAACAGAATATCATTTGT TTATTCAAACTATTATCACITATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	---	---	---	AGGTCCACATTATGCTGATGTTGCTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTGTTATTAAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAATATGGTCAGGTACAGCTGATATCCC AGAAGTGAACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTCCGCTTCACGAIGG CAGGTATGAAATATAATAATCTGCTCTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATCTCCTTGTATCCATGGACTGCAGAAATAAATGTATTT TAGCTGTCAGAAAACAATACTATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCATGAGTAG
ESTD- D4S95	--	--	---	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAAACAACTTTCAAGG ATAATGGGGCAATCACCTTCTTCTCTTCTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGCTGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGAGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCCTGTGGGTAGGGGAGCTGCTTCCAAAGCC TCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	--	---	---	---	TCCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCACCTGAACCTCGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	--	--	--	--	---	---	---	TCTGCCCTTGGTGCAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACACAGCTGACTCTCCCGGACCCCG TCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCAAACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	--	---	---	---	AAGCAGTGGCCAGGATGAGGGCAGTAGGAGAGGCGATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCAAGGTGTAGTTAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ER8B2	--	--	--	--	---	---	---	TCTTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTGAGCGGCTCCACAGCTGG GGTGAGGGGTGGTGGTCACTGCGGGGGCGGTGCAGACCCACGCGGGCTGGGAGGACTTCACCC CGCTCACTCCGTTCTCGACGAGTCTCCGCTCGTACT
ESTD- ETS2	--	--	--	--	---	---	---	ACTCACAGTGCTTTTAAAGTAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCGGCGCTGGCA GTCCGTGGAGCGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGTGACACACAC AGACTATTTTATGATTTCTTTTGCCTTTTGCAACAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	--	--	--	--	---	---	---	GATAAGTACACTGAGGCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCC AGCCAGTCCCGGGGTGGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGAGAGGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCTCAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- GODH	--	--	--	---	---	---	CGCAGACCGGTGAGTGGGGTCGGGAGTGTGAGGGAAGGAGGGAGGAACCTGGGGGTTAGGGACT TTCCGGGGTACTTCCCGTTCTGTGCTTGCAGAGAAAGGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGGTCGCACCGTGTGTTCTGCTGCOOCTGTCAGCTGCTGCTGCGGCAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	---	GTTTATGTCATGGAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGTGTCACCATGAC AACCACAGGCCCTCTCAGGACACAGTAAGCCCTGGCAGGAGATCCCCCACCCACACCTGGCTGG AGCAGGAATGCGAGCGCGCTGAGCCCGAGGAGGAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG
ESTD- GNAT2	--	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTTACGGTAAGTGCATGGTTCCTTAGG
ESTD- GPPK2L	--	--	--	---	---	---	AGTCTTCATCTGGGGTGTCCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HPAS	--	--	--	---	---	---	CTGGGCTGCCCCGACGAGCTGCTGGCACTGGAGCGGGGCGCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACACTTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCCTCACAAAGCTATGATAACCTTAATACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTTTATCCCTGATGATGATTGGATTGGCTTCTGCTG
ESTD-HT2	--	--	--	---	---	---	GGGCTAAAATTTCCGAGCAACTTTCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGAATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	ACCAACGAGCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCCCTTCTATCGGCAAGAAATCGTACTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	AACACAAAGCCCCAGCGAGAATTGAACTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGGTTTTCTCTTTCATCTTATAGATTGATGTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTCACCGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTCCTACATTTGTGTGAGTACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACGAAAGT ATGTAATACITTCACAAAATACTAATAACGGAGTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGCACCCTAAATGTTAGCTATTACTATCATTAATTATTATTTATTTTATTTTGG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCCCTCAGCTCCGAGTAGCTGGGAATACAGGCCACCGGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTAATCTTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCTTAGCCGTGGGAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAAATGTAAACGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAAAATTTCCAATATGTAGTGTGTATACCTGCCTCGCCATGCAGCATCATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGTTTTGCTTAATCTCAATCAATGCTCTTTCATCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCGTTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACACATTTTATAAAATTTTTCACCTG
ESTD-MOC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCAAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGGTTTGGTCTAAGTGTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCACTGGTTCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAATATACCAGATCCACAGACTGATATGGCTGTT

ESTD-NFKB1	--	--	--	---	---		AACATGGACTTGTATATTGTACAAAAAAGTTTATTTTTCTAAAAAAGAAAAAGAAGAA AAATTTAAAGGTTGTAATAATCCACACTGCACACTGCTAGCCCCAAAACGCTTATTGTGTAGG ATCAGCCCTCATTTTGTTCCTTTGTGAACCTTTTGAGGGACGAGAAAGATCATTGAAATTTCTGAG AAVACTTCTTTTAAACCCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	--	--	--	---	---		TGTCCTTAGGCCAGCCCTGCTTGCTCCCTGGCTGTATCTTCAGTACTGCAAAAGAGAACACAGAC AT
ESTD-NRAMP	--	--	--	---	---		GGAAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCOCACAGACCAGAGAAGCGGCCCTCAGTG TATCCCACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAAGT
ESTD-NRAS	--	--	--	---	---		GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCAIATITCTTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTATGTAGGTGATATGGACTTTTTTTGTGTGATATATAIATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---		GTGACCTTCTCACITTTAAAAAACITTTACGGGAGAAAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAACAGAAAGGAGAGGTATGTAACA
ESTD-PAI1	--	--	--	---	---		GCCACCACCCACCCAGCACACCTCCAACCTCAGCCACAGCAAGGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGAGTCAGCCGTGTATCATCGGAGGGCGCGGGCAC ATGGCAGGGATGAGGGAAGACCAGAGTCTCTGTGTTGGGCCCAAGTCTAGACAGACAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---		CTCTCAGGAACCCAGTCTCTTACCACACAGCACTTATGCTGCCGAGAGGTACAACCCGTAAGA ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTCCTTTCACITTTCTGTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCCC
ESTD-PBDA	--	--	--	---	---		CCTTCTCATGCCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAATCTCTACCCGAGCTTGTCTGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	--	---	---		GGGGAGTAAACCTTGATTGGGAGATTTCAITTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAAACACACCAATAGCCTATTTCGTAGCCATATTAATTTGTGTGCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCAITGGCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTGTGA
ESTD-POMP1	--	--	--	---	---		ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTIA ATGCAGAAAGAGGGGAAAAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTTATAATCTT
ESTD-PeIRDS	--	--	--	---	---		ACCTACAGACGTGCTGGATGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGGCTGGCTG CTGGAAGAGCGTGC CGGAGACCTGGAAGCCCT

ESTD-FDS	--	--	--	---	---	---	CCCGAGGAATCTGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAAGCGTGCGCGGAGACCTGGAAAGG CCCTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAAGGTGGAAACAGGTGGAAACCGAGGGCGCAGACGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAGAAACGTGGATCTCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTGTGACGGGAGGTCAAGTCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGGAGTGTGCACTCATGCCCCG TCCTCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGGATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTTCTCTGGGAGCCTGAGGAGTGTGTGTGTGTG CAGTCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCCCTTTGGCCCCGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCCCTCC CCCACCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTCACTTTGTGGATTGTTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAGAGATCTTGGCAGTCCATGTCTTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTGATTCTGTGA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAAGTGGTACCATTTTCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCACTTCAATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACACCTTCTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THPB	--	--	--	---	---	---	TGCGGCCTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTTGATTTCCAAAGAGAAAGATGCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAATCAGAGGATCACTTCATCCA CACTGGATTGCCCAACAAGTCTGAGTGCCAGCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGTCTTACACACAAATCAGTCAGTG GCCCCAAGACCCCCCTCAGATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCCAACTTCCAATCCCCCGCCCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATATAATATGCATCCAGACAAAGAGGTCAATAATTGATGTCGTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

-300-

ESTD- TVRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTGATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTCTTTTTCACCTTTATTACCTTCTTTCT AATACAGCATATGTTAGAATTAAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCAAAGGCTCAATACAAAGTCTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACAAAGTCAAGAGTCAAGACAGGAAACCCAGTG ACTCTGAGATGTCACCACTGAGAACCCAGTATATGTTACTGGTATCGACAAGACCCCGGGCATG GGCTGAGGCTGATCCTACTCATAT
ESTD-VWF	--	--	--	---	---	AGTAGGAAAGCAAAGAGTTGATTAGTGMGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAAGTGAAGAAACGCCCTT CATGTGTCTTAACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAACTTAAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCAAAGTTGAATGTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGTCAAGCCTCAGCACAGATGCTTCTTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAAGATACAGCTGTTGGTGAAGG AGTGCCCAAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCCTCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCCCCG GTCACTC
EST51976 7	--	--	--	---	---	AGGAGAAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAGGACCTGA GGGACAAGGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAAGGAACAGCAGGAGGAGCAGCAGGAGGAGGAGGATGCTGGGC CCTTGGAGAGCTGAGCTGCCCCCTGGTGC

EST11458 6	--	--	---	---	---	CCACITTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGITTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAACTTCTATGAGCCAGGAGAGAGATTACGTAITTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGATGAGAAAGTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTTCCAGGTATTGTTGCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGTGGTGAACCTGTCTCTTGGCATTGCCGGCCCTCTCTGGGGCCCGTGG TCCTCTGTGCTGTGGTAGTCTGTGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGGTCCCAAGGTGCGATGGTCAACCCGGACACAAGGAGAGCGGGTTAOCCTGG CAATAT
EST38027 2	--	--	---	---	---	AGTGACTTCCAAAGGAAATGGCTACCCCACTTGCCCTTCATGCGCTGTGGCCCACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGATGATGGTGTCTTAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTCCAAATAGAGCCTTACCAAGTGTAT TACATAAAGAAAGTCAAGTGTCTTCTCTCATGACCAATATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTCAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAGCCACAGAGCTGCCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAAGACCCCTGTGAGCCGATTGTCTATCTCCAGCGCCCTGTCTC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCAACCCTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGAGCAGCCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAATCTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAAGTACTTGTAGTAAGGGAACCTTGAATGTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGCTGTGGGACCTGAGACCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTGTCTACTA TAGTCCAAAGTGAA



EST26021 1	--	--	--	---	---	TAATGTAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACAATTCCTCTGCAGCACATTCACATAACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAATGCATTATGGAGTGAACCGGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCCITTTGCAACAAGACAAAGCAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAAATAGCTTCTTGTTCTACTTCTCTTCACAAAGCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCTGGAGCCTTGTGCTCCACTCAATACAAAAGGCCCTCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGGTGCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGCGTGCACTCAAGCTCT GAGAGCAACCTCCTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGCGTGCACTCAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCACAGAAGAGAGGGGTGGTCACTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAAGAAATAAATTCACAGTCAA AGAATCAAGCACATTTTCGAACATGAAGTTGTTTTGAAGTGGTGTGACCTTTAATACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCCAAGAGACCGGCTCAAGG ATCCCAAGGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAAGAGACCCAGAAAT CACAGGTGGGCACGTGGGTCTACGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAACT
EST74082	--	--	--	---	---	TCCAGGTGGCTGGAOCCAGGCCCCAGCTCTGCAGCAGGAGGAGCGTGGGCTGCTGAAGCATG TGGGGTGAGCCAGGGGCCCCAAGGCAGGCACTGGCTTCAGCTGCTCAGCCCTGCTGCTGAC CCAGTACTGTCTCTGCCATGGCCCTGTGGATGCGGCTCTGCGCTGCTGGGCTGCTGGGCTC TGGGACCTGACCCAGCCGCGAGCCTTTGTGAACCAACAGCTGTGGC
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTCCAAATCTGTCCTATAGTTTCTCTATTAGTGAACATACATGCTTTTAGT GGATAGATGCACACAACACACAGCCATTATGGGGAAGGATCCAGGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST65258 8	---	---	---	---	---	TGCCCCATCAGCGGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAAGAAAT CCAGTTATTTTCCACCTCAAATGACAGCCATGGCCGGCGGCTCTTGGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCAGCTTTTGATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGGCTGTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	---	---	---	---	---	ATCAGAGTAAGGTGGAGAGGAGGAGGAGGGCCAACTGTCTCCAGGGCCCTGCAGATGTGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 2	---	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCAATTTGTTTAGCATTACCTAA TTTTTTTCCCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTTTCCCTCGAAGTCCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCGTGTGA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGATGCA
EST35879 9	---	---	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTCGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA
EST68308 5	---	---	---	---	---	GGAAAGAGATTAAAGAGCTTGATTGGACAATCTGCTTTTGGTGTGGAAGAGTTCATGCTCT GCCTGAGTTACACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	---	---	---	---	---	GGAAATTTAAAAATATTTTAAATACCTCCATTTTGTCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTGGCAATTTGTTTCTTACAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAATGTGACTTTATCAT
EST52908 0	---	---	---	---	---	ATCACAGGTCTGTGCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590 2	---	---	---	---	---	AGGAGAAGCTGAGGAGGGGAGAGAGACAAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST76136 2	---	---	---	---	---	TGAAGCTTCTGCCCAAGCTTGCTTTCTAGGAGAACCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGCTCT
EST58607 0	---	---	---	---	---	CTCTGGATGGTTACAGGTGGCAGGACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGAGAACAGGACAGCCACATGCGCGGATGCGCGGGAGTCTGGT TGCGGCACGGCTGTGGCTGTTGTGAACGGTAGCCTTTGGGTTGCGATGCTAAACCTTTGTTTCT TGCCCAAGGAGGGGGGGTGGCCTGAGATGTAGATGGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer  
6=SNP Reverse Primer 7=Sequence

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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.

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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/US98/12442 <b>(22) International Filing Date:</b> 11 June 1998 (11.06.98)  <b>(30) Priority Data:</b> 60/049,612 13 June 1997 (13.06.97) US  <b>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application</b> US 60/049,612 (CIP) Filed on 13 June 1997 (13.06.97)  <b>(71) Applicant (for all designated States except US):</b> AFFYMETRIX, INC. [US/US]; 3380 Central Expressway, Santa Clara, CA 95051 (US).  <b>(72) Inventor; and</b> <b>(75) Inventor/Applicant (for US only):</b> CHEE, Mark [AU/US]; 3199 Waverly Street, Palo Alto, CA 94306 (US).  <b>(74) Agents:</b> LIEBESCHUETZ, Joe et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> METHOD TO DETECT GENE POLYMORPHISMS AND MONITOR ALLELIC EXPRESSION EMPLOYING A PROBE ARRAY  <b>(57) Abstract</b>  The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to determine the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to determine relative proportions of polymorphic forms in transcript of the gene. Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. The methods are amenable to analyzing large collections of genes simultaneously using arrays of immobilized probes.		

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## METHOD TO DETECT GENE POLYMORPHISMS AND MONITOR ALLELIC EXPRESSION EMPLOYING A PROBE ARRAY

5

## CROSS-REFERENCE TO RELATED APPLICATIONS

The present application derives priority from USSN 60/049,612 filed June 13, 1997, which is incorporated by  
10 reference in its entirety for all purposes.

## BACKGROUND

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution  
15 generating variant forms of progenitor sequences (Gusella, Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not  
20 transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both  
25 progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP)  
30 means a variation in DNA sequence that alters the length of a restriction fragment as described in Botstein et al., Am. J.

Hum. Genet. 32, 314-331 (1980). Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. Some polymorphisms take the form of single nucleotide variations between  
5 individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Single nucleotide polymorphisms can occur anywhere in protein-coding sequences, intronic sequences, regulatory sequences, or intergenomic regions.

10 Many polymorphisms probably have little or no phenotypic effect. Some polymorphisms, principally those occurring within coding sequences, are known to be the direct cause of serious genetic diseases, such as sickle cell anemia. Polymorphisms occurring within a coding sequence typically  
15 exert their phenotypic effect by leading to a truncated or altered expression product. Still other polymorphisms, particularly those in promoter regions and other regulatory sequences, may influence a range of disease-susceptibility, behavioral and other phenotypic traits through their effect on  
20 gene expression levels. That is, such polymorphisms may lead to increased or decreased levels of gene expression without necessarily affecting the nature of the expression product.

#### SUMMARY OF THE INVENTION

25 The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to determine the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of  
30 interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to determine relative proportions of polymorphic forms in transcript of the gene.

In some methods, genomic DNA is analyzed by amplifying a segment of genomic DNA from a sample and hybridizing the amplified genomic DNA to an array of immobilized probes. In some methods the array used for  
5 analyzing genomic DNA comprises a first probe group comprising one or more probes exactly complementary to a first polymorphic form of the gene and a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene. In some methods, RNA is  
10 analyzed by reverse transcribing and amplifying mRNA expressed from the gene to produce an amplified nucleic acid and hybridizing the amplified nucleic acid to an array of immobilized probes. In some such methods, the amplified nucleic acid is cDNA. In some methods, the array of  
15 immobilized probes for analyzing RNA comprises a first probe group comprising one or more probes exactly complementary to a first polymorphic form of the gene, a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene.

20 In some method, genomic DNA and the RNA are analyzed by hybridizing the genomic DNA or an amplification product thereof, and the RNA or an amplification product thereof, to the same array of immobilized probes comprising a first probe group comprising one or more probes exactly complementary to a  
25 first polymorphic form of the gene, and a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene.

In some methods, the genomic DNA, or amplification product, and the RNA, or amplification product, bear different labels  
30 and are hybridized simultaneously to the array.

Some methods further comprise comparing a genomic DNA hybridization intensity of the first probe group to the

subset to identify a further polymorphism in a promoter, enhancer or intronic sequence of the gene.

5

## DEFINITIONS

A nucleic acid is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated.

10

An oligonucleotide is a single-stranded nucleic acid ranging in length from 2 to about 500 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides.

15

A probe is an oligonucleotide capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation.

20

Oligonucleotide probes are often 10-50 or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, oligonucleotide probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

25

30

Specific hybridization refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. Stringent conditions are conditions under which a probe will hybridize to its target subsequence,

but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances.

Longer sequences hybridize specifically at higher

temperatures. Generally, stringent conditions are selected to

5 be about 5°C lower than the thermal melting point ( $T_m$ ) for the

specific sequence at a defined ionic strength and pH. The  $T_m$

is the temperature (under defined ionic strength, pH, and

nucleic acid concentration) at which 50% of the probes

complementary to the target sequence hybridize to the target

10 sequence at equilibrium. (As the target sequences are

generally present in excess, at  $T_m$ , 50% of the probes are

occupied at equilibrium). Typically, stringent conditions

include a salt concentration of at least about 0.01 to 1.0 M

Na ion concentration (or other salts) at pH 7.0 to 8.3 and the

15 temperature is at least about 30°C for short probes (e.g., 10

to 50 nucleotides). Stringent conditions can also be achieved

with the addition of destabilizing agents such as formamide.

For example, conditions of 5X SSPE (750 mM NaCl, 50 mM

NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C

20 are suitable for allele-specific probe hybridizations.

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion

(subsequence) of the target sequence. The term "mismatch

25 probe" refer to probes whose sequence is deliberately selected not to be perfectly complementary to a particular target

sequence. Although the mismatch(s) may be located anywhere in

the mismatch probe, terminal mismatches are less desirable as

a terminal mismatch is less likely to prevent hybridization of

30 the target sequence. Thus, probes are often designed to have

the mismatch located at or near the center of the probe such

that the mismatch is most likely to destabilize the duplex

with the target sequence under the test hybridization conditions.

Transcriptions levels can be quantified absolutely or relatively. Absolute quantification can be accomplished by inclusion of known concentration(s) of one or more target nucleic acids (e.g. control nucleic acids such as Bio B or with known amounts the target nucleic acids themselves) and referencing the hybridization intensity of unknowns with the known target nucleic acids (e.g. through generation of a standard curve). Alternatively, relative quantification can be accomplished by comparison of hybridization signals between two or more polymorphic forms of a transcript.

A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as a the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

A single nucleotide polymorphism (SNP) occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is

usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

5 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms  
10 can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

#### DESCRIPTION

##### I. General

15 A substantial number of polymorphic sites in humans and other species have been described in the published literature, and many other polymorphic sites in human genomic DNA are described in commonly owned copending patent applications, such as PCT/US98/04571, filed March 5, 1998  
20 (incorporated by reference in their entirety for all purposes). The genomic locations of these sites are known, as is the nature of the polymorphic forms occurring at the sites. Many of the known polymorphic sites occur within so-called expressed sequence tags and are therefore represented in the  
25 transcript of genomic DNA, as well as genomic DNA itself. The present invention uses polymorphisms within the transcribed region of a gene as a means to monitor the relative expression of different allelic forms of the gene. Having identified alleles of a gene that are expressed at different levels, the  
30 alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. Often, the causative polymorphism is found

outside the coding sequence of a gene; for example, in a promoter, other regulatory sequence or an intronic sequence.

In the present methods, nucleic acid samples from individuals are characterized at both the genomic and transcriptional levels. The genomic analysis screens genomic DNA from an individual to identify one or more genes that are heterozygous for a polymorphism occurring within a transcribed region of a gene. RNA from the individual is then analyzed to determine the relative levels of polymorphic forms in the transcript of the heterozygous genes identified by the genomic analysis. If the levels of polymorphic forms in the transcript of a gene differ significantly from each other, further analysis is performed to identify the cause of the different levels. It is possible that the polymorphism within the transcript that is used for monitoring expression levels may itself affect expression levels. However, it is more likely that the difference in expression levels stems from another polymorphic difference between the alleles. Such polymorphisms are particularly likely to reside in promoter sequences, enhancers, intronic splice sites, or other regulatory sequences.

## II. Analyzing Polymorphic Forms at the Genomic Level

Strategies for identification and detection of polymorphisms are described in commonly owned USSN 08/831,159, EP 730,663, EP 717,113, and PCT US97/02102, filed February 7, 1997 (incorporated by reference in their entirety for all purposes). The present methods usually employ precharacterized polymorphisms. That is, the genotyping required by the present methods is usually performed after the location and nature of polymorphic forms present at a site have already been determined. The availability of this

information allows sets of probes to be designed for specific identification of the known polymorphic forms.

In the simplest form of analysis, a biallelic polymorphism forms can be characterized using a pair of allele specific probes respectively hybridizing to the two polymorphic forms. However, analysis is more accurate using specialized arrays of probes tiled based on the respective polymorphic forms. Tiling refers to the use of groups of related immobilized probes, some of which show perfect complementarity to a reference sequence and others of which show mismatches from the reference sequence (see EP 730,663). A typically array for analyzing a known biallelic single nucleotide polymorphism contains two group of probes tiled based on two reference sequences constituting the respective polymorphic forms.

The first group of probes includes at least a first set of one or more probes which span the polymorphic site and are exactly complementary to one of the polymorphic forms. The group of probes can also contain second, third and fourth additional sets of probes, which contain probes identical to probes in the first probe set except at one position referred to as an interrogation position. When such a probe group is hybridized with the polymorphic form constituting the reference sequence, all probes in the first probe show perfect hybridization and all of the probes in the other probe sets show background hybridization levels due to mismatches.

When such a probe group is hybridized with the other polymorphic form, a different pattern is obtained. That is, all but one probes in the array show a mismatch to the target and produce only background hybridization. The one probe that shows perfect hybridization is a probe from the second, third or fourth probe sets whose interrogation position aligns with

the polymorphic site and is occupied by a base complementary to the other polymorphic form.

When the probe group is hybridized with a heterozygous sample in which both polymorphic forms are present, the patterns for the homozygous polymorphic forms are superimposed. Thus, the probe group shows distinct and characteristic hybridization patterns depending on which polymorphic forms are present and whether an individual is homozygous or heterozygous.

Typically, an array also contains a second group of probes tiled using the same principles as the first group but with a reference sequence constituting the other polymorphic form. That is, the first probe set in the second group spans the polymorphic site and shows perfect complementarity to the other polymorphic form. Hybridization of the second probe group to homozygous or heterozygous target sequences yields a mirror image of hybridization patterns from the first group. By analyzing the hybridization patterns from both probe groups, one can determine with a high accuracy which polymorphic form(s) are present in an individual.

The principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

Arrays can also be designed to analyze many different polymorphisms in many different genes simultaneously.

simply by including multiple subarrays of probes. Each subarray has first and second groups of probes designed for analyzing a particular polymorphism according to the strategy described above.

5           For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis.

10   Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. The target is usually labelled in the course of amplification. The amplification product can be RNA or DNA, single stranded

15   or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with

20   DNase-free RNase.

### III. Expression Monitoring

          The invention monitors the levels of RNA transcripts expressed from genes of interest. The RNA transcript can be

25   nuclear RNA, mRNA, rRNA or tRNA. Nuclear RNA contains intronic sequences that have been spliced out of mRNA. Analysis of nuclear RNA can be useful in analyzing the effects on expression of polymorphisms occurring within intronic regions. In some methods, RNA is monitored directly and in

30   other methods RNA is monitored indirectly via an amplification product, such as cDNA or cRNA.

Strategies for analysis and quantification of transcript are described in detail in commonly owned WO 96/14839 and WO 97/01603. In general, the same probe arrays that are used for analyzing polymorphic forms in genomic DNA can be used for analyzing polymorphic forms of transcript. The hybridization patterns of the probe arrays can be analyzed in the same manner for genomic and RNA (or RNA-derived) targets. Comparison of the hybridization intensities of the first probe group that are perfectly matched with one polymorphic form to the hybridization intensities of the second probe group that are perfectly matched with the second polymorphic form indicates approximately the relative proportions of the polymorphic forms in the transcript.

In some instances, it can be useful to compare the ratio of hybridization intensities of perfectly matched probes from the first and second probe groups for genomic DNA and RNA targets (or amplification products thereof). Preferably, the comparison is performed between like forms of amplification products (i.e., both DNA or both RNA). In genomic DNA from a diploid individual, the polymorphic forms at a heterozygous gene are expected to be present in equal molar ratio. However, in practice, the ratio of hybridization intensities may differ somewhat from the expected molar ratio due to, for example, base-composition effects on hybridization intensity. By comparing the ratios of hybridization intensities for genomic DNA and RNA (or amplification products thereof) to the same groups of probes, factors other than molar ratio of polymorphic forms that might influence hybridization intensities can largely be eliminated from the analysis. If the ratio of hybridization intensities differs significantly for the genomic and RNA targets (or amplification products

thereof), then it can be concluded that the polymorphic forms are differently expressed in the transcript.

Some arrays contain additional probes for measuring the level of transcript of a gene without distinguishing between the polymorphic forms. These probes exhibit perfect complementarity to a segment of the gene distal from the polymorphism used to distinguish polymorphic forms. The presence and level of the transcript can be inferred from the hybridization intensities of these probes, optionally relative to control probes lacking complementarity to the target and designed to measure the background level of hybridization intensity.

RNA transcript for analysis is isolated from a biological sample obtained from a biological tissue or fluid in which the gene of interest is expressed. Samples include sputum, blood, blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

Methods of isolating total mRNA are described in Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation*, P. Tijssen, ed. Elsevier, N.Y. (1993) and Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation*, P. Tijssen, ed. Elsevier, N.Y. (1993)).

Frequently, it is desirable to amplify RNA prior to hybridization. The amplification product can be RNA or DNA, single-stranded, or double-stranded. In one procedure, mRNA can be reverse transcribed with a reverse transcriptase and a

primer consisting of oligo dT and a sequence encoding the phage T7 promoter to provide single stranded DNA template. The second DNA strand is polymerized using a DNA polymerase. After synthesis of double-stranded cDNA, T7 RNA polymerase is added and RNA is transcribed from the cDNA template.

Successive rounds of transcription from each single cDNA template result in amplified RNA. Alternatively, cDNA can be amplified to generate double stranded amplicon, and one strand of the amplicon can be isolated, i.e., using a biotinylated primer that allows capture of the undesired strand on streptavidin beads. Alternatively, asymmetric PCR can be used to generate a single-stranded target.

Typically, amplification product is labelled either in the course of amplification or subsequently. If RNA amplification product is to be hybridized simultaneously with genomic DNA, or an amplification product thereof, to an array, then the two targets are differentially labelled. A variety of different fluorescent labels are available. For example, one sample can be labelled with fluorescein and the other with biotin, which can be stained with phycoerythrin-streptavidin after hybridization. Two target samples can be diluted, if desired, prior to hybridization to equalize fluorescence intensities.

Detailed protocols for PCR are provided in *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990). Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics*, 4: 560 (1989), Landegren, et al., *Science*, 241: 1077 (1988) and Barringer, et al., *Gene*, 89: 117 (1990), transcription amplification (Kwoh, et al., *Proc. Natl. Acad. Sci. USA*, 86: 1173 (1989)), and self-sustained sequence replication (Guatelli, et al., *Proc. Nat.*

Acad. Sci. USA, 87: 1874 (1990)). In some methods, a known quantity of a control sequence is co-amplified using the same primers to provide an internal standard that may be used to calibrate the PCR reaction to ensure that the amplification products are produced in approximately the same molar ratio as the starting ratio of templates. The probe array then includes probes specific to the internal standard for quantification of the amplified nucleic acid.

#### IV. Correlation of Genotype with Expression Levels

Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to identify a difference between them that accounts for the different expression levels. The difference may reside in the same polymorphism that was used to distinguish the different allelic forms in the analyses described above. However, more typically, the difference in expression levels resides in a second polymorphism located in a promoter, enhancer or other regulatory regions. Such polymorphisms can be identified by sequencing the regulatory regions of the differentially expressed alleles and identifying sequence differences between the alleles.

A possible causative role of a polymorphism within a regulatory sequence in differential expression of alleles can be analyzed by both molecular biological and genetic approaches. For example, if differentially expressed alleles differ from each other at a polymorphic site within a promoter, the different forms of the promoter can be cloned and placed in operable linkage with a reporter gene. If the reporter gene is expressed at different levels from the two forms of the promoter, it is likely that the polymorphism within the promoter has a causative role in the observed

differential expression levels of allelic forms of the gene with which it is naturally associated. Similar reporter assays can be devised to assess the effect of polymorphisms in other regulatory sequences.

5                   Polymorphisms within promoters and other regulatory sequences can also be characterized by association analysis. Association analysis identifies correlations between polymorphic forms and a population of individuals who have been tested for the presence or absence of a phenotypic trait  
10 of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a polymorphism is determined for a set of the individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of the polymorphism are then reviewed to  
15 determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a  $\chi^2$ -squared test and statistically significant correlations between a polymorphic form and phenotypic characteristics are  
20 noted.

#### V. Alternative Method of Correlating Expression Levels with Genotype

25                   In an alternative or additional approach, a population of individuals is genotyped at one or more polymorphic sites within a gene including flanking sequences. Expression levels of the gene transcript are then determined in individuals without distinguishing between the polymorphic forms. Optionally expression levels from different  
30 individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such that isolates in a given cluster tend to be similar and isolates in

different clusters tend to be dissimilar. See commonly owned  
USSN 08/797,812, filed February 7, 1997 (incorporated by  
reference in its entirety for all purposes). The population  
of individuals on which the analysis is performed should  
5 preferably be matched for characteristics that might have  
indirect affects on expression levels such as age, sex and  
ethnicity, and expression levels should be determined from the  
same tissue type. The genotype of an individual with respect  
to one or more polymorphisms within the gene is then  
10 correlated with the expression level of gene transcript in the  
same individual throughout the population. Polymorphic forms  
showing strong correlation with expression levels of  
transcript may have a causative role in determining the  
expression level. This role can be further investigated using  
15 the molecular biological and genetic approaches described  
above.

#### VI. Association Analysis

Phenotypic traits suitable for association analysis  
20 include diseases that have known but hitherto unmapped genetic  
components (e.g., agammaglobulinemia, diabetes insipidus,  
Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
syndrome, Fabry's disease, familial hypercholesterolemia,  
polycystic kidney disease, hereditary spherocytosis, von  
25 Willebrand's disease, tuberous sclerosis, hereditary  
hemorrhagic telangiectasia, familial colonic polyposis,  
Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute  
intermittent porphyria). Phenotypic traits also include  
symptoms of, or susceptibility to, multifactorial diseases of  
30 which a component is or may be genetic, such as autoimmune  
diseases, inflammation, cancer, diseases of the nervous  
system, and infection by pathogenic microorganisms. Some

examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Such correlations can be exploited in several ways. In the case of a strong correlation between a polymorphic form and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of

several treatment regimes for a disease indicates that this treatment regime should be followed.

#### VII. Probe Array Design and Construction

5 VLSIPS™ technology provides methods for synthesizing arrays of many different oligonucleotide probes that occupy a very small surface area. See US 5,143,854 and WO 90/15070. For example, high density arrays can be produced which comprise greater than about 100, preferably greater than about  
10 1000, 16,000, 65,000, 250,000 or 1,000,000 different oligonucleotide probes. The oligonucleotide probes range from about 5 to about 50 or about 5 to about 45 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length.  
15 In some embodiments, the oligonucleotide probes are 20 or 25 nucleotides in length. The oligonucleotide probes are usually less than 50 nucleotides in length, generally less than 46 nucleotides, more generally less than 41 nucleotides, most generally less than 36 nucleotides, preferably less than 31  
20 nucleotides, more preferably less than 26 nucleotides, and most preferably less than 21 nucleotides in length. The probes can also be less than 16 nucleotides or less than even 11 nucleotides in length.

The location and sequence of each different  
25 oligonucleotide probe sequence in the array are generally known. Moreover, the large number of different probes can occupy a relatively small area providing a high density array having a probe density of generally greater than about 60, 100, 600, 1000, 5,000, 10,000, 40,000, 100,000, or 400,000  
30 different oligonucleotide probes per cm<sup>2</sup>. The small surface area of the array (often less than about 10 cm<sup>2</sup>, preferably less than about 5 cm<sup>2</sup> more preferably less than about 2 cm<sup>2</sup>,

and most preferably less than about 1.6 cm<sup>2</sup>) permits uniform hybridization conditions, such as temperature regulation and salt content.

5 Finally, because of the small area occupied by the high density arrays, hybridization may be carried out in extremely small fluid volumes (e.g., 250  $\mu$ l or less, more preferably 100  $\mu$ l or less, and most preferably 10  $\mu$ l or less). In small volumes, hybridization may proceed very rapidly. In addition, hybridization conditions are extremely uniform  
10 throughout the sample, and the hybridization format is amenable to automated processing.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication  
15 or patent application were specifically and individually indicated to be so incorporated by reference. Although the present invention has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be apparent that certain changes and  
20 modifications may be practiced within the scope of the appended claims.

What is claimed is:

3           1. A method of monitoring expression levels of  
4 different polymorphic forms of a gene, comprising:  
5           analyzing genomic DNA from an individual to  
6 determine the presence of heterozygous polymorphic forms at a  
7 polymorphic site within a transcribed sequence of a gene of  
8 interest;  
9           analyzing RNA from a tissue of the individual in  
10 which the gene is expressed to determine relative proportions  
11 of polymorphic forms in transcript of the gene.

1           2. The method of claim 1, wherein analyzing genomic  
2 DNA comprises amplifying a segment of genomic DNA from a  
3 sample and hybridizing the amplified genomic DNA to an array  
4 of immobilized probes.

1           3. The method of claim 2, wherein the array of  
2 immobilized probes comprises a first probe group comprising  
3 one or more probes exactly complementary to a first  
4 polymorphic form of the gene and a second probe group  
5 comprising one or more probes exactly complementary to a  
6 second polymorphic form of the gene.

1           4. The method of claim 1, wherein analyzing the  
2 RNA, comprises reverse transcribing and amplifying mRNA  
3 expressed from the gene to produce an amplified nucleic acid  
4 and hybridizing the amplified nucleic acid to an array of  
5 immobilized probes.

1           5. The method of claim 4, wherein the amplified  
2 nucleic acid is cDNA.

1           6. The method of claim 4, wherein the array of  
2 immobilized probes comprises a first probe group comprising  
3 one or more probes exactly complementary to a first  
4 polymorphic form of the gene, a second probe group comprising  
5 one or more probes exactly complementary to a second  
6 polymorphic form of the gene.

1           7. The method of claim 1, wherein the genomic DNA  
2 and the RNA are analyzed by hybridizing the genomic DNA or an  
3 amplification product thereof, and the RNA or an amplification  
4 product thereof, to the same array of immobilized probes  
5 comprising a first probe group comprising one or more probes  
6 exactly complementary to a first polymorphic form of the gene,  
7 and a second probe group comprising one or more probes exactly  
8 complementary to a second polymorphic form of the gene.

1           8. The method of claim 7, wherein the genomic DNA,  
2 or amplification product, and the RNA, or amplification  
3 product, bear different labels and are hybridized  
4 simultaneously to the array.

1           9. The method of claim 7, further comprising  
2 comparing a genomic DNA hybridization intensity of the first  
3 probe group to the second group to determine a genomic  
4 hybridization ratio, and comparing an RNA hybridization  
5 intensity of the first group to the second group to determine  
6 an RNA hybridization ratio, whereby a difference in the  
7 genomic DNA and RNA ratios indicates that the polymorphic  
8 forms of the gene are expressed at different levels in the  
9 individual.

1           10. The method of claim 1, further comprising  
2 sequencing a nontranscribed region of the gene to identify a  
3 second polymorphic site in a promoter or enhancer region of  
4 the gene.

1           11. A method of monitoring expression levels of  
2 different polymorphic forms of a collection of genes,  
3 comprising:

4           hybridizing genomic DNA, or an amplification product  
5 thereof, from an individual to an array of immobilized probes  
6 comprising a subarray of probes for each gene in the  
7 collection, wherein each subarray comprises a first group of  
8 one or more probes exactly complementary to a first  
9 polymorphic form of the gene and a second group of one or more  
10 probes exactly complementary to a second polymorphic form of  
11 the gene;

12           analyzing the relative hybridization of the first  
13 and second group of probes to the genomic DNA or amplification  
14 product thereof for each subarray to identify heterozygous  
15 genes in the individual;

16           hybridization RNA or an amplification product  
17 thereof from the individual to the array of immobilized  
18 probes;

19           comparing the hybridization intensities of the first  
20 and second groups of probes to the RNA or amplification  
21 product to identify a subset of the heterozygous genes for  
22 which different polymorphic forms are expressed at different  
23 levels.

1           12. The method of claim 11, wherein the collection  
2 of genes comprises at least 100 genes.

1           13. The method of claim 11, wherein the collection  
2 of genes comprises at least 1000 genes.

1           14. The method of claim 11, wherein the collection  
2 of genes comprises at least 100,000 genes.

1           15. The method of claim 11, further comprising  
2 sequencing a nontranscribed region of a gene in the subset to  
3 identify a further polymorphism in a promoter, enhancer or  
4 intronic sequence of the gene.

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12442

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12Q 1/68; C12P 19/34; C07H 21/04, 21/00

US CL :435/6, 91.1, 91.2; 536/24.3, 24.31, 25.32

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 91.2; 536/24.3, 24.31, 25.32

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GUO, Z. Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide arrays on glass supports. Nucleic Acids Research. 1994, Vol. 22, No. 24, pages 5456-5464, especially page 5456.	1-7
Y	SOUTHERN, E.M. Analyzing and Comparing Nucleic Acid Sequences by Hybridization to Arrays of Oligonucleotides: Evaluation Using Experimental Models. Genomics. 1992, Vol. 13, pages 1008-1017, especially pages 1008 & 1011.	1-15
Y	US 5,567,809 A (APPLE et al) 22 October 1996, see entire document, especially column 53.	1-15



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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*O* document referring to an oral disclosure, use, exhibition or other means	
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Date of the actual completion of the international search

26 AUGUST 1998

Date of mailing of the international search report

28 SEP 1998

Name and mailing address of the ISA/US  
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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12442

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,503,980 A (CANTOR) 02 April 1996, see entire document, especially column 7, lines 19-61.	1-15
Y	US 5,631,134 A (CANTOR) 20 May 1997, see entire document, especially column 2, lines 64-67.	1-15
A,E	US 5,795,714 A (CANTOR et al) 18 August 1998, see entire document.	

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12442

### B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN CAPLUS, MEDLINE, BIOSIS, WPIDS, GENBANK, SCISEARCH, EMBASE, CANCERLIT, JAPIO,  
LIFESCI, DISSABS, TOXLINE, AIDSLINE, BIOTECHDS, DGENE, PHIC, PHIN, TOXLIT,  
NTIS, BIOBUSINESS

SEARCH TERMS: PROBE, OLIGONUCLEOTIDE, ARRAY, CHIP, CARRIER, SUPPORT  
IMMOBILIZED, BOUND OR BIND, DETECT RNA, RIBONUCLEO?, POLYMORPH?  
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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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			(43) International Publication Date: 9 April 1998 (09.04.98)
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(74) Agents: FITTS, Renee, A. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).			<b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>

(54) Title: POLYMORPHISMS AND NEW GENES IN THE REGION OF THE HUMAN HEMOCHROMATOSIS GENE

## (57) Abstract

Polymorphic sites in the region surrounding the HFE gene are provided. These polymorphisms are useful as surrogate markers in diagnostic assays for hemochromatosis. Additionally, a fine structure map of the 1 megabase region surrounding the HFE gene is provided, along with 235 kb of DNA sequence and 8 loci corresponding to candidate genes within the 1 megabase region, and in the purification of related proteins.

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BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NI	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CJ	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

## Polymorphisms and New Genes in the Region of the Human Hemochromatosis Gene

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### BACKGROUND OF THE INVENTION

Hereditary hemochromatosis (HH) is an inherited disorder of iron metabolism wherein the body accumulates excess iron. In symptomatic individuals, this excess iron leads to deleterious effects by being deposited in a variety of organs leading to their failure, and resulting in cirrhosis, diabetes, sterility, and other serious illnesses. The gene which is defective in this disease was disclosed in copending U.S.S.N. 08/652,265.

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Fine structure mapping of the region to which the gene responsible for HH, HFE (denoted HH or HFE in some publications), was mapped makes possible the identification of candidate sequences comprising the HFE gene, along with structural elements for regulation and expression and neighboring genes.

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A variety of techniques is available for fine structure mapping, including direct cDNA selection, exon-trapping, and genomic sample sequencing. The direct selection approach (Lovett *et al.* Proc. Natl. Acad. Sci. U.S.A. 88:9628-9623 (1991)) involves the hybridization of cDNA fragments to genomic DNA. This technique is extremely sensitive and capable of isolating portions of rare transcripts. Exon-trapping (Church *et al.* Nature Genetics 6:98-105 (1994)) recovers spliced introns from *in vivo* expressed genomic DNA clones and produces candidate exons without requiring any prior knowledge of the target's gene expression. High-throughput genomic DNA sequencing with comparison of the sequence data to databases of expressed sequences has also been used, such as in the positional cloning of the Werner syndrome gene (Yu *et al.* Science 277:258-262 (1996)) and in cloning by homology of the second Alzheimer's disease gene on chromosome 1 (Levy-Lahad *et al.* Science 269:973-977 (1995)).

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HH is typically inherited as a recessive trait; in the current state of knowledge, homozygotes carrying two defective copies of the gene are most frequently affected by the disease. In addition, heterozygotes for the HFE gene are more susceptible to sporadic porphyria cutanea tarda and potentially other disorders (Roberts *et al.*, Lancet 349:321-323 (1997)). It is estimated that approximately 10-15% of Caucasians carry one copy of the HFE gene mutation and that there are about one million homozygotes in the United States. HH, thus, represents one of the most common genetic disease mutations in Caucasian individuals. Although ultimately HH produces debilitating symptoms, the majority of homozygotes and heterozygotes have not been diagnosed.

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The need for such diagnostics is documented, for example, in Barton, J.C. *et al.* Nature Medicine 2:394-395 (1996); Finch, C.A. West J Med 153:323-325 (1990); McCusick, V. Mendelian Inheritance in Man pp. 1882-1887, 11th ed., (Johns Hopkins University Press, Baltimore (1994)); Report of a Joint World Health Organization/Hemochromatosis Foundation/French Hemochromatosis Association Meeting on the Prevention and Control of Hemochromatosis (1993); Edwards, C.Q. *et al.* New Engl J Med 328:1616-1620 (1993); Bacon, B.R. New Engl J Med 326:126-

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127 (1992); Balan, V. et al. Gastroenterology 107:453-459 (1994); Phatak, P.D. et al. Arch Int Med 154:769-776 (1994).

A single mutation in the HFE gene, designated 24d1 in copending U.S.S.N. 08/630,912, gave rise to the majority of disease-causing chromosomes present in the population today.

5 This is referred to herein as the "common" or "ancestral" or "common ancestral" mutation. These terms are used interchangeably. It appears that about 80% to 90% of all HH patients carry at least one copy of the common ancestral mutation which is closely linked to specific alleles of certain genetic markers close to this ancestral HFE gene defect. These markers are, as a first approximation, in the allelic form in which they were present at the time the ancestral HFE mutation occurred. See, for  
10 example, Simon, M. et al. Am J Hum Genet 41:89-105 (1987); Jazwinska, E.C. et al. Am J Hum Genet 53:242-257 (1993); Jazwinska, E.C. et al. Am J Hum Genet 56:428-433 (1995); Worwood, M. et al. Brit J Hematol 86:863-866 (1994); Summers, K.M. et al. Am J Hum Genet 45:41-48 (1989).

Several polymorphic markers in the HFE region have been described and shown to have alleles that are associated with HH disease. These markers include the published microsatellite  
15 markers D6S258, D6S306 (Gyapay, G. et al. Nature Genetics 7:246-339 (1994)), D6S265 (Worwood, M. et al. Brit J Hematol 86:833-846 (1994)), D6S105 (Jazwinska, E.C. et al. Am J Hum Genet 53:242-257 (1993); Jazwinska, E.C. et al. Am J Hum Genet 56:428-433 (1995)), D6S1001 (Stone, C. et al. Hum Molec Genet 3:2043-2046 (1994)), D6S1260 (Raha-Chowdhury et al. Hum Molec Genet 4:1869-1874 (1995)) as well as additional microsatellite and single-nucleotide-polymorphism markers  
20 disclosed in co-pending PCT application WO 96/06583, the disclosure of which is hereby incorporated by reference in its entirety. Additionally, copending U.S.S.N. 08/630,912 disclosed additional markers 24d2 and 24d7.

The symptoms of HH are often similar to those of other conditions, and the severe effects of the disease often do not appear immediately. Accordingly, it would be desirable to provide a  
25 method to identify persons who may be destined to become symptomatic in order to intervene in time to prevent excessive tissue damage associated with iron overload. One reason for the lack of early diagnosis is the inadequacy of presently available diagnostic methods to ascertain which individuals are at risk, especially while such individuals are presymptomatic.

Although blood iron parameters can be used as a screening tool, a confirmed  
30 diagnosis often employs liver biopsy which is undesirably invasive, costly, and carries a risk of mortality. Thus, there is a clear need for the development of an inexpensive and noninvasive diagnostic test for detection of homozygotes and heterozygotes in order to facilitate diagnosis in symptomatic individuals, provide presymptomatic detection to guide intervention in order to prevent organ damage, and for identification of heterozygote carriers.

35 Furthermore, a need exists for both methods for fine structure mapping and a fine structure map of the region of the chromosome to which the HH locus maps. This and other needs are addressed by the present invention.

**SUMMARY OF THE INVENTION**

One aspect of the invention is an oligonucleotide comprising at least 8 to about 100 consecutive bases from the sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100 consecutive bases includes at least one polymorphic site of Table 1.

Another aspect of the invention is an oligonucleotide pair selected from the sequence of Figure 9 or its complement for amplification of a polymorphic site of Table 1.

Another aspect of the invention is an isolated nucleic acid molecule comprising about 100 consecutive bases to about 235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at least one polymorphic site of Table 1.

Another aspect of the invention is a method to determine the presence or absence of the common hereditary hemochromatosis (HFE) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a haplotype of

Table 1,

wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

Another aspect of the invention is a method to determine the presence or absence of the common hereditary hemochromatosis (HFE) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a genotype

defined by a polymorphic allele of Table 1,

wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

Another aspect of the invention is a culture of lymphoblastoid cells having the designation ATCC CRL-12371.

One aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF1.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF2.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF3.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF4.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF5.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to NPT3.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to NPT4.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to RoRet.

5 Additional aspects of the invention include nucleic acid sequences that are cDNAs, polypeptides encoded by the nucleic acids of the invention and antibodies specifically immunoreactive thereto, vectors comprising the nucleic acid sequences of the invention, and host cells stably transfected with the nucleic acids of the invention.

10 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF1.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF2.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF3.

15 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF4.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF5.

20 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of NPT3.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of NPT4.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of RoRet.

## 25 **BRIEF DESCRIPTION OF THE DRAWINGS**

Figure 1 depicts a combination genetic, physical and transcription map of the HFE gene region. The first line shows the relative positions of selected genetic markers that define the HFE region. The heavy bar below represents the YAC clone used in the direct selection experiment. The order and positions of the bacterial clones employed in the exon-trapping and sample sequencing is indicated under the YAC. The thin bar under the bacterial clones represents the approximate locations of a subset of the expressed sequence fragments mapped to the contig. The thicker bars show the location of the cDNAs cloned. Two regions are bracketed; the butyrophilin family of genes (BTF), and the region where complete genomic sequencing was carried out.

35 Figure 2 is a schematic of the 250 kb of genomic sequence including the HFE gene. Both the structure of the overall cDNA (top) and that corresponding to the coding regions (bottom), as well as the direction of transcription are shown. The positions of the histone genes, the zinc  $\alpha$ -2 glycoprotein pseudogene, and the ESTs are also shown.

40 Figure 3 depicts an alignment of the predicted amino acid sequence of the BTF proteins. Sequences were aligned in a pair-wise fashion using CLUSTAL W (Thompson *et al.* Nucl. Acids Res. 22:4673-4680) to deduce the most parsimonious arrangement. The asterisks under the

alignment represent amino acids conserved in all 6 proteins; the "dots" represent conserved amino acids substitutions. Boxed are the regions within the proteins which correspond to three conserved motifs: 1) the B-G domain, 2) the transmembrane domain (TM), and 3) the B30-2 exon domain.

Figure 4, panel (A) depicts a Northern blot analysis of representative members of the two groups of BTF proteins, BTF1 and BTF5. BTF1 hybridized to all tissues on the blot as a major transcript at 2.9 kb and a minor one at 5.0 kb. BTF5 hybridized to several transcripts ranging between 4.0 and 3.1 kb and as a similar expression profile to BTF1. Autoradiography was for 24 hours. The  $\beta$ -actin hybridization demonstrated the variation in poly (A)+ RNA between the lanes. Autoradiography was for 1 hour. In panel (B), RT-PCR analysis demonstrated that the expression of both genes was widespread. Included in the (+) lane are cDNA 21 and 44 as positive controls; the (-) lane represents the no-DNA control. Amplification using primers for the RFP gene (Isomura *et al.* Nucleic Acid Res. 20:5305-5310 (1992)) controlled for the integrity of the cDNA. All first strand cDNAs were checked for contaminating genomic DNA amplification by carrying out an identical experiment excluding the reverse transcriptase. In all cases, no amplification was obtained (data not shown).

Figure 5(A) depicts an alignment of the predicted amino acid sequence of the RoRet gene to the 52 kD Ro/SSA auto-antigen protein. The asterisks under the alignment represent conserved amino acids; the "dots" represent conserved amino acids substitutions. The putative DNA binding cysteine-rich domain and the B30-2 exon domain are boxed. Figure 5(B) depicts an alignment of the predicted amino acid sequence of the two novel putative sodium phosphate transport proteins to that of the NPT1.

Figure 6, panel (A) depicts a Northern blot analysis of the RoRet gene. The RoRet cDNA hybridized to 4 different transcripts, ranging from 7.1 kb to 2.2 kb. Autoradiography was performed for 4 days. The re-hybridization of the blot with a  $\beta$ -actin probe showed the variation in poly (A)+ RNA between the lanes. Autoradiography was for 1 hour. Panel (B) depicts RT-PCR analysis of the RoRet gene. Included in the (+) lane was a cDNA 27 positive control. Weak amplification of the correct size was observed in the small intestine, kidney and liver. The other tissues were negative as was the no DNA control lane (-). The RFP primers demonstrated the integrity of the cDNA. Panel (C) depicts Northern blot analysis of NPT3 and NPT4. NPT3 was expressed at high abundance in the heart and muscle as a single 7.2 kb transcript. Lesser amounts were found in the other tissues. The expression pattern of NPT4 was more restricted, being found only in the liver and kidney as a smear of transcripts ranging from 2.8 to 1.7 kb. Panel (D) depicts RT-PCR analysis of the NPT3 and NPT4 genes. Included in the (+) lane were the respective cDNA22E and 22B positive controls. The NPT3 gene was expressed as the proper size PCR fragment in kidney, liver, spleen and testis. A smaller fragment was detected in all tissues with the exception of the liver. The no DNA control lane (-) was negative. NPT4 was expressed as the proper size fragment in the small intestine, kidney, liver and testis. Larger and smaller size fragments were found in all other tissues with the exception of the brain. For both genes these different size fragments may indicate alternative splice events. The no DNA control lane (-) was negative. The RFP primers demonstrated the integrity of the cDNA.

Figure 7 depicts the sequences of cDNA 21 (BTF1), cDNA 29 (BTF3), cDNA 23 (BTF4), cDNA 44 (BTF5), cDNA 32 (BTF2), cDNA 27 (RoRet), cDNA 22B (NPT3), cDNA22E (NPT4).

Figure 8 depicts the nucleotide sequence of approximately 235 kb in the HFE subregion from an unaffected individual.

Figure 9 depicts the nucleotide sequence of approximately 235 kb in the HFE subregion from an HH affected individual. Polymorphic sites in the HH affected individual determined by comparing a sequence of the corresponding region from an HH unaffected individual are listed and described in Table I.

### DETAILED DESCRIPTION

#### **A. Definitions**

Abbreviations for the twenty naturally occurring amino acids follow conventional usage. In the polypeptide notation used herein, the left-hand direction is the amino terminal direction and the right-hand direction is the carboxyl-terminal direction, in accordance with standard usage and convention. Similarly, unless specified otherwise, the left hand end of single-stranded polynucleotide sequences is the 5' end; the left hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences".

The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. It includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence.

"Nucleic acid probes" may be DNA or RNA fragments. DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR, or synthesized by either the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett. 22:1859-1862 (1981), or by the triester method according to Matteucci, *et al.*, J. Am. Chem. Soc. 103:3185 (1981), both incorporated herein by reference. A double stranded fragment may then be obtained, if desired, by annealing the chemically synthesized single strands together under appropriate conditions or by synthesizing the complementary strand using DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The phrase "selectively hybridizing to" refers to a nucleic acid probe that hybridizes, duplexes or binds only to a particular target DNA or RNA sequence when the target sequences are present in a preparation of total cellular DNA or RNA. "Complementary" or "target" nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe's length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For

discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook *et al.*, Molecular Cloning: a Laboratory Manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989) or Current Protocols in Molecular Biology, F. Ausubel *et al.*, ed. Greene Publishing and Wiley-Interscience, New York (1987).

5           The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein or peptide. The nucleic acid sequence includes both the DNA strand sequence that is transcribed into RNA and the sequence translated into protein. The nucleic acid sequences include both full length sequences derived from the full length sequence as well as non-full length sequences derived from the full length sequence that the sequence includes the degenerate codons of the native sequence be introduced to provide codon preference in a specific host cell.

10           The phrase "isolated" or "substantially purified" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell.

15           The phrase "expression cassette" refers to nucleotide sequences which are capable of affecting expression of a structural gene in hosts compatible with such sequences. Such cassettes include at least promoters and optionally, transcription termination signals. Additional factors necessary or helpful in effecting expression may also be used as described herein.

20           The term "operably linked" as used herein refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence.

25           The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector," this includes both extrachromosomal circular DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

30           The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, and termination regions. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

35           The term "plasmid" refers to an autonomous circular DNA molecule capable of replication in a cell, and includes both the expression and nonexpression types. Where a recombinant microorganism or cell culture is described as hosting an "expression plasmid", this includes both extrachromosomal circular DNA molecules and DNA that has been incorporated into the host chromosome(s). Where a plasmid is being maintained by a host cell, the plasmid is either being stably replicated by the cells during mitosis as an autonomous structure or is incorporated within the host's genome.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence.

Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 85:2444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

The terms "substantial identity" or "substantial sequence identity" as applied to nucleic acid sequences and as used herein and denote a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, and more preferably at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 25-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. The reference sequence may be a subset of a larger sequence.

As applied to polypeptides, the terms "substantial identity" or "substantial sequence identity" mean that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 90 percent sequence identity, more preferably at least 95 percent sequence identity or more. "Percentage amino acid identity" or "percentage amino acid sequence identity" refers to a comparison of the amino acids of two polypeptides which, when optimally aligned, have approximately the designated percentage of the same amino acids. For example, "95% amino acid identity" refers to a comparison of the amino acids of two polypeptides which when optimally aligned have 95% amino acid identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. For example, the substitution of amino acids having similar chemical properties such as charge or polarity are not likely to effect the properties of a protein. Examples include glutamine for asparagine or glutamic acid for aspartic acid.

The phrase "substantially purified" or "isolated" when referring to a peptide or protein, means a chemical composition which is essentially free of other cellular components. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein which is the predominant species present in a preparation is substantially purified. Generally, a substantially purified or isolated protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the protein is purified to represent greater than 90% of all macromolecular species present. More preferably the protein is purified to greater than 95%, and most preferably the protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional techniques.

The phrase "specifically binds to an antibody" or "specifically immunoreactive with", when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

As used herein, "EST" or "Expressed Sequence Tag" refers to a partial DNA or cDNA sequence of about 150 to 500, more preferably about 300, sequential nucleotides of a longer sequence obtained from a genomic or cDNA library prepared from a selected cell, cell type, tissue or tissue type, or organisms which longer sequence corresponds to an mRNA or a gene found in that library. An EST is generally DNA. One or more libraries made from a single tissue type typically provide at least 3000 different (i.e. unique) EST's and potentially the full complement of all possible EST's representing all possible cDNAs, e.g., 50,000 - 100,000 in an animal such as a human. (See, for example, Adams *et al.* Science 252:1651-1656 (1991)).

"Stringent" as used herein refers to hybridization and wash conditions of 50% formamide at 42°C. Other stringent hybridization conditions may also be selected. Generally, stringent conditions are selected to be about 5° C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is at least about 0.02 molar at pH 7 and the temperature is at least about 60°C. As other factors may significantly affect the stringency of hybridization, including, among others, base composition and size of the complementary strands, the presence of organic solvents and the extent of base mismatching, the combination of parameters is more important than the absolute measure of any one.

**B. Transcript Map and New Genes near HH**

The instant invention provides a fine structure map of the 1 megabase region surrounding the HFE gene. As part of that map the instant invention provides approximately 250 kb of DNA sequence of which about 235 kb are provided in Figure 8 and eight loci of particular interest corresponding to candidate genes within the 1 megabase region. These loci are useful as genetic and physical markers for further mapping studies. Additionally, the eight cDNA sequences corresponding to those loci are useful, for example, for the isolation of other genes in putative gene families, the identification of homologs from other species, and as probes for diagnostic assays. In particular, isolated nucleic acid sequences of at least 18 nucleotides substantially identical to contiguous nucleotides of a cDNA of the invention are useful as PCR primers. Typically, the PCR primer will be used as part of a pair of primers in a PCR reaction. Isolated nucleic acid sequences preferably comprising about 18-100 nucleotides, more preferably at least 18 nucleotides, substantially identical to contiguous nucleotides in a cDNA of the invention are useful in the design of PCR primers and probes for hybridization assays. Additionally, the proteins encoded by those cDNAs are useful in the generation of antibodies for analysis of gene expression and in diagnostic assays, and in the purification of related proteins.

Thus, in one embodiment of the invention, a 235 kb sequence is provided for the HFE subregion within the 1 megabase region mapped. This sequence can serve as a reference in genetic or physical analysis of deletions, substitutions, and insertions in that region. Additionally, the sequence information provides a resource for the further identification of new genes in that region. Thus, nucleic acid sequences substantially identical to the 235 kb sequence are also included in the scope of this invention.

In a further embodiment of the invention, a family of five genes, BTF1-5, is provided which are related by sequence homology to the milk protein butyrophilin (BT) (Figures 1, 3, and 7). The predicted amino acid sequences of the proteins encoded by these genes are provided in Figure 3. These cDNAs are useful for the identification of further members of the BT family and to study regulation of expression of this family of genes. The proteins encoded by these cDNAs can be useful in the identification and isolation of ligands for the BT protein, and in the generation of agonists or antagonists of BT function. Nucleic acid sequences substantially identical to BTF1-5 and the proteins encoded by them are also included in the scope of this invention, including allelic forms.

In a further embodiment of the invention, a novel gene RoRet is provided, which is related by sequence homology to the 52 kD Ro/SSA Lupus and Sjogren's syndrome autoantigen. This sequence is especially useful in the identification of other genes that may be involved in Lupus or Sjogren's syndrome. The protein encoded by this cDNA can be useful in the identification and isolation of ligands for the autoantigen, and in the generation of agonists or antagonists of the antigen. Nucleic acid sequences substantially identical to RoRet and the proteins encoded by them are also included in the scope of this invention.

In a further embodiment of the invention, two genes, NPT3 and NPT4, with structural homology to a type 1 sodium transport gene are provided. These cDNAs and the proteins expressed by them are useful in determining the etiology of hypophosphatemia, along with being useful as probes

in the identification and isolation of further members of the gene family. Nucleic acid sequences substantially identically to the NPT1-like sequences and the proteins encoded by them are also included in the scope of this invention.

### C. Polymorphic Markers

The invention provides 397 new polymorphic sites in the region of the HFE gene. These polymorphisms are listed in Table 1. As described below, these polymorphisms were identified by comparison of the DNA sequence of an affected individual homozygous for the common ancestral HH mutation with that of an unaffected individual disclosed in copending U.S. 08/724,394.

Table 1. Polymorphic Sites in the HH Region

Base Location	Difference	Base Location	Difference
35-36	AC DEL	19755	G-A
841	T-C	19949	C-T
2662-2663	TT DEL	20085	C-T
3767	T-C	20366-20367	A INS
3829	C-G	20463	C-A
4925-4928	TAAA DEL	20841	A-T
5691	C-T	21059	A-T
5839	T-C	21117	A-G
6011	G-A	21837	A-C
6047	C-G	22293	A-C
6231	G-A	22786	C-A
6643	A DEL	23009	G-A
6698	T-C	24143	T-A
7186	T-C	26175	G-C
7273	G-A	26667	C-A
7545-7558	TCACACACCGATTGG DEL	26994	T-C
7672	G DEL	27838	G-T
7933	T-C	27861	T DEL
8746	T-G	28132	G-A
9115	G-A	29100	G-A
9823	G-A	29454-29457	TTTT DEL
10027	G-A	29787	T-G
10214	C-T	29825	A-C
10828	A-G	30009	T-C
10918	C-G	30177	A-G
10955	A-G	30400	A-G
11524	C-A	31059	T-A
11674	A-G	31280	C-T
11955	T-C	31749	C-T
12173-12175	TTT DEL	32040	C-G
13304	G-A	32556-32559	TGTG DEL
13455	G-A	33017	T-G
14416-14417	A INS	33026	T DEL
14998	C-T	34434	C-T
15564	T-C	35179	A-C
15887	A-G	35695	G-A
15904-15919	CCAACTGATCTTTGA DEL	35702	G-A
16019	T DEL	35983	A-G
16211	A-T	37411	A-G
17461	A-G	38526	C-T

	Base Location	Difference	Base Location	Difference
	40431	C-A	72688	C-G
	42054-42055	TT DEL	75323-75324	T INS
	43783-43784	TTTT INS	75887	G-C
5	45120	C DEL	77519	T-C
	45567	A-C	77749	G-A
	46601	A-T	77908	T-C
	47255	C-G	78385	C-G
	47758	C-A	78592-78593	AG INS
	47994	G-C	80189	T-G
10	48440	G-A	80279	T DEL
	48650	T-G	80989-80990	A INS
	48680	A-G	81193	T-C
	50240	C-T	81273	A DEL
	50553	G-A	82166	G-A
15	50586	G-T	83847	T DEL
	51322	G-C	84161-84162	CA-GG
	51747	A-G	84533	A-G
	52474	C-G	84638	T-G
	52733	C-A	85526	T-G
20	52875	G-A	85705	G-T
	53631-53637	TTTTTTT DEL	86984	T-C
	53707	G-A	87655	T-C
	54819	A-G	87713	A-C
	55913	T-C	87892	C-T
25	56225	A-C	88192	T DEL
	56510	T-C	88528	A-G
	56566	G-A	89645	A-T
	56618	A-T	89728	A-G
	57815	A-G	90088	T-C
30	58011	T DEL	91193-91194	2209bp INS
	58247-58248	T INS	91373	T-C
	58926	C-G	91433-91434	A INS
	59406	C-G	91747	G-A
	59422	G-C	93625	T DEL
35	60221-60222	A INS	95116-95117	T INS
	60656-60657	CA DEL	96315	G-A
	61162	G-A	97981	A-G
	61465	G-A	98351	T DEL
	61607	A DEL	99249	C-T
40	61653	T-C	100094-100095	T INS
	61794-61795	T INS	100647-100648	TTC INS
	62061	G-C	100951	C-T
	62362	T-G	101610	C-G
	62732	C-G	102589	C-T
45	63364	G-A	103076-103077	TATATATATATA INS
	63430-63431	GT INS	103747	T-C
	63754	C-T	105638	A-C
	63785	A-C	107024	C-T
	63870-63871	A INS	107322	C-T
50	64788	A-G	107858	C-G
	64962	G-A	109019	A DEL
	65891	C-T	109579	T DEL
	66675	G-C	110021	C-A
	67186-67187	ATT INS	111251	C-A
55	67746-67747	TT INS	111425	G-A
	68259	T-C	112644	T-A
	68836	T-C	113001	G-C
	68976	C-G	113130	C-T
	72508	T-G	114026	G-A

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	Base Location	Difference	Base Location	Difference
	114250	A DEL	176222	T-C
	115217	C-G	176524	A-T
	117995	G-A	176684	G-A
5	118874	A-G	176815	T-C
	119470	T-C	177049	T-C
	119646	G-T	177065	G-T
	120853	C-T	178285	T-C
	121582	G-A	178551-178552	CTTTTTTTTTTTT INS
10	123576	A-C	179114-179115	A INS
	125581	C-T	179260	C-G
	125970	G-T	179281	C-G
	126197	A-G	180023	G-C
	126672	A DEL	180430	T-C
	126672	G-C	180773	T-C
15	128220-128221	A INS	180824	T-C
	132569	C-T	181097	C-T
	133572	A-C	181183	A-T
	134064	T-G	182351	C-T
	136999	G-A	183197	G-A
20	137784	C-T	183623	A-T
	138903	G-A	183653	G-T
	139159-139160	A INS	183657	T-G
	140359	G-A	183795-183796	A INS
	140898	C-T	184060	G-A
25	141313	C DEL	184993	G-A
	141343	T-C	185918	A-G
	142148	T-C	186036	T-C
	142178	C-A	186506-186507	TAAC INS
30	142433-142434	ATAGA INS	186561-186568	TATTTATT DEL
	143783	C-T	186690	G DEL
	144090	C-T	186751	T-A
	144220-144221	A INS	187221	A-G
	144725	A-C	187260	A-G
35	145732-145733	AAAAAAAAAAAAA INS	187444-187447	CTCT DEL
	147016-147017	CG DEL	187831-187832	C INS
	147021	G-T	188638	G-A
	147536	T-G	188642	C-T
	148936	T-A	189246	T-C
40	149061	T-C	190340	A-C
	154341	A-T	190354	A-G
	154588	G-A	190762	A-G
	155464	G-A	191260	G-T
	158574	C-G	193018-193019	AGAT INS
45	160007	C-T	193147	T-G
	164348	A-T	193196-193197	C INS
	164499	C-G	193499	C-T
	166677-166678	AAAG INS	193738	C-G
	167389	G-A	193984-193985	ACACACAC INS
50	168506-168507	AGGATGGTCT INS	194064	C-G
	168515	T-C	194504	A DEL
	169413-169414	AA INS	194734	G-A
	170300-170301	TTGTTGTTGTTG INS	194890	A-C
	170491	G-A	195404	G-A
55	173428	T-C	195693	A-T
	173642	G-A	196205	G-A
	173948	T-G	197424	C-T
	175330	T-C	197513	C-T
	175836	T-C	197670	G-A
	176200	G-C	198055	C-A

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Base Location	Difference	Base Location	Difference
198401	C-T	215947	C-A
198692	A-G	216232	A-G
198780	T DEL	217478	G-A
199030	T-G	219052	T-C
199933	C-T	219082-219083	ATATATATATATATATAT INS
200027	G-A	219314	C-A
200439	T-A	219327	G-A
200452	A-G	219560	C-T
200472-200483	AATAATAATAAT DEL	219660	C-T
200559	A-T	219889	G-A
200745	A-G	220198	G-T
200919	T-A	220384	G-A
201816	C-T	220451-220452	CAAAAA INS
201861-201862	42bp INS	221363	G-A
202682	T-C	221645	G-A
202880	T-C	222119	T-C
204341	C-T	222358	A-G
204768	A-T	222367	A-C
205284	T-G	222686	A-G
207400	C-A	222959	T-C
208634	T-C	223270-223271	TT DEL
208718	T DEL	223283	T-C
208862	A-C	224964	T-C
209419-209420	TT DEL	225232	A-C
209802	G-A	225366-225367	TTTT INS
209944	C-G	225416	G-C
210299	A-G	225486	T-C
211142	G-A	226088	A-G
212072	G-A	228421	A-G
212146	T-C	230047	G-A
212379	G-A	230109	G-C
212637-212639	TCT DEL	230376	C-G
212696	T-C	230394	A-G
213042	T-A	231226	A-G
214182	A-G	231447	G-A
214529-214530	TTTTTTTTTTT INS	231835	A-G
214549	T-C	232400-232402	AAA DEL
214795	C-T	232402-232403	G INS
214908	T-G	232515	T-C
214977	A-G	232703	G-T
215769	C-T	232750	A-G

\* D6S2238 occurs at base 1. 24d1 occurs at base 41316. D6S2239 occurs at base 84841. D6S2241 occurs at base 235032

Table 2. Polymorphic Allele Frequencies

Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
232703	53%	47%
231835	53%	47%
230394	85%	15%
230376	25%	75%
230109	53%	47%
225486	45%	55%
225416	75%	25%
220198	43%	57%
219660	58%	42%

	Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
	219560	53%	47%
	214977	65%	35%
	214908	50%	50%
	214795	24%	76%
5	214549	53%	47%
	214192	65%	35%
	210299	53%	47%
	208862	80%	20%
	208634	48%	52%
10	207400	25%	75%
	205284	50%	50%
	204341	53%	47%
	202880	58%	42%
	202662	98%	2%
15	200027	25%	75%
	199030	58%	42%
	198692	55%	45%
	198401	55%	45%
	198055	55%	45%
20	195693	60%	40%
	195404	25%	75%
	194890	55%	45%
	175330	53%	47%
	173948	83%	17%
25	173642	55%	45%
	173428	80%	20%
	168515	80%	20%
	160007	18%	82%
	149061	58%	42%
30	148936	82%	18%
	147536	100%	0%
	147021	46%	54%
	141343	55%	45%
	140359	55%	45%
35	138903	55%	45%
	132569	81%	19%
	125581	18%	82%
	121582	80%	20%
	120853	18%	82%
40	118874	85%	15%
	115217	50%	50%
	113130	40%	60%
	113001	48%	52%
	107858	48%	52%
45	103747	50%	50%
	96315	25%	75%
	91194	80%	20%
	90088	75%	25%
	89728	50%	50%
50	89845	50%	50%
	88528	63%	37%
	87892	75%	25%
	87713	60%	40%
	87655	50%	50%
55	86984	79%	21%
	85705	50%	50%
	85526	50%	50%

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Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
84638	50%	50%
84533	50%	50%
82166	78%	22%
81193	58%	42%
80189	50%	50%
78385	80%	20%
77908	88%	12%
68976	50%	50%
68259	51%	49%
66675	80%	20%
62732	50%	50%
62362	40%	60%
61653	48%	52%
61465	5%	95%
61162	60%	40%
53707	100%	0%
52875	50%	50%
52733	74%	26%
52474	47%	53%
50588	50%	50%
50553	50%	50%
50240	50%	50%
48680	53%	47%
48650	63%	37%
48440	50%	50%
47255	50%	50%
46601	53%	47%
45567	49%	51%
41316	5%	95%
40431	20%	80%
38526	23%	77%
37411	70%	30%
35983	5%	95%

These polymorphisms provide surrogate markers for use in diagnostic assays to detect the likely presence of the mutations 24d1 and/or 24d2, in preferably 24d1, in homozygotes or heterozygotes. Thus, for example, DNA or RNA from an individual is assessed for the presence or absence of a genotype defined by a polymorphic allele of Table 1, wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

These markers may be used singly, in combination with each other, or with other polymorphic markers (such as those disclosed in co-pending PCT application WO 96/06583) in diagnostic assays for the likely presence of the HFE gene mutation in an individual. For example, any of the markers defined by the polymorphic sites of Table 1 can be used in diagnostic assays in combination with 24d1 or 24d2, or at least one of polymorphisms HHP-1, HHP-19, or HHP-29, or microsatellite repeat alleles 19D9:205; 18B4:235; 1A2:239; 1E4:271; 24E2:245; 2B8:206; 3321-1:98; 4073-1:182; 4440-1:180; 4440-2:139; 731-1:177; 5091-1:148; 3216-1:221; 4072-2:170; 950-1:142; 950-2:164; 950-3:165; 950-4:128; 950-6:151; 950-8:137; 63-1:151; 63-2:113; 63-3:169; 65-1:206; 65-

2:159; 68-1:167; 241-5:108; 241-29:113; 373-8:151; and 373-29:113, D6S258:199, D6S265:122, D6S105:124; D6S306:238; D6S464:206; and D6S1001:180.

Table 2 lists the frequency of about 100 of the alleles defined by the polymorphic sites of the invention in the general population. As is evident from the Table, certain of these alleles are present rarely in the general population. These polymorphisms are thus preferred as surrogate markers in diagnostic assays for the presence of a mutant HFE allele ("gene mutation") such as 24d1 or 24d2. Preferably, the frequency of the polymorphic allele used in the diagnostic assay in the general population is less than about 50%, more preferably less than about 25%, and most preferably less than about 5%. Thus, of the genotypes defined by the alleles listed in Table 2, polymorphisms occurring at base 35983 and base 61465 of Figure 1 are preferred.

It will be understood by those of skill in the art that because they were identified in an ancestral HH homozygote, the haplotypes defined by the polymorphic sites of Table 1 are predictive of the likely presence of the HFE gene mutation 24d1. Thus, for example, the likelihood of any affected individual having at least two or more of any of the polymorphic alleles defined by Table 1 is greater than that for any unaffected individual. Similarly, the likelihood of any affected individual having at least three or more of any of the polymorphic alleles defined by Table 1 is greater than that for any unaffected individual.

Thus, for example, in a diagnostic assay for the likely presence of the HFE gene mutation in the genome of the individual, DNA or RNA from the individual is assessed for the presence or absence of a haplotype of Table 1, wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

The markers defined by the polymorphic sites of Table 1 are additionally useful as markers for genetic analysis of the inheritance of certain HFE alleles and other genes which occur within the chromosomal region corresponding to the sequence of Figure 9 which include, for example, those disclosed in copending U.S.S.N. 08/724,394.

As the entire nucleotide sequence of the region is provided in Figure 9, it will be evident to those of ordinary skill in the art which sequences to use as primers or probes for detecting each polymorphism of interest. Thus, in some embodiments of the invention, the nucleotide sequences of the invention include at least one oligonucleotide pair selected from the sequence of Figure 9 or its complement for amplification of a polymorphic site of Table 1. Furthermore, in some embodiments of the invention a preferred hybridization probe is an oligonucleotide comprising at least 8 to about 100 consecutive bases from the sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100 consecutive bases includes at least one polymorphic site of Table 1. In some embodiments the polymorphic site is at base 35983 or base 61465.

It will also be appreciated that the nucleic acid sequences of the invention include isolated nucleic acid molecules comprising about 100 consecutive bases to about 235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at least one polymorphic

site of Table 1. Such isolated DNA sequences are useful as primers, probes, or as the component of a kit in diagnostic assays for detecting the likely presence of the HFE gene mutation in an individual.

#### D. Nucleic Acid Based Screening

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. The genomic DNA used for the diagnosis may be obtained from body cells, such as those present in peripheral blood, urine, saliva, bucca, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically *in vitro* through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other *in vitro* amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods Appl. 1:25-33 (1992)), prior to mutation analysis. The methodology for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art.

The detection of polymorphisms in specific DNA sequences, such as in the region of the HFE gene, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl Acids Res 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. U.S.A. 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and Southern Nucl Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. Acad. Sci. U.S.A. 85:4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvänen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. Nucl Acids Res 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res. 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984 (1996)).

In addition to the genotypes defined by the polymorphisms of the invention, as described in co-pending PCT application WO 96/35802 published November 14, 1996, genotypes characterized by the presence of the alleles 19D9:205; 18B4:235; 1A2:239; 1E4:271; 24E2:245; 2B8:206; 3321-1:98 (denoted 3321-1:197 therein); 4073-1:182; 4440-1:180; 4440-2:139; 731-1:177; 5091-1:148; 3216-1:221; 4072-2:170 (denoted 4072-2:148 therein); 950-1:142; 950-2:164; 950-3:165; 950-4:128; 950-6:151; 950-8:137; 83-1:151; 63-2:113; 63-3:169; 65-1:206; 65-2:159; 68-1:167; 241-

5:108; 241-29:113; 373-8:151; and 373-29:113, alleles D6S258:199, D6S265:122, D6S105:124, D6S306:238, D6S464:206; and D6S1001:180, and/or alleles associates with the HHP-1, the HHP-19 or HHP-29 single base-pair polymorphisms can also be used to assist in the identification of an individual whose genome contains 24d1 and/or 24d2. For example, the assessing step can be performed by a process which comprises subjecting the DNA or RNA to amplification using oligonucleotide primers flanking a polymorphism of Table 1, and oligonucleotides flanking 24d1 and/or 24d2, oligonucleotide primers flanking at least one of the base-pair polymorphisms HHP-1, HHP-19, and HHP-29, oligonucleotide primers flanking at least one of the microsatellite repeat alleles, or oligonucleotide primers for any combination of polymorphisms or microsatellite repeat alleles thereof.

Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides. Such oligonucleotides can be derived from either the genomic DNA of Figure 8 or 9, or cDNA sequences derived therefrom, or may be synthesized.

Additionally, the proteins encoded by such cDNAs are useful in the generation of antibodies for analysis of gene expression and in diagnostic assays, and in the purification of related proteins.

#### E. General Methods

The nucleic acid compositions of this invention, whether RNA, cDNA, genomic DNA, or a hybrid of the various combinations, may be isolated from natural sources, including cloned DNA, or may be synthesized *in vitro*. The nucleic acids claimed may be present in transformed or transfected whole cells, in a transformed or transfected cell lysate, or in a partially purified or substantially pure form.

Techniques for nucleic acid manipulation of the nucleic acid sequences of the invention such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like are described generally in Sambrook *et al.*, Molecular Cloning - a Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook *et al.*"

There are various methods of isolating the nucleic acid sequences of the invention. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein. Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known. See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook *et al.*

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments

are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, *et al.* Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-182 (1977). Colony hybridization is carried out as generally described in  
5 M. Grunstein *et al.* Proc. Natl. Acad. Sci. USA, 72:3961-3965 (1975).

DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, *et al.*

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of  
10 the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired.

15 PCR can be used in a variety of protocols to isolate cDNA's encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from sequence obtained.

20 Oligonucleotides for use as primers or probes are chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage, S.L. and Carruthers, M.H., Tetrahedron Lett., 22(20):1859-1862 (1981) using an automated synthesizer, as described in Needham-VanDevanter, D.R., *et al.*, Nucleic Acids Res., 12:6159-6168 (1984). Purification of oligonucleotides is by either native acrylamide gel electrophoresis or by anion-exchange HPLC as  
25 described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). The sequence of the synthetic oligonucleotide can be verified using the chemical degradation method of Maxam, A.M. and Gilbert, W., in Grossman, L. and Moldave, D., eds. Academic Press, New York, Methods in Enzymology 65:499-560 (1980).

#### 1. Expression

30 Once DNA encoding a sequence of interest is isolated and cloned, one can express the encoded proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

35 In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and  
40 promoters useful for regulation of the expression of polynucleotide sequence of interest. To obtain

high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, *i.e.*, shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook *et al.* Examples of expression of ATP-sensitive potassium channel proteins in both prokaryotic and eukaryotic systems are described below.

a. Expression in Prokaryotes

A variety of prokaryotic expression systems may be used to express the proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacteriol. 158:1018-1024 (1984) and the leftward promoter of phage lambda (P<sub>L</sub>) as described by Herskowitz, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook *et al.* for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503.

Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

b. Expression in Eukaryotes

A variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, are known to those of skill in the art. As explained briefly below, a sequence of interest may be expressed in these eukaryotic systems.

Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., *et al.*, Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast.

Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, *et al.*, Gene 8:17-24 (1979); Broach, *et al.*, Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucylase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, a., *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., *et al.*, *J. Bact.* 153:163-168 (1983)).

The proteins of the invention, once expressed, can be isolated from yeast by lysing the cells and applying standard protein isolation techniques to the lysates. The monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay or other standard immunoassay techniques.

The sequences encoding the proteins of the invention can also be ligated to various expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen *et al.* *Immunol. Rev.* 89:49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of ATP-sensitive potassium channel proteins are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)).

Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider *J. Embryol. Exp. Morphol.* 27:353-365 (1987)).

As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences.

As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 Intron from SV40 (Sprague, J. *et al.*, *J. Virol.* 45: 773-781 (1983)).

Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus type-vectors.

Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238.

The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

## 2. Purification

The proteins produced by recombinant DNA technology may be purified by standard techniques well known to those of skill in the art. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide.

The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

## 3. Antibodies

As mentioned above, antibodies can also be used for the screening of polypeptide products encoded by the polymorphic nucleic acids of the invention. In addition, antibodies are useful in a variety of other contexts in accordance with the present invention. Such antibodies can be utilized for the diagnosis of HH and, in certain applications, targeting of affected tissues.

Thus, in accordance with another aspect of the present invention a kit is provided that is suitable for use in screening and assaying for the presence of polypeptide products encoded by the polymorphic nucleic acids of the invention by an immunoassay through use of an antibody which specifically binds to polypeptide products encoded by the polymorphic nucleic acids of the invention in combination with a reagent for detecting the binding of the antibody to the gene product.

Once hybridoma cell lines are prepared, monoclonal antibodies can be made through conventional techniques of priming mice with pristane and interperitoneally injecting such mice with the hybrid cells to enable harvesting of the monoclonal antibodies from ascites fluid.

In connection with synthetic and semi-synthetic antibodies, such terms are intended to cover antibody fragments, isotype switched antibodies, humanized antibodies (mouse-human, human-

mouse, and the like), hybrids, antibodies having plural specificities, fully synthetic antibody-like molecules, and the like.

This invention also embraces diagnostic kits for detecting DNA or RNA comprising a polymorphism of Table 1 in tissue or blood samples which comprise nucleic acid probes as described herein and instructional material. The kit may also contain additional components such as labeled compounds, as described herein, for identification of duplexed nucleic acids.

The following examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims.

## 10 F. EXPERIMENTAL EXAMPLES

### 1. Megabase transcript map

In these studies direct selection, exon-trapping, and genomic sample sequencing were used to generate a transcript map of a 1 megabase region approximately 8.5 megabases telomeric to HLA-A in the vicinity of HFE. This region 6p21.3 was flanked by the genetic markers D6S2242 and D6S2241. The starting material for these experiments was a 1 megabase YAC labeled y899g1 and a bacterial clone contig of this region (Feder *et al.* Nature Genetics 13:399-408 (1996)). These techniques and other methods used in the study are outlined below.

#### a. Direct Selection (DS)

Poly A<sup>+</sup> RNA from human fetal brain, liver and small intestine (Clontech, Palo Alto, CA) were converted into cDNA using random primers and a Superscript cDNA synthesis kit (Life Technologies, Gaithersburg, MD). The cDNA was digested with Mbo I and ligated to cDNA Mbo I linker-adaptors. Unligated linker-adaptor were removed by passage through cDNA spun columns (Pharmacia, Piscataway, NJ). The 5 ng of each of the ligated cDNAs were amplified using the cDNA Mbo I-S primer (5'-CCTGATGCTCGAGTGAATTC-3'). The amplified products were purified on S-400 spin columns (Pharmacia, Piscataway, NJ), ethanol precipitated and resuspended at 1mg/ml in TE. Gel-purified yac899g1 (Centre d'Etude du Polymorphisme Humain) was processed as described by Morgan *et al.* (Nucl. Acids Res. 20:5173-5179 (1992)). The cDNAs were mixed in equal molar amounts for a total of 3 mg, and blocked with a mixture of 4 mg Cot-1 DNA (Life Technologies, Gaithersburg, MD), and a cocktail of Sau 3A-digested ribosomal and five different histone DNAs. The blocked cDNAs were hybridized to biotinylated yac899g1 DNA and streptavidin capture was carried out as described by Morgan *et al.* (*ibid.*). After the second round of selection, the eluted cDNAs were amplified using the cDNA Mbo I-S primer which included a (CUA)<sub>4</sub> repeat at the 5' end to facilitate cloning into a version of pSP72 (Promega, Madison, WI) constructed for use with uracil-DNA glycosylase cloning (UDG, Life Technologies, Gaithersburg, MD). Recombinants were transformed in DH5 $\alpha$ , 1000 clones picked into a 96 well format, and clones prepped for DNA sequencing using AGTC boiling 96-well mini-prep system (Advance Genetic Technologies, Gaithersburg, MD).

Four hundred and sixty five clones were sequenced and the resulting data searched by BLAST (Altschul *et al.* J. Mol. Biol. 215:403-410 (1990)). Those clones representing repetitive, bacterial, yeast, mitochondrial and histone sequences were eliminated from future considerations. The remaining sequences were then searched for overlaps and assembled into 108 unique DS contigs.

The number of clones per DS contig varied between 1 to 22 with the length of each contig ranging from 250bp to 850 bp. Small sequence-tag-sites PCR assays were developed for each DS contig and two experiments were carried out concomitantly; mapping each DS contig back to the bacterial clone contig of the region and testing for the presence of each DS contig in cDNA libraries. Overall, 86 or 80% of the DS contigs mapped back to the region and were found to be in cDNA libraries. The number of 80% mapping to the region was probably an underestimate of the fidelity of the direct-selection since PCR assays which cross exon-intron boundaries would be expected to fail or give larger size products, thereby being scored negative.

#### b. Exon-Trapping

CsCl-purified genomic P1 (Genome Systems), BAC (Research Genetics) and PAC (Genome Systems) DNAs were digested with BamHI, Bgl II, Pst I Sac I and Xho I and 125 ng of each digest ligated into 500 ng pSPL3 (Church *et al.* Nature Genetics 6:98-105 (1994)) (Life Technologies, Gaithersburg, MD) digested with the appropriate restriction enzyme and phosphatased with calf intestinal alkaline phosphatase (USB, Cleveland, OH). One tenth of the ligation was used to transform XL1-Blue MRF<sup>+</sup> cells (Stratagene, La Jolla, CA) by electroporation. Nine tenths of the electroporation was used to inoculate 10 ml of LB + 100µg/ml of carbenicillin and after overnight growth, DNA was prepared using Qiagen Q-20 tips (Qiagen GmbH, Hilden Germany). The remaining one tenth was plated on LB + 100 µg/ml carbenicillin plates to evaluate the efficiency on cloning and to test individual clones for the presence of single inserts. COS-7 cells were seeded overnight at a density of 1.4 x10<sup>5</sup>/well in 6 well dishes. One µg of DNA was transfected using 6ml of Lipofect-Ace. Cytoplasmic RNA was isolated 48 hr post-transfection. RT-PCR was carried out as described by Church *et al.* (*ibid*) using commercially available reagents Life Technologies, Gaithersburg, MD). The resulting CUA-tailed PCR fragments for each restriction digested bacterial clone were pooled and UDG cloned into pSP72-U (a derivative of pSP72). The DNA was transformed in DH5α and the cells plated onto nylon membranes. After overnight growth, duplicates were made and the DNA hybridized to <sup>32</sup>P end-labeled oligos designed to detect various background products associated with the pSPL3 vector. One set of filters was hybridized with the following gel-purified oligos in 6X SSC aqueous hybridization solution at 42° C:

	vector-vector splicing	5'-CGACCCAGCAACCTGGAGAT-3'
30	cryptic donor-1021	5'-AGCTCGAGCGGCCGCTGCAG-3'
	cryptic donor-1134	5'-AGACCCCAACCCACAAGAAG-3'

The filters were washed twice in 6X SSC, 10 mM sodium pyrophosphate (NaPPi) at 60°C, 30 mins.

After overnight autoradiography, non-hybridizing clones were picked and grown in 250 µl of LB + 100µg/ml of carbenicillin in 96 well mini-rack tubes. The samples were analyzed by PCR using the secondary PCR primers supplied in the kit (Life Technologies, Gaithersburg, MD) and those clones with inserts greater than 200 bp were selected for sequencing.

Ninety-six exon traps per bacterial clone were sequenced for a total of 768 reactions and the resulting data analyzed by BLAST. In addition, each potential exon was searched against a database of the 86 DS contigs to eliminate redundant sequences. PCR assays were developed for

each of the potential exons and they were tested for their presence in cDNA libraries. A total of 48 potential exons remained after these screening steps.

### c. Sample Sequencing

A minimal set of bacterial clones chosen to cover y899g1 were prepped with the Qiagen Maxi-Prep system and purified on CsCl. Ten micrograms of DNA from each bacterial clone was sonicated in a Heat Systems Sonicator XL and end-repaired with Klenow (USB) and T4 polymerase (USB). The sheared fragments were size selected between three to four kilobases on a 0.7% agarose gel and then ligated to BstXI linkers (Invitrogen). The ligations were gel purified on a 0.7% agarose gel and cloned into a pSP72 derivative plasmid vector. The resulting plasmids were transformed into electrocompetent DH5 $\alpha$  cells and plated on LB-carbenicillin plates. A sufficient number of colonies was picked to achieve 15-fold clone coverage. The appropriate number of colonies was calculated by the following equation to generate a single-fold sequence coverage: Number of colonies = size of bacterial clone (in kb)/average sequence read length (0.4 kb). These colonies were prepped in the 96-well AGCT system and end-sequenced with oligo MAP1 using standard ABI Dye Terminator protocols. MAP1 was CGTTAGAACGCGGCTACAAT. The MAP1 sequences were screened locally with the BLAST algorithm against all available public databases. All sequence identities were catalogued and cross referenced to the DS and exon-trapped databases.

A total of 3794 end sequence reactions were run to achieve the theoretical 1X coverage. Eighty-five percent of these sequences contained non-bacterial non-vector inserts. An additional 1060 end sequence reactions were run from the opposite end of the cloning vector to augment the sequence coverage and to prepare for contigging across selected regions. BLAST searches to all publicly available databases identified 12 histone genes and 74 unique expressed sequence fragments (ESF). The ESF represent a collection of ESTs and other expressed sequence fragments that were selected due to their sequence identity over a significant portion of genomic DNA. The ESF were cross referenced against the DS and exon-trapped databases to eliminate redundancies. 58 unique ESF remained, representing 39 distinct clones. Included in these ESF are 5 sequences homologous to histone genes.

Table 3. EST's found by Sample Sequencing Large Insert Bacterial Clones

Clone name	Bacterial clone	Homology 5' blastx	Homology 3' blastx	Poly A + signal <sup>1</sup>	Genomic poly (A) <sub>cat</sub>	cDNA Homology
EST03556	pc157c3	na <sup>2</sup>	none <sup>3</sup>	+	-	cDNA 28
ym33f11	pc157c3	ZNF	na	na	na	
EST04698	pc157c3	na	NSH <sup>4</sup>	+	-	
EST04812	pc157c3	na	NSH	-	-	
yb89b08	pc157c3	NSH	na	na	na	
yd88g11	pc157c3	na	nsh	+	-	
yj49b01	pc157c3	NSH	na	na	na	
yv81d05	pc157c3	HG17 Human	NSH	+	-	cDNA 30
yg57h09	p196e20	BUTYBOVIN	NSH	+	-	cDNA 21
yq23d08	p196e20	BUTYBOVIN	NSH	+	-	cDNA 21

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	Clone name	Bacterial clone	Homology 5' blastx	Homology 3' blastx	Poly A+ signal <sup>1</sup>	Genomic poly (A) <sub>on</sub>	cDNA Homology
30	yo65f06	p196e20	NSH	na	na	na	cDNA 29
	yv88c09	p196e20	BUTYBOVIN	na	na	na	cDNA 29
	yd17d06	p196e20	NSH	na	na	na	cDNA 23
	ye25g03	p196e20	BUTYBOVIN	NSH	na	na	cDNA 44
5	ys04h08	pc45p21	NSH	NSH	+	-	cDNA 44
	yn01c05	p196e20	BUTYBOVIN	na	na	na	cDNA 32
	YG78F10	PC45P21	NSH	NSH	na	na	
	yh54f11	p196e20	none	NSH	-	-	
	ys05b08	pc157c3	NSH	Alu	-	+	
10	yb12h11	b132a12	NSH	Histone H3.1	-	-	
	HSC2EE082	b132a12	na	NSH	+	-	
	HUM160h11b	b132a12	none	na	na	na	
	yg04f09	b132b12	Line element	Alu	-	+	
	yd37d11	b132a12	NSH	Alu	-	+	
15	ym29g03	b132a12	Histone H2A	NSH	+	-	cDNA 37
	yi77b02	b132a12	NSH	NSH	-	-	cDNA 37
	yh76b05	b132a12	NSH	Alu	-	-	
	yu98e02	b132a12	NSH	Alue	-	+	
	yd72h12	b132a12	Alu	NSH	+	+	
20	yd19d03	pc222k22	Histone H2B.1	NSH	+	-	
	ye98g01	b132a12	NSH	NSH	+	-	cDNA
	yi61f07	b132a12	NSH	NSH	-	+	
	ESTO5340	b3e17	na	Alu	-	+	
	yd35d05	pc222k22	NSH	NSH	-	+	
25	yc52a05	pc75L14	NSH	na	na	na	
	yd84a05	pc75L14	none	none	-	? <sup>5</sup>	
	yr42a05	pc75L14	NaPi transport	none	+	-	cDNA 22B
	yd83h08	b20h20	NSH	none	+	-	
	ye38c09	b20h20	NSH	Alu	-	+	
30	yp74c05	b20h20	NaPi transport	Alu	? <sup>6</sup>	na	

Bracketed area is the critical region

1	Signal of ATAAA or ATTAA	4	No Significant Homologies
2	Not available	5	3' splice that is not on contig
35	3 "NONE" reported by blast	6	Poor EST sequence

#### d. cDNA library screening

Superscript plasmid cDNA libraries, brain, liver and testis, were purchased from Life Technologies, Gaithersburg, MD. Colonies were plated on Hybond N filters (Amersham) using

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standard techniques. Insert probes from DS, exons and EST (I.M.A.G.E. clones; Genome Systems) were all isolated by PCR followed by purification in low-melting point agarose gels (Seakem). The DNAs were labeled in gel using the Prime-it II kit (Stratagene, La Jolla, CA). Small exon probes were labeled using their respective STS PCR primers instead of random primers. Up to 5 different probes were pooled in a hybridization. Filters were hybridized in duplicate using standard techniques. Putative positives were screened by PCR using the probe's STSs to identify clones. Inserts from positive clones were subcloned in pSP72 and sequenced.

#### **e. Northern blots and RT-PCR analysis**

Multiple tissue northern blots were purchased from Clontech and hybridized according to the manufacturer's instructions. RT-PCR was carried out on random primed first strand cDNA made from poly A+ RNA (Clontech) using AmpliTaq Gold (Perkin-Elmer). Control reactions were performed on RNA samples processed in the absence of reverse transcriptase to control for genomic DNA contamination.

#### **f. Genomic Sequencing**

The MAP1 sequences from the bacterial clones b132a2, 222K22, and 75L14 were assembled into contigs with the Staden package (available from Roger Staden, MRC). A minimal set of 3 kb clones was selected for sequencing with oligo labeled MAP2 that sits on the opposite end of the plasmid vector. The sequence of MAP2 was GCCGATTCATTAATGCAGGT. The MAP2 sequences were entered into the Staden database in conjunction with the MAP1 sequences to generate a tiling path of 3 kb clones across the region. These sequences were also screened with the BLAST algorithm and all novel sequence identities were noted. The plasmid 3 kb libraries were concurrently transformed in 96 well format into pox38UR (available from C. Martin, Lawrence Berkeley Laboratories). The transformants were subsequently mated with JGM (Strathman *et al.* P.N.A.S. 88:1247-1250 (1991) in 96 well format. All matings of the 3 kb clones within the tiling path were streaked on LB-carbenicillin-kanamycin plates and a random selection of 12 colonies per 3 kb clone was prepped in the AGCT system. The oligos -21: CTGTAAAACGACGGCCAGTC, and REV: GCAGGAAACAGCTATGACC were used to sequence off both ends of the transposon. Each 3 kb clone was assembled in conjunction with the end sequence information from all bacterial clones to generate complete sequence across the region. The genomic sequence was analyzed with the BLAST nucleotide and protein homology algorithms and the GRAIL 1.2 software to identify novel open reading frames (ORF) for gene finding.

#### **g. Discussion**

A compilation of 174 ESF led to the construction of an expressed sequence map of the region that served as the framework for the isolation of full-length cDNAs (Figure 1). (The map shows the subset of ESF that were actually mapped). Probes were developed for 82 best ESFs which appeared to be derived from the coding portions of cDNAs and the appropriate cDNA libraries were screened. This led to the isolation of 19 cDNAs, 17 of which represented novel sequences. 70 of the 174 ESF were included in the cDNAs isolated (40%). 36 probes failed to produce any clones even after repeated screening of several libraries. 51 ESF which were not accounted for in the cDNAs

cloned were not used in any screen. Therefore, it is possible that some additional genes within this 1 megabase region may have escaped detection.

A list of these cDNAs cloned and a comparison of the methods used to find them is presented in Table 4. Direct selection found 14 out of the 18 cDNAs contained within the boundaries of the YAC used in the experiment. Exon trapping found 15 out of the 19 cDNAs contained within the boundaries of the large insert bacterial clone contig. Sample sequencing identified 11 genes that had corresponding ESTs in the public database.

Table 4. Comparison of gene finding methods

	Bacterial Clone	CDNA #	Homology	EST	DS	Exon Trap
	157c	28	zinc finger	EST03556	2	1
	157c3	30	nonhistone	yv81d05	1	none
				yvh07a10		
	157c3	46	ORF	yd88g11	1	
15	157c3	20	BT	none	none	3
	p18696	21	BTF1	yn01G5	4	5
				yg23d08		
				yg57h09		
				yu15h03		
	45p21	32	BTF2	yg78f10	7	3
				yn01c05		
	45p21	29	BTF3	ye25g03	2	9
				yo65f06		
	45p21	23	BTF4	yd17d06	4	6
20	45p21	44	BTF5	ys04h08	2	4
	3e17	41	genomic?	none	none	1
	132a2	43	genomic?	none	none	3
	132a2	36	genomic?	none	1	none
	132a2	37	histone 2A	ym29g03	3	none
				yh87a03		
25	75114	24	MHC class I	ye98g01	1	2
	132a2	39	genomic?	none	none	4
	132a2	27	Ro/SSA	none	3	4
	132a2	22B	NPT1-like	yr42a05	1	7
				yf09g06		
	20h20	22E	NPT1-like	none	2	5
30	20h20	NPT1	NPT1	yp74c05	N/A	3

As a final approach, a tiling path with overlapping end sequences from the sample sequence database was generated. Each 3 kb clone within the path was shotgun-sequenced using transposable elements as platforms for dual end sequencing. These individual clones were assembled in conjunction with the end sequences from all bacterial clones in the region. The resulting sequence (Figure 2) was analyzed systematically with BLAST homology searches and the Grail 1.2 program to identify novel open reading frames (ORF) and other gene-like structures. The BLAST homology searches did not produce any probes that had not already been identified by sample sequencing. Grail predicted exons for all the genes in the region, but was only able to assemble the histones into any representative form. A detailed analysis of BLAST homology searches to protein databases identified an enticing homology to a zinc alpha 2 glycoprotein approximately 25 kb upstream of HFE, but the lack of a substantial ORF and the presence of a stop codon suggested that it was a pseudogene. Figure 2 shows the positions, the exon and intron structures, and the relative orientation of transcription of novel genes within this region. Also shown are the positions and transcriptional orientations of the histone genes. A total of 12 histone genes were identified in this study.

In an effort to account for the ESTs that did not associate with the characterized genes in the 250 kb region, the genomic sequence around the putative 3' ends were examined for polyadenylation signals to determine whether certain EST sequences may have originated from genomic DNA contamination in the normalized cDNA libraries used in EST generation. The positions of the 14 ESTs found in this region are indicated in Figure 2 to show those associated with the cDNAs cloned and those which did not associate with genomic DNA of obvious coding potential. Four ESTs corresponded to 3 of the 4 cDNAs cloned from the region (Table 2). One EST encoded a histone H2B.1 gene and another was a repetitive element. Of the remaining 8, 6 EST clones were used as probes of cDNA libraries with negative results. Those sequences representing putative 3' ends of cDNA were searched for the presence of poly (A)+ addition signals. Five of the 13 ESTs which had 3' end sequence, had the sequence ATAAA or ATTAA. Five of the remaining 8 ESTs that did not have a poly (A)+ addition signal had genomic encoded stretches of poly (A) near the end of EST sequence and, therefore, may have been created by oligo d(T) priming of contaminating genomic DNA. This analysis was expanded to include all ESTs in the large-insert bacterial contigs with definitive 3' ends. Of the remaining 26, 15 had 3' end sequence and, of these, 8 had poly (A)+ addition signals. Five of these 8 ESTs were associated with the cloned cDNAs. Of the remaining 7 which did not have poly (A)+ addition signals, 4 had genomic encoded stretches of poly (A).

#### i. Butyrophilin gene family

The human homolog of the bovine butyrophilin gene (BT) was cloned and mapped to approximately 480 kb centromeric to HFE (Figure 1). BT is a transmembrane protein of unknown function which constitutes 40% of the total protein associated with the fat globule of bovine milk (Jack *et al.* J. Biol. Chem. 265:14481-14486 (1990)). A human homolog of BT has recently been cloned by Tayloer *et al.* (Biochem Biophys Acta 1306:1-4 (1996)). The results in this study indicated that BT is a member of a gene family with at least five other members of the family residing in this region (Figure 1). A comparison of these proteins is shown in Figure 3. The proteins were aligned based on their descending order of relatedness and to minimized gaps in the sequence. Each of the five proteins

display varying degrees of homology to BT. BTF1 (cDNA 21), BTF2 (cDNA 32), BTF5 (cDNA 44), and BTF3 (cDNA 29) are 45%, 48%, 46%, and 49%, identical to BT, whereas BTF4 (cDNA 23), which is more similar to BTF3 (cDNA 29), is only 26% identical. This low degree of identity to BT is largely due to a truncation at the carboxyl terminus of the protein. The BTF family falls into two groups: BTF1 and 2 which are more related to each other than to BT or the other BTF members, and BTF5, 3 and 4, which appear to have a common evolutionary origin. The order of these genes on the chromosome suggests that the BT gene has duplicated two times, giving rise to BTF1 and BTF5. Subsequently, it appears likely these two genes experienced further duplication events to give rise to the other members in their groups.

The three major components of BT, the B-G immunoglobulin superfamily domain (containing the V consensus sequence) (Miller *et al.* Proc. Natl. Acad. Sci. U.S.A. 88:4377-4381 (1991)), the transmembrane region, and the B30-2 exon are found in all of these proteins (with the exception of BTF4 (cDNA 23) which lacks the B30-2 exon by virtue of the carboxyl terminal truncation). The exon B30-2 is a previously noted feature of the MHC class 1 region found approximately 200 kb centromeric to the HLA-A gene (Vernet *et al.*, J. Mol. Evol. 37:600-612 (1993)). In addition this exon is found in several genes of diverse function telomeric to HLA-A namely MOG (approximately 200 kb) and RFP (approximately 1 megabase) (Amadou *et al.* Genomics 26:9-20 (1995)).

The levels of the BTF mRNA were analyzed by northern blot analysis (Figure 4A). The expression of the BTF genes fell into two patterns. BTF1 and BTF2 were expressed as a single major transcript of 2.9 kb and one minor transcript of 5.0 kb. These genes were expressed at high levels in all the tissues tested with the exception of the kidney where the expression level was less. The two genes are 90% identical at the DNA sequence level, therefore, it is possible that the signal observed on the northern blots was the result of cross-hybridization and only one of the two genes was actually expressed. To address this possibility RT-PCR experiments were carried out on a panel of different tissues in order to detect possible tissue dependent expression that would suggest that both genes are expressed. Identical, and thus equivocal, results were obtained with both BTF1 and BTF2 amplification (Figure 4B).

The second group of genes, BTF3-5, are expressed as three (BTF5) (Figure 4A) and two (BTF3 and 4) transcripts ranging from 4.0 to 3.3 kb. BTF5 is expressed at moderate levels in all tissues tested with the exception of the kidney where the expression level is less. RT-PCR experiments showed that mRNA from the BTF5 gene can be found in all tissues tested, including the kidney (Figure 4B). Identical results were obtained with primers from the other genes of this group (data not shown). These genes are also 90% identical to each other at the DNA sequence level (but only 58% identical to BTF1 and 2), hence like BTF1 and BTF2, cross-hybridization could account for the similarity in size and patterns on the northern blots and RT-PCR. This might be particularly true for BTF4 which lacks the B30-2 exon but still hybridizes to larger size transcripts like BTF5 and BTF3.

#### ii. A gene with similarity to 52 kD Ro/SSA auto-antigen

Located approximately 120 kb telomeric to the HFE gene is a gene, RoRet, that has 58% amino acid similarity to the 52 kD Ro/SSA protein, an auto-antigen of unknown function that is frequently recognized by antibodies in patients with systemic lupus and Sjogren's syndrome (Anderson

*et al. Lancet* 2:456-560 (1961); Clark *et al. J. Immunol.* 102:117-122 (1969)) (Figures 1 and 2).

Alignment of the predicted amino acid sequence of this cDNA with that of 52 kD Ro/SSA indicated two features associated with the 52 kD Ro/SSA protein: a putative DNA binding cysteine rich motif (C-X-(I,V)-C-X(11-30)-C-X-H-X-(F,I,L)-C-X(2)-C-(I,L,M)-X(10-18)-C-P-X-C) found at the N terminus (Freemont *et al. Cell* 64: 483-484 (1991)) and the B30-2 exon found near the carboxyl terminus, are both conserved in RoRet (Figure 5). Northern blot analysis indicated the RoRet gene was expressed as two major transcripts of 2.8 and 2.2 kb and two minor transcripts of 7.1 and 4.4 kb in all of the tissues on the blot at levels reflective of the RNA amounts as determined by  $\beta$ -actin probing (Figure 6A). Using RT-PCR, expression can also be detected in small intestine, kidney liver, and spleen (Figure 6B).

### iii. Two genes with homology to a sodium phosphate transporter

A cDNA for a sodium phosphate transport protein (NPT1) was previously cloned and mapped to 6p21.3 using a somatic cell hybrid panel (Chong *et al. Genomics* 18:355-359 (1993)). NPT1 maps 320 kb telomeric to the HFE gene (Figures 1 and 2). Two additional cDNAs were cloned which show appreciable homology to NPT1 (Figure 5). These genes, NPT3 and NPT4, mapped 1.5 megabases and 1.3 megabases centromeric to the NPT1 gene (Figure 1). Like NPT1, the gene products of NPT3 and NPT4 were extremely hydrophobic, which may reflect a membrane location. Both proteins gave hydrophilicity profiles which were indistinguishable from NPT1 in this study (data not shown). Northern blot analysis indicated that the two genes have different patterns of expression (Figure 6C). NPT3 was expressed at high levels as a 7.2 kb transcript predominately in muscle and heart. Lesser amount of the mRNA were also found in brain, placenta, lung, liver and pancreas. RT-PCR analysis indicated that expression of the proper size PCR fragment for NPT3 was clearly absent in fetal brain, bone marrow and small intestine (Figure 6D). A smaller size fragment was detectable in all tissues with the exception of the liver, which may represent evidence for alternative splicing. Although expression was apparently absent from the kidney by northern blot analysis, it was detectable by RT-PCR. Expression was also noted in the mammary gland, spleen and testis. NPT4, on the other hand, was expressed only in the liver and the kidney as a smear of transcripts approximately 2.6 - 1.7 kb (Figure 6C). RT-PCR confirmed these results, although a small amount of the proper size PCR fragment was also found in the small intestine and testis (Figure 6D). Other tissues showed amplification, but the fragments were of larger and smaller size than that produced by the cDNA 22E positive control. Hence, these two genes which apparently have the structural characteristics of a sodium phosphate transporter, appeared to be under the control of different regulatory mechanism that lead to differential patterns of expression.

### 2. Sequencing of 235 kb from a Homozygous Ancestral (Affected) Individual

In these studies the entire genomic sequence was determined from an HH affected individual for a region corresponding to a 235,033 bp region surrounding the HFE gene between the flanking markers D6S2238 and D6S2241. The sequence was derived from a human lymphoblastoid cell line, HC14, that is homozygous for the ancestral HH mutation and region. The sequence from the ancestral chromosome (Figure 9) was compared to the sequence of the region in an unaffected individual (Figure 8) disclosed in copending U.S.S.N. 08/724,394 to identify polymorphic sites. A

subset of the polymorphic alleles so defined were further studied to determine their frequency in a collection of random individuals.

The cell line HC14 was deposited with the ATCC on June 25, 1997, and is designated ATCC CRL-12371.

5

a. Cosmid Library Screening

The strategy and methodology for sequencing the genomic DNA for the affected individual was essentially as described in copending U.S.S.N. 08/724,394, hereby incorporated by reference in its entirety. Basically, a cosmid library was constructed using high molecular weight DNA from HC14 cells. The library was constructed in the supercos vector (Stratagene, La Jolla, CA).

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Colonies were replicated onto Biotrans nylon filters (ICN) using standard techniques. Probes from genomic subclones used in the generation of the sequence of the unaffected sequence disclosed in 08/724,394 were isolated by gel electrophoresis and electroporation. Subclones were chosen at a spacing of approximately 20 kb throughout the 235 kb region. The DNA was labeled by incorporation of <sup>32</sup>P dCTP by the random primer labeling approach. Positively hybridizing clones were isolated to purity by a secondary screening step. Cosmid insert ends were sequenced to determine whether full coverage had been obtained, and which clones formed a minimal path of cosmids through the 235 kb region.

15

b. Sample Sequencing

A minimal set of cosmid clones chosen to cover the 235 kb region were prepped with the Qiagen Maxi-Prep system. Ten micrograms of DNA from each cosmid preparation were sonicated in a Heat Systems Sonicator XL and end-repaired with Klenow (USB) and T4 DNA polymerase (USB). The sheared fragments were size selected between three to four kilobases on a 0.7% agarose gel and then ligated to BstXI linkers (Invitrogen). The ligations were gel purified on a 0.7% agarose gel and cloned into a pSP72 derivative plasmid vector. The resulting plasmids were transformed into electrocompetent DH5α cells and plated on LB-carbenicillin plates. A sufficient number of colonies was picked to achieve 15-fold clone coverage. The appropriate number of colonies was calculated by the following equation to generate a single-fold sequence coverage: Number of colonies = size of bacterial clone (in kb)/average sequence read length (0.4 kb). These colonies were prepped in the 96-well Qiagen REAL, and the 5' to 3' DNA Prep Kit, and AGCT end-sequenced with oligo MAP1 using standard ABI Dye Terminator protocols. MAP1 was CGTTAGAACGCGGCTACAAT.

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c. Genomic Sequencing

The MAP1 sequences from the cosmid clones HC182, HC187, HC189, HC195, HC199, HC200, HC201, HC206, HC207, and HC212 were assembled into contigs with the Staden package (available from Roger Staden, MRC). A minimal set of 3 kb clones was selected for sequencing with oligo labeled MAP2 that sits on the opposite end of the plasmid vector. The sequence of MAP2 was GCCGATTCATTAATGCAGGT. The MAP2 sequences were entered into the Staden database in conjunction with the MAP1 sequences to generate a tiling path of 3 kb clones across the region. The plasmid 3 kb libraries were concurrently transformed in 96 well format into pox38UR (available from C. Martin, Lawrence Berkeley Laboratories). The transformants were subsequently mated with JGM (Strathman et al. P.N.A.S. 88:1247-1250 (1991) in 96 well format. All matings of the

35

40

3 kb clones within the tiling path were streaked on LB-carbenicillin-kanamycin plates and a random selection of 12 colonies per 3 kb clone was prepped in the AGCT system. The oligos -21: CTGTAAAACGACGGCCAGTC, and REV: GCAGGAAACAGCTATGACC were used to sequence off both ends of the transposon. Each 3 kb clone was assembled in conjunction with the end sequence information from all cosmid clones in the region.

In some regions, the coverage of the genomic sequence by cosmids was incomplete. Any gaps in the sequence were filled by using standard PCR techniques to amplify genomic DNA in those regions and standard ABI dye terminator chemistry to sequence the amplification products.

#### d. Identification of Polymorphic Sites

The assembled sequence of the cosmid clones in connection with the PCR amplified genomic DNA was compared to the genomic sequence of the unaffected individual using the FASTA algorithm. Numeric values were assigned to the sequenced regions of 1 to 235,303, wherein base 1 refers to the first C in the CA repeat of D6S2238 and base 235,303 is the last T in the GT repeat of D6S2241 of the unaffected sequence (Figure 8). Table 1 lists the differences between the two compared sequences. Note that previously disclosed (Feder et al., Nature Genetics 13:399-408 (1996)) polymorphic sites D6S2238 (base 1), D6S2241 (base 235,032), 24d1 (base 41316), and D6S2239 (base 84841) are not included in the list of new polymorphisms, although they are provided for reference in a footnote to the Table and were observed in the ancestral sequence. In the Table, a single base change such as C-T refers to a C in the unaffected sequence at the indicated base position that occurred as a T in the corresponding position in the affected sequence. Similarly, an insertion of one or more bases, such as TTT in the affected sequence, is represented as "TTT INS" between the indicated bases of the unaffected sequence. A deletion of one or more bases occurring in the affected sequence, such as AAA DEL, is represented as the deletion of the indicated bases in the unaffected sequence.

#### e. Characterization of Rare Polymorphisms

In this study about 100 of the polymorphisms of Table 1 were arbitrarily chosen for further characterization. Allele frequencies in the general population were estimated by OLA analysis using a population of random DNAs (the "CEPH" collection, J. Dausset et al., Genomics 6(3):575-577 (1990)). These results are provided in Table 2.

One single base pair difference, occurring at base 35983 and designated C182.1G7T/C (an A to G change on the opposite strand) was present in the ancestral chromosome and rare in the random DNAs. This change occurred in a noncoding region of the hemochromatosis gene near exon 7 approximately 5.3 kb from the 24d1 (Cys282Tyr) mutation. OLA was used to genotype 90 hemochromatosis patients for the C182.1G7T/C base pair change. The frequency for C occurring at this position in the patients was 79.4% as compared to 5% in the random DNAs. Eighty-five of the 90 patients assayed contained identical 24d1 and C182.1G7T/C genotypes. Four of the remaining 5 patients were homozygous at 24d1 and heterozygous at C182.1G7T/C; one was heterozygous at 24d1 and homozygous at C182.1G7T/C. The primers used for this analysis were as follows.

PCR primers for detection:

182.1G7.F 5'-GCATCAGCGATTAACCTTCTAC -3'

182.1G7.R 5'-TTGCATTGTGGTGAAATCAGGG -3'

For the detection assay, the biotinylated primers used were as follows.

5 182.1G7.C 5' (b)CTGAGTAATTGTTTAAGGTGC -3'

182.1G7.T 5' (b)CTGAGTAATTGTTTAAGGTGT -3'

The phosphorylated digoxigenin-labeled primer used was:

182.1G7.D 5' (p)AGAAGAGATAGATATGGTGG -3'

10 A further rare single base pair change was detected at 61,465bp. The inheritance pattern of this polymorphism, C195.1H5C/T (a G to A change on the opposite strand), is identical to that of 24d1. The frequency of T occurring at that position (C195.1H5T) observed in a set of 76 patients was 78.5% as compared to 5% in random individuals.

15 PCR primers for detection:

1951H5.3F 5'-GAATGTGACCGTCCCATGAG-3'

1951H5.3R 5'-CAACTGAATATGCAGAAAAAAGTACACC-3'

For the detection assay, the biotinylated primers used were:

1951H5.3.4 5' (b)AGTAGCTGGGACTCACGGTGT-3'

20 1957H5.3.5 5' (b)AGTAGCTGGGACTCACGGTGC-3'

The phosphorylated digoxigenin-labeled primer used was:

1951H5.3.6 5' (p)GCGCCACCACTCCCAGCTCAT-3'

25 These rare alleles are thus preferred surrogate markers for 24d1 and are especially useful in screening assays for the likely presence of 24d1 and/or 24d2.

All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety.

WHAT IS CLAIMED IS:

- 1           1.       An oligonucleotide comprising at least 8 to about 100 consecutive bases from the  
2       sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100  
3       consecutive bases includes at least one polymorphic site of Table 1.
- 1           2.       The oligonucleotide of claim 1, wherein the polymorphic site is selected from the  
2       group consisting of base 35983 or base 61465.
- 1           3.       An oligonucleotide pair selected from the sequence of Figure 9 or its complement for  
2       amplification of a polymorphic site of Table 1.
- 1           4.       An isolated nucleic acid molecule comprising about 100 consecutive bases to about  
2       235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at  
3       least one polymorphic site of Table 1.
- 1           5.       The isolated nucleic acid molecule of claim 4, wherein the polymorphic site is selected  
2       from the group consisting of base 35983 or base 61465.
- 1           6.       The isolated nucleic acid molecule of claim 4, wherein the nucleic acid is selected  
2       from the group consisting of cDNA, RNA, or genomic DNA.
- 1           7.       A polypeptide encoded by the nucleic acid molecule of claim 4.
- 1           8.       An antibody which specifically recognizes the polypeptide of claim 7.
- 1           9.       A method to determine the presence or absence of the common hereditary  
2       hemochromatosis (HFE) gene mutation in an individual comprising:  
3               providing DNA or RNA from the individual; and  
4               assessing the DNA or RNA for the presence or absence of a haplotype of Table 1,  
5               wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the  
6       HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the  
7       likely presence of the HFE gene mutation in the genome of the individual.
- 1           10.      The method of claim 9, wherein the method further comprises assessing the RNA or  
2       DNA for the presence of at least one of the polymorphisms 24d1, 24d2, HHP-1, HHP-19, or HHP-29;  
3       or microsatellite repeat alleles 19D9:205, 18B4:235, 1A2:239, 1E4:271, 24E2:245, 2B8:206, 3321-  
4       1:98, 4073-1:182, 4440-1:180, 4440-2:139, 731-1:177, 5091-1:148, 3216-1:221, 4072-2:170, 950-  
5       1:142, 950-2:164, 950-3:165, 950-4:128, 950-6:151, 950-8:137, 63-1:151, 63-2:113, 63-3:169, 65-

6 1:206, 65-2:159, 68-1:167, 241-5:108, 241-29:113, 373-8:151, 373-29:113, D6S258:199, D6S265:122,  
7 D6S105:124, D6S306:238, D6S464:206, or D6S1001:180.

1 11. The method of claim 9, wherein the haplotype comprises at least two polymorphic  
2 sites of Table 1.

1 12. The method of claim 11, wherein one of the at least two polymorphic sites of Table 1  
2 is at base 35983 or 61465.

1 13. The method of claim 11, wherein the haplotype comprises at least three polymorphic  
2 sites of Table 1.

1 14. A method to determine the presence or absence of the common hereditary  
2 hemochromatosis (HFE) gene mutation in an individual comprising:  
3 providing DNA or RNA from the individual; and  
4 assessing the DNA or RNA for the presence or absence of a genotype defined by a  
5 polymorphic allele of Table 1,  
6 wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1  
7 indicates the likely absence of the HFE gene mutation in the genome of the individual and the  
8 presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the  
9 individual.

1 15. The method of claim 15, wherein the polymorphic allele occurs in less than about 50%  
2 of a random population of individuals.

1 16. The method of claim 15, wherein the polymorphic allele occurs in less than about 25%  
2 of a random population of individuals.

1 17. The method of claim 15, wherein the polymorphic allele occurs in less than about 5%  
2 of a random population of individuals.

1 18. The method of claim 15, wherein the genotype is C182.1G7C or C195.1H5T.

1 19. A kit comprising one or more oligonucleotides of claim 1.

1 20. A kit comprising at least one oligonucleotide pair of claim 3.

1 21. A culture of lymphoblastoid cells having the designation ATCC CRL-12371.

- 1 22. An isolated nucleic acid sequence comprising a sequence substantially identical to  
2 BTF1.
- 1 23. The isolated nucleic acid sequence of claim 23, wherein the nucleic acid is cDNA.
- 1 24. The polypeptide encoded by the isolated nucleic acid sequence of claim 23.
- 1 25. A vector comprising the nucleic acid sequence of claim 23.
- 1 26. A host cell stably transfected with the nucleic acid sequence of claim 23.
- 1 27. An antibody that is specifically immunoreactive with the polypeptide of claim 24.
- 1 28. An isolated nucleic acid sequence comprising a sequence substantially identical to  
2 BTF2.
- 1 29. The isolated nucleic acid sequence of claim 28, wherein the nucleic acid is cDNA.
- 1 30. The polypeptide encoded by the isolated nucleic acid sequence of claim 28.
- 1 31. A vector comprising the nucleic acid sequence of claim 28.
- 1 32. A host cell stably transfected with the nucleic acid sequence of claim 28.
- 1 33. An antibody that is specifically immunoreactive with the polypeptide of claim 30.
- 1 34. An isolated nucleic acid sequence comprising a sequence substantially identical to  
2 BTF3.
- 1 35. The isolated nucleic acid sequence of claim 34, wherein the nucleic acid is cDNA.
- 1 36. The polypeptide encoded by the isolated nucleic acid sequence of claim 34.
- 1 37. A vector comprising the nucleic acid sequence of claim 34.
- 1 38. A host cell stably transfected with the nucleic acid sequence of claim 34.
- 1 39. An antibody that is specifically immunoreactive with the polypeptide of claim 36.

- 1           40.    An isolated nucleic acid sequence comprising a sequence substantially identical to  
2    BTF4.
- 1           41.    The isolated nucleic acid sequence of claim 40, wherein the nucleic acid is cDNA.
- 1           42.    The polypeptide encoded by the isolated nucleic acid sequence of claim 40.
- 1           43.    A vector comprising the nucleic acid sequence of claim 40.
- 1           44.    A host cell stably transfected with the nucleic acid sequence of claim 40.
- 1           45.    An antibody that is specifically immunoreactive with the polypeptide of claim 42.
- 1           46.    An isolated nucleic acid sequence comprising a sequence substantially identical to  
2    BTF5.
- 1           47.    The isolated nucleic acid sequence of claim 46, wherein the nucleic acid is cDNA.
- 1           48.    The polypeptide encoded by the isolated nucleic acid sequence of claim 46.
- 1           49.    A vector comprising the nucleic acid sequence of claim 46.
- 1           50.    A host cell stably transfected with the nucleic acid sequence of claim 46.
- 1           51.    An antibody that is specifically immunoreactive with the polypeptide of claim 48.
- 1           52.    An isolated nucleic acid sequence comprising a sequence substantially identical to  
2    NTP-3.
- 1           53.    The isolated nucleic acid sequence of claim 52, wherein the nucleic acid is cDNA.
- 1           54.    The polypeptide encoded by the isolated nucleic acid sequence of claim 52.
- 1           55.    A vector comprising the nucleic acid sequence of claim 52.
- 1           56.    A host cell stably transfected with the nucleic acid sequence of claim 52.
- 1           57.    An antibody that is specifically immunoreactive with the polypeptide of claim 54.

1           58.     An isolated nucleic acid sequence comprising a sequence substantially identical to  
2     NTP-4.

1           59.     The isolated nucleic acid sequence of claim 58, wherein the nucleic acid is cDNA.

1           60.     The polypeptide encoded by the isolated nucleic acid sequence of claim 58.

1           61.     A vector comprising the nucleic acid sequence of claim 58.

1           62.     A host cell stably transfected with the nucleic acid sequence of claim 58.

1           63.     An antibody that is specifically immunoreactive with the polypeptide of claim 60.

1           64.     An isolated nucleic acid sequence comprising a sequence substantially identical to  
2     RoRet.

1           65.     The isolated nucleic acid sequence of claim 64, wherein the nucleic acid is cDNA.

1           66.     The polypeptide encoded by the isolated nucleic acid sequence of claim 64.

1           67.     A vector comprising the nucleic acid sequence of claim 64.

1           68.     A host cell stably transfected with the nucleic acid sequence of claim 64.

1           69.     An antibody that is specifically immunoreactive with the polypeptide of claim 66.

1           70.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of BTF1.

1           71.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of BTF2.

1           72.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of BTF3.

1           73.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of BTF4.

1           74.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of BTF5.

1           75.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of NPT3.

1           76.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of NPT4.

1           77.     An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides  
2     substantially identical to 18 contiguous nucleotides of RoRet.



## BACTERIAL CLONES

157c3	45p21	132o2	75i14	136i7
PI 8696	3e17	222k22	20h20	

**PI 8696**

3e17

222k22

20h20

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**EXPRESSED  
SEQUENCE  
FRAGMENTS**

[illegible]

**cDNAs**

28 30 2082129 234432

**ZNF**

## NON-HISTONE

**BTF**

BTF

**FIG. 1.**

**HISTONE HLA-H RoRet**

**NPT3 NPT4**

SEQUENCED REGION

**FIG. 1.**

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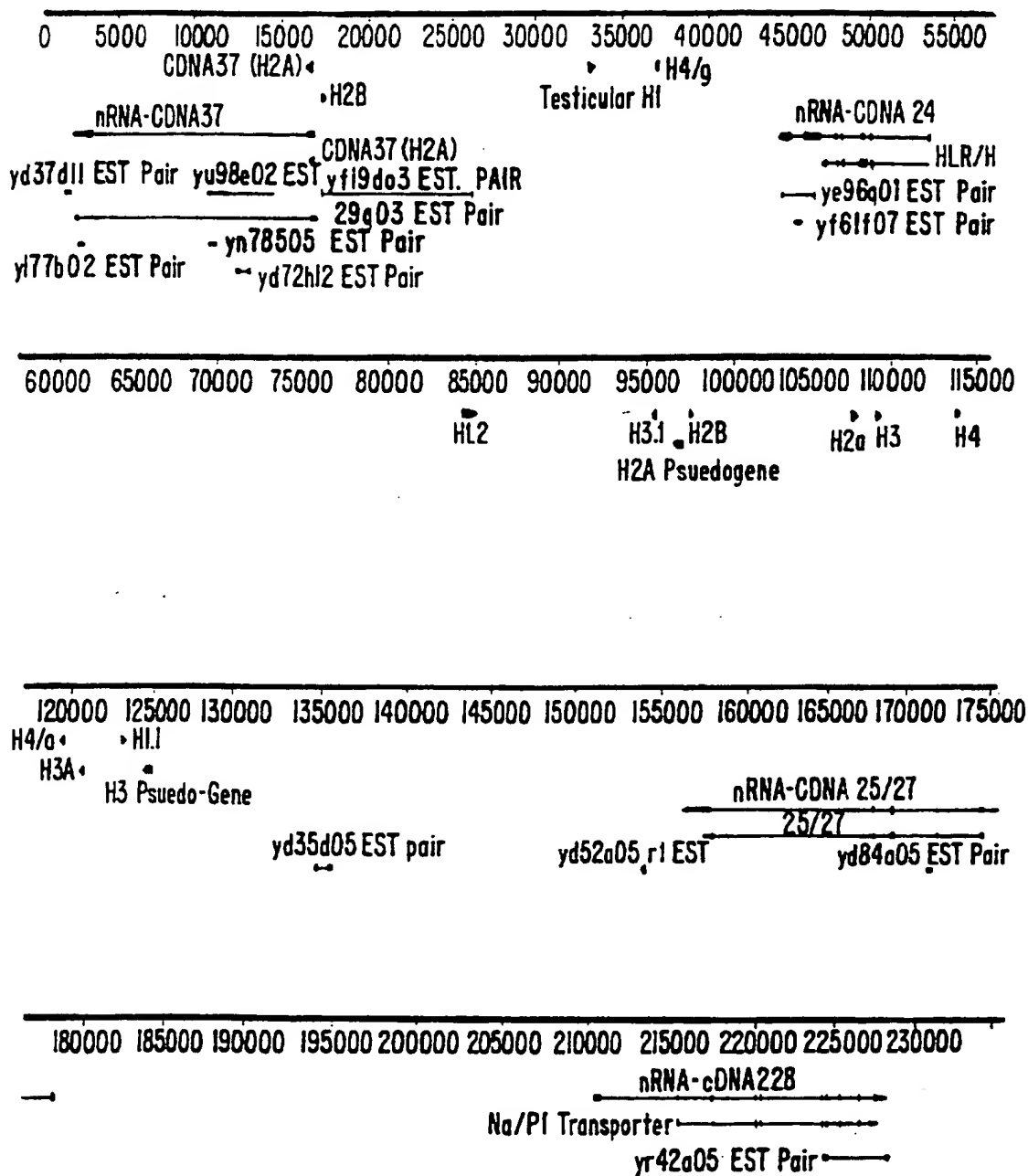


FIG. 2.

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BT      --MAVFPSSGLPRCL---LTLILLQLPKLDSAPFDVIGPPEPILAVVGEDAELPCRISP
BTf1    MESAAALHFSRPAS----LLLLLLSLCALVSAQFIVVGPTDPILATVGENTTLRCHLSPE
BTf2    MEPAAALHFSLPASLLLLLLLLLLLLSLCALVSAQFTVVGPNPILAMVGENTTLRCHLSPE
BTf5    MKMASFLAFLLLNFR---VCLLLQLLMPHSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
BTf3    MKMASSLAFLLLNFH---VSLFLVQLLTPCSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
BTf4    MKMASSLAFLLLNFH---VSLLLVQLLTPCSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
      *      * * * * * * * * * * * * * * * *

BT      ASAEHLELRWFRKKVSPAVLVHRDGREQAEQMPEYRGRATLVQDGIAGRVALRIRGVR
BTf1    KNAEDMEVRWFRSQFSPAVFVYKGGRETEEQMEEYRGRITFVSKDISRGSVALVIHNIT
BTf2    KNAEDMEVRWFRSQFSPAVFVYKGGRETEEQMEEYRGRITFVSKDINRGSVALVIHNVT
BTf5    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
BTf3    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
BTf4    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
      * * * * * * * * * * * * * * * *

BT      VSDDGEYTCFFREDGSYEEALVHLKVAALGSDPHISMVQENGEICLECTSVGWYPEPQV
BTf1    AQENGTYRCYFQEGRSYDEAILHLVVAGLGSKPLISMRGHEDGGIRLECISRGWYPKPLT
BTf2    AQENGIYRCYFQEGRSYDEAILRLVVAGLGSKPLIEIKAQEDGSIWLECISGGWYPEPLT
BTf5    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSDLHVDVKGKDGGIHLECRSTGWYPQPQI
BTf3    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSDLHIEVKGYEDGGIHLECRSTGWYPQPQI
BTf4    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSLNHVEVKGYEDGGIHLECRSTGWYPQPQI
      * * * * * * * * * * * * * * * *

BT      QWRTSKGEKFPSTSESERNPDEEGLFTVAASVIIRDSTKNVSCYIQNLLLGQEKKEVEISI
BTf1    VWRDPYGGVAPALKEVSMPPDADGLFMVTTAVIIRDKSVRNMSCSINNTLLGQKKESVIFI
BTf2    VWRDPYGEVVPALKEVSIADADGLFMVTTAVIIRDKYVRNVSCSVNNTLLGQEKETVIFI
BTf5    QWSNNKGENIPTVEAPVVADGVGLYAVAASVIMRGSSGEGVSCITRSSLLGLEKTASISI
BTf3    KWSDTKGENIPAVEAPVVADGVGLYAVAASVIMRGSSGGGVSCIIRNSLLGLEKTASISI
BTf4    QWSNAKGENIPAVEAPVVADGVGLYAVAASVIMRGSSGEGVSCIIRNSLLGLEKTASISI
      * * * * * * * * * * * * * * * *

BT      PASSLPRLTPWIVAVAV-----ILMVLGLLTIGSIFFTWRLYNER-----
BTf1    PESFMPSVSPCAVALP-----IIVVILMPIAVCIYWINKLQKEKKILSGEK
BTf2    PESFMPSASPWMVALAVILTASPWMVSMTVILAVFIIFMAVSICCIKKLQREKKILSGEK
BTf5    ADPFFRSAQRWIAALAR-----TLPVLLLLLLGGAGYFLWQQQEEKKTQFRKK
BTf3    ADPFFRSAQPWIAALAG-----TLPISLLLLLAGASYFLWRQQKEKIALSRET
BTf4    ADPFFRSAQPWIAALAG-----TLPILLLLLLAGASYFLWRQQKEITALSSEI
      *      *      *      *      *      *      *

BT      PRER-----RNEFS-----SKERLLEELKWKATLHA-----
BTf1    EFERETREIALKELEKERVQKEELQVKEKLQEELRWRRTFLHA-----
BTf2    KVEQE-----EKE-----IAQQLQEELRWRRTFLHA-----
BTf5    KREQELREMAWSTMKQEQS-----TRVKLLEELRWRSIQYASRGERHSAYNEWKKALF
BTf3    EREREMKEMGYAATEQEIS-----LREKLQEELKWRKIQYMARGEKSLAYHEWKMALE
BTf4    ESEQEMKEMGYAATEREIS-----LRESLQEELKRKKSST-----
      *      *      *      *      *      *      *

BT      --VDVTLDPDTAHPHFLYEDSKSVRLSDSRQK---LPEKTERFDSWPCVLGRETFTSGR
BTf1    --VDVLDLPDTAHPDLFLSEDRRSVRRCPFRHLGESVPDNPERFDSQPCVLGRESFASGK
BTf2    --ADVLDLPDTAHPDLFLSEDRRSVRRGPYRQR---VPDNPERFDSQPCVLGWESFASGK
BTf5    KPADVILDPKTANPILLVSEDQRSVQRAKEPDQ---LPDNPERFNWHYCVLGCESFISGR
BTf3    KPADVILDPDTANAILLVSEDQRSVQRAEPRD---LPDNPERFEWRYCVLGCENFTSGR
BTf4    -----

BT      HYWEVEVGDRDWAIGVCRENVMKK-GFDPMTPENGFWAVELY-GNGYWALTPLRTPLPL
BTf1    HYWEVEVENVIEWTVGVCRDVERK-GEVLLIPONGFWTLEMH-KGQYRAVSSPDRIPLPL
BTf2    HYWEVEVENVMVTVGVCRHSVERK-GEVLLIPONGFWTLEMF-GNQYRALSSPERILPL
BTf5    HYWEVEVGDRKEWHIGVCSKNVQRK-GWVKMTPENGFWTMGLTDGNKYRTLTEPRTNLKL
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BTf4    -----

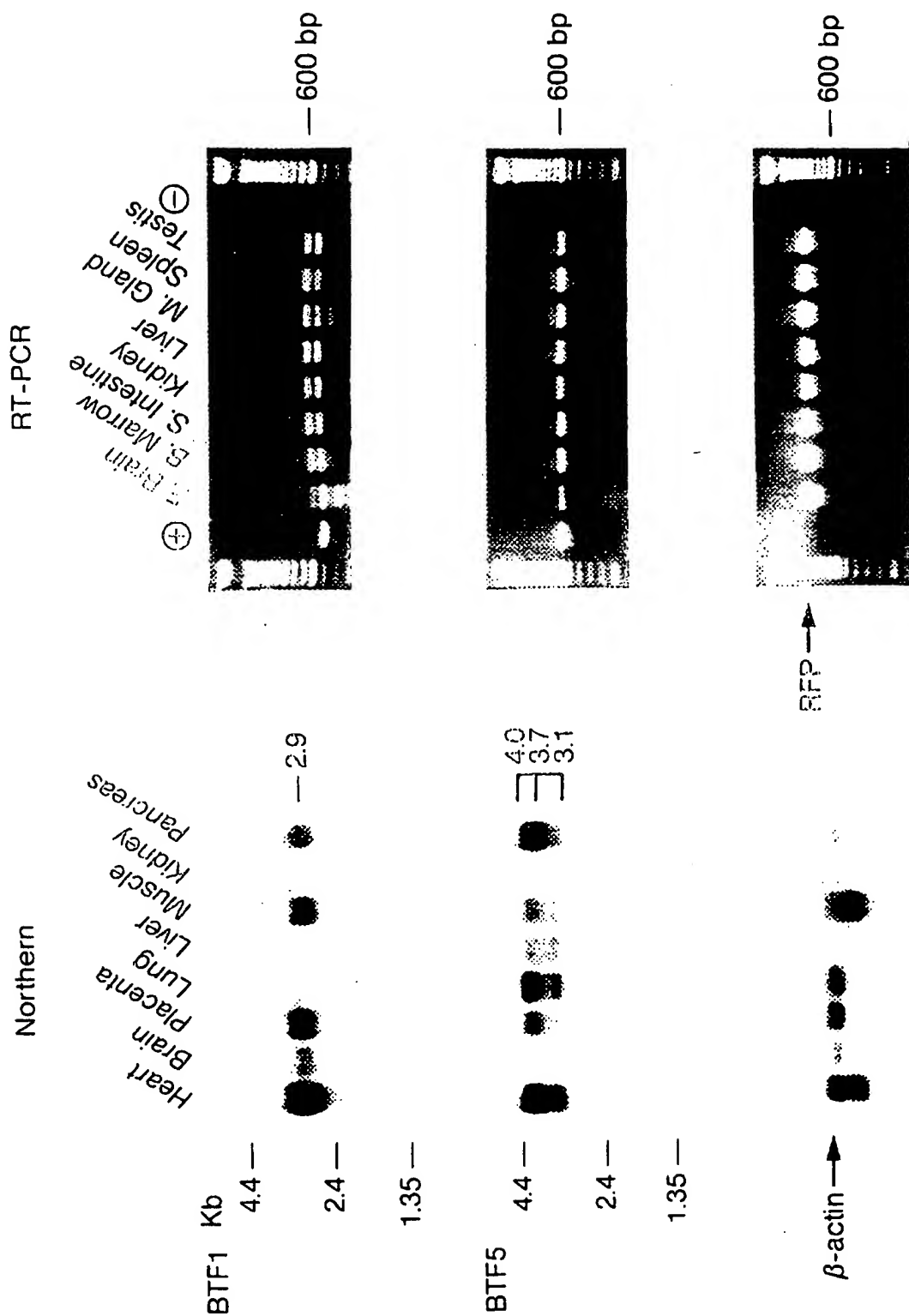
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BT	AGPPRRVGIFLDYESGDISFYNMNDGSDIYTFNSVTFSGLRPPFFCLWSSGKKPLTICPI
BTF1	KESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFSVPVRPFFRLGC-EDSPIFICPA
BTF2	KESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFTVPVRPFFRLGS-DDSPIFICPA
BTF5	PKPPKKVGVFLDYETGDISFYNAVDGSHIHTFLDVSEALYPVFRILTLEPTALSICPA
BTF3	PEPPRKVGIFLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRILTLEPTALTICPI
BTF4	-----
BT	ADGPERVTVIANAQDLSKEIPLSPMGEEASAPRDADTLHSLIPTQPSQGAP-----
BTF1	LTGANGVTVP-----EEGLTLHRVGTHQSL-----
BTF2	LTGASGVMVP-----EEGLKLHRVGTHQSL-----
BTF5	-----
BTF3	PKEVESSPDPLVPDHSLETPLTPGLANESGEPQAEVTSLLLPAHPGAEVSPSATTNQNH
BTF4	-----
BT	-----
BTF1	-----
BTF2	-----
BTF5	-----
BTF3	KLQARTEALY
BTF4	-----

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**FIG. 4B.**

**FIG. 4A.**

		CYSTEINE-RICH DOMAIN																			
52 kD	Ro	MASAARLTMMWEEVTCPICLDPFVEPVSVIECGHSFCQECISQVGKGGG	-----	VCPVCRQRFLLKNLNPRLAMMVN																	
RoRet		MASTTSTKKMMEEATCSICLSLMTNPVSINCGHSYCHLCITDFFKNPSQQLRQETFCPCQCRAPFHMDSLRLPNKQLGSLIE																			
		***	*	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
52 kD	Ro	NLKKISQEAAREGTQGERCAVHGERLHLFCEKDGKALCWVCAQSKKHRDHAMVPLEEAAQYQEKQLQVALGELRRKQELAEKL																			
RoRet		ALKKTDQEM-----	SCEEHGEQFHLFCEDEGQLICWRCERAPQHKGHTT	TALVEDVCQGYKEKLQKAVTKLKQLEDRCTEQ																	
		***	**	*	***	***	*	***	*	***	*	***	*	***	*	***	*	***	*	***	*
52 kD	Ro	EVEIAIKRADWKKTVETQKSRIHAEFVQQNFLVEEEQRLQLEKEKDEREQRLILGEKEAKLAQQSQALQELISELDRRCHS																			
RoRet		KLSTAMRITKWKEKVQIQORQKIRSDFKNLQCFLHEEEKSYLWRLEKEEQTLRLRDYEAGLGLKSNELKSHILELEKCCQG																			
		*	**	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
52 kD	Ro	SALELLQEVIIVLERSESNLKDLDITSPELRSVCHVP	----	GLKKMLRTCAVHITLDPDTANPWLILSEDRRQVRLGDTQQ																	
RoRet		SAQKLLQNVDNLTLSRSWAVKLETSEAVSLELHTMCNVSKLYFDVKKMLRSHQVSVTLDPDTAHHELILSEDRRQVTRGYTQE																			
		**	***	*	**	*	**	*	**	*	**	*	**	*	**	*	**	*	**	*	**
52 kD	Ro	SIPGNEERFDSYPMVLGAQHFGHSGKHYWEVDVTGKEAWDLGVCRDVSRRKGHFLSSKSGFWT IWLWNKQKYEAGTYPQTPL																			
RoRet		NQDTSSRRFTAFPCVLGCEGFTSGRRRYFEVDVGEVGTGWDLGVCMENVQVQGTGMKQEPQSGFWTLRLCKKKGYVALTSPPTSL																			
		**	*	**	*	**	*	**	*	**	*	**	*	**	*	**	*	**	*	**	*
52 kD	Ro	HLQVPPCQVGIFLDYEAGMVSFYNITDHGSLIYSFSECAFTGPLRPF																			
RoRet		HLHEQPLLVGIFLDYEAGVVSFYNG-NTGCHIFTEPKASFSDTLRPFYQVYQYS-----																			
		**	*	*****	*****	*****	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*

FIG. 5A.



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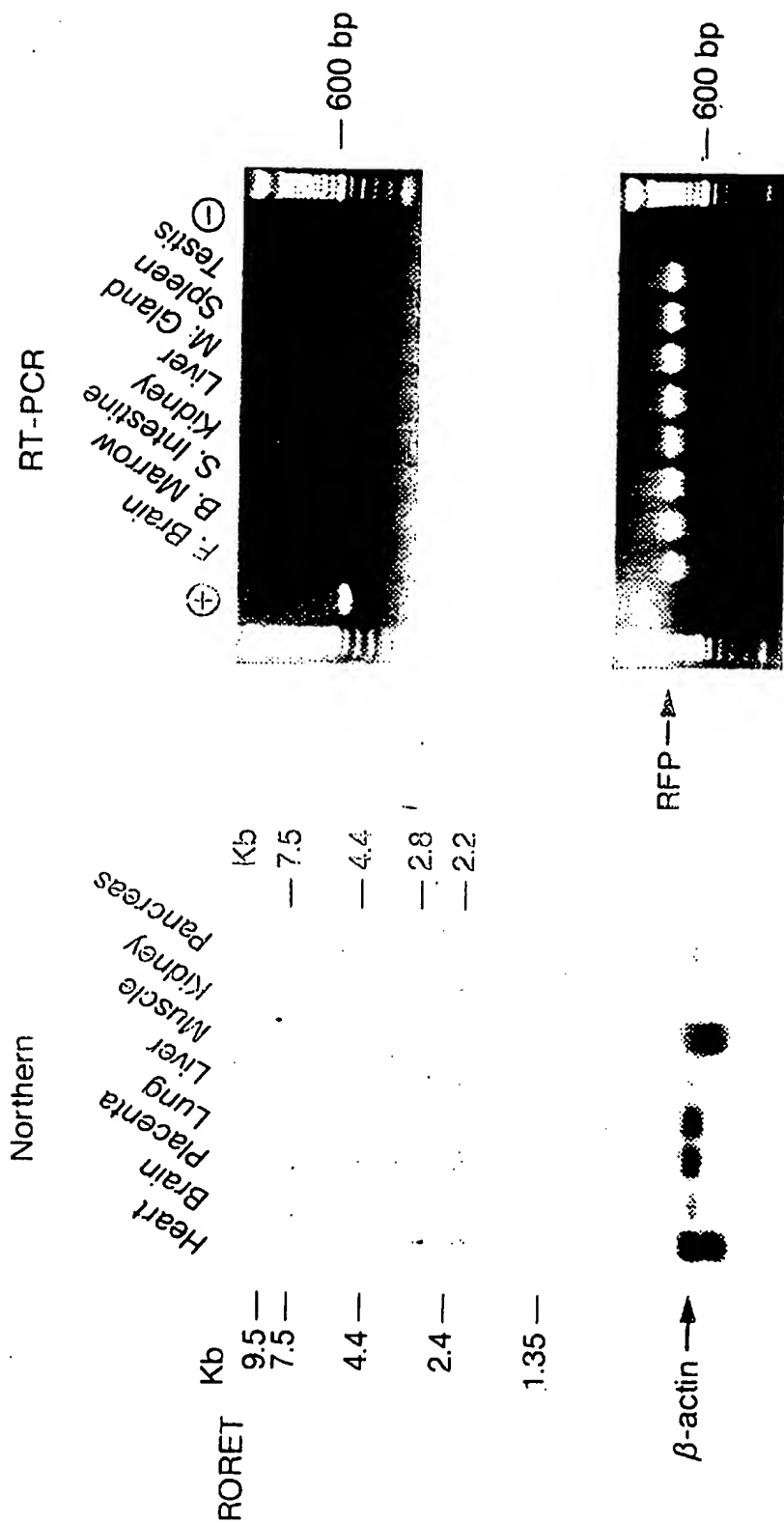
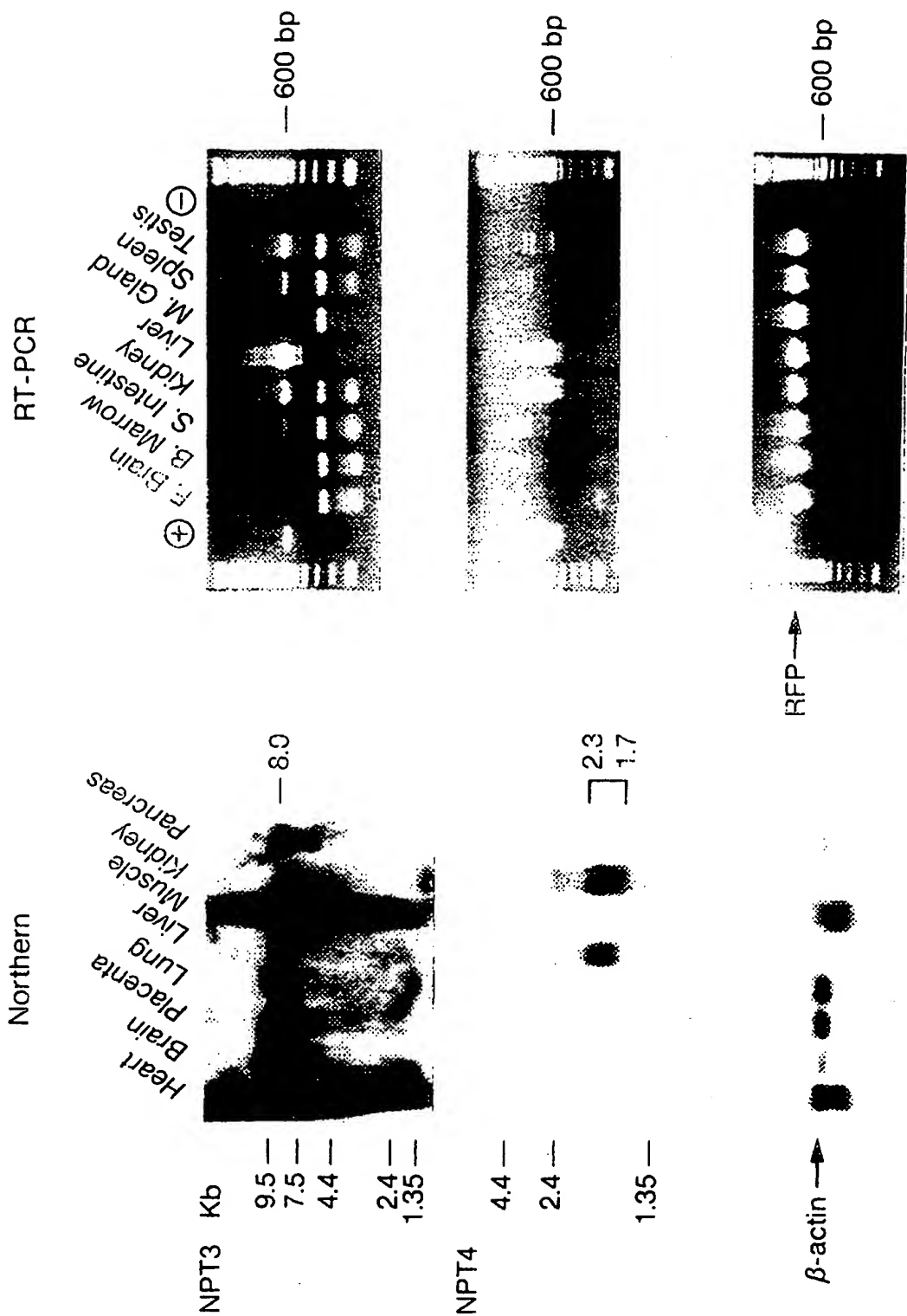


FIG. 6B.

FIG. 6A.

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Figure 7 (5 of 6)

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SUBSTITUTE SHEET (RULE 26)

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3541 TGGGATGGAA TAATTTTTTT TTTTTTTTGG AGACGGAGTC TAGCTCTGTC GCCCAGGCTG  
3601 GAGTGCAGTG GCACCATCTT GGCTCACTGC AAGCTCTGCC TCCCGGGTTT ATGCCATTCT  
3661 CATGTCTCAG CCTCCAGAGT AGCTGGGACT ACAGGCGCCC GCCACCACGC CTGGCTAATT  
3721 TTTTTTTTAT TTTAGTAGAG ATGGGGTTTC ACCGTGTTAG CCAGAATGGT CTCGATCTCT  
3781 TGACCTTCTG ATCCGCCTGC CTGGCTTCC CAAAGTGCTG GGATTACACG TGTGAGCCAC  
3841 CATGCCCCGC TGGGATGGAA TAAATTTATC TTGTATGGGA GAAGGACATA CATTTTGGCA  
3901 GGTCAAGGAC AGAATGTTAT GGACTAAACT GTGTCCCCCA AAATTCATTT ATTAAACCC  
3961 TAAACCCAG TGTGACTGCA TTTGGACATA GAGCCTTTAG GGGGTACATA AACTTAAAGA  
4021 TCACAGGATA GGGCCCTAAT CCCATTGGGG CTGGTGTCTT TACAGAAGAT GAGACACTTA  
4081 GAGCTCTCTC TCCACGCAGG CACCAAGGAA ACACCATAA AACACACAGT GAGATGGCAG  
4141 CCATCTGTTA GCCAGGAACA GATTCTCACC ATAAACTATG TTGGCACCTT GATCTTAAAC  
4201 TTCCAGGCTC CAAAAGTGT AGAAAATGAA TTTCTGTTCC AAGCCTCTTA GATATGAAAA  
4261 AAAAGATTCT GTTGTTTAAG CCATCCAGTC TCTGGTATTT TGTTATGGCA GCCTGAGTAG  
4321 GCTAAGACAA TGAAGGATGT GGTAAAACCT TACGTCCCAA CCACATACCA AAGAGGCTGG  
4381 AATTTAGCAT GCTTTCTTCT TTCAACTGTA TACGTCCCAA CCACATACCA AAGAGGCTGG  
4441 CATGTTGGCT CCTTTACTCT GCCCAAACCT CAACTCAAAC AAACAACGT AATATAATAA  
4501 CATCCAATGA AGTTCTGACA TTTCTTCAAC ATGAGTACAG TAATTCAATG CCAGAGAATT  
4561 CATTTTATTT TGAAATCTAC ATGCCATATT CCAATTTCTG TTGAAGATGC AATGGTTATA  
4621 TTTATTCTTT TTAATATAGA TTTATCAGAC TGGGCGCGGT GGCTCATACC TGTAATCCTA  
4681 GCATTGAGAG GGCTGAGGTG GGCATATCAC CTGAGGTCAG GAGTTTGAGA CCAGGCTGGC  
4741 CAACATGGTG AAACCCTGTC TCTACTATAA ATATAAAAAT TAGCTGGGTG TGGTGGTGCA  
4801 TGCCTGTAGT CCCAGTTACT AGGGAGGCTG AGGTAGAATT GCTTGAACCT GGGAGCAGGA  
4861 GGTGCAATG AGTGGAATC GCACCACTAC ACTCCAGCCT GGATGACAGA GCAAAATAAT  
4921 AAATAAATAC ATAAATAGA TTTATCAGTT TATCAATAAT ATAGTTTTCT TTTCTAGGTG  
4981 TAAATATAGG TAATGACTGT CCTTTAGTAC ATTTTCTCAT GATGCTCCTC TTACTTGGTT  
5041 TGGTACAATA TTAAGTATTG AAATAAATA GAGAATCCTG TCGCTACACA TGAGCACTTA  
5101 TTCCATTGTC TCATCTCCAA TATGCACGGG AAATTCTCAA ATTGCTAATA ATCTTGTAAC  
5161 ACACATGCAT TATATTCAAC AGGAATATAT AAATTTATAA TTATAATTTA GGATCAACAG  
5221 ATGACAAACC TTTAGAAGGT TTGTATTTAA CCTTAAATA TAATTTTTTA AAAATTGGTT  
5281 ATAAATTTT TAATACTTTC TTTTTTGGA CCTCAAGGGG AAAATATAAT TCTTATAAAA  
5341 GTTCAAATGA TTTACAGAAT ACAAAGAGTG AATAGAGATG ATGAATGAAT TAAAGGAAAG  
5401 GATATTGCTA CATAGATTG GAAATTTAA AAGGGAAAT ACGATTGTTG ATTTTGTGTT  
5461 AAAGTATCT GCTTTGTTCA AGATACTTA TGTACCAAAA AATGATTTTA TCTCAGCCTC  
5521 ATATCTCAGT AAATTCCTGA GACAACTTT AGTCCCTGGT GCCCAGGTGC CTTTGGTAAT  
5581 TGGGAGACCT CTAGGTTTAG CATCCTCATC CACTCGCCCC AATTTAAATA GTCCTCCCCA  
5641 GGGCCATTCA GGCAAGGGAG ATGAAACTT GCTCAAGAGT TGGAATCCAA CTGAAGCTAC  
5701 CGAAATTCAT TGCTCAATAG ATAATTTTCC CTGGAAGTAA CTAGGGCTTT TGAATATAAT  
5761 AGTGGGCATT TCAAAGTAGA AGGTAAAGTA TTTTGGAGAT GAGGAGACAG GACAGAGCTA  
5821 CGAGGAATGT CCTTGCTTA GGGACTAGGC TCTTAGCAGT ACCTCTTAGG TAAGAAGCTGG  
5881 TTAACCTGGCA CCTTCTGTGT TTCTCTGAAG CTCCCTTTGC TTAGGGACTA GGCTCTTAGC  
5941 AGTACCTCTT AGGTAAAGAC TGGTTAACTG ACACCTTCTA TGTGTCTGAA GCTCCCAGAA  
6001 CAACTGCCA GTGAAATTTG GATTTTGGGA ATATAGTTTC TTTTTTCTTG TTACTTTTTG  
6061 TTTTGTGTT TTTTTTTGAG AGTCTCACTC TCACTGCAAC CTCCCCCTCC TATATTCAAG  
6121 TGATTCTCTT GCCTCAGCCT CCCGAGTAGC TGGGACTACA GGCCTGCACT AGCATGCCCCA  
6181 GCTAATTTTT GTATTTTTTA GTAGAGATGG GGTGTTTGT TTTTGTAGAC GGAGTTTCAC  
6241 TTTGTGCCCC AGGCTGGAGT GCAGTGGCAC GATCTGGCT CACTACAACC TCCACCTCCC  
6301 GGGGTTCAAG TGATCTTCT GCCTCAGTCT CCTGAGTAGC TGGGACTACA GGCCTTACA  
6361 GGTGAACACC GCCACACCTG ACTAATTTGT GTAGTTTTAT TAGAGATGGG GTTTCGCCAT  
6421 GTTGGCCAGG CTGGTCTCAA ACTCTGACC TCAGGTGATC TACCCACCTC AGCCTCCCCA

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6481 AGTGCTGGGA TTACAGATGT GAGACACCAG ATCAGCCTCA GAAGACATTT TCTATTGGAA  
6541 AGAGAAAACA CTATTAGCAA CCTATTAGTC TAATATTTAA TACTTAATGT CTTCCTTAGT  
6601 AATAAACCAA CTCTCTACAA CAAAGTGCTT CCTGGCTGCC TAAGTCATTG ATTCATTGAG  
6661 TTCAACATTT TCTCAATGCC CAACAGCCAA GTGTCTCTTG TATGCCAAGT TCTATGCTGA  
6721 TTATCAGTAT TTGAATAAGA GGGGGTCTAC ATCTTAAGTA CTGCTTAAGA TGAAAGCCTC  
6781 TAGGTTAACA AACTTAACAC AATGTATCAT TCACTACTAA ATAGACCGAA TACAAAATCT  
6841 TGTTATTGGA GCCCAGAGAG AAGAATTGAA ATTCAAGTTT TCTCTCTCTC CTTTTCTCAC  
6901 TCACCACAAT AAGTCAGTTG CACCAAGTCT TGTAGCTCTT TACTGAGCCA TGTTTTCACG  
6961 TGTCCCTTTG TTTTATTTGC CACACCCTAA ATAAAAATTG TACTGGCTTT TTTTCCCTGG  
7021 GTTTACAGTA TTAATACATT GTCAAGATTT ACCTCTTCGT GTAGATTCCC TGGGGAAAAT  
7081 TACCTTTCCT CCTTCCCTTA AATTCTTCAG AGGTTAGAAA GCCATTAGTA ACATTCTGGT  
7141 ATGTGGACAA AGTTTACCCA TTATGTATGG ATGTTTTACT CTTTCTATTT TTCTGACAAT  
7201 AATCTCTTAA GGAGGTGTGG TTATAGAATA GTCAGCTGTT ATAAGTACTG TTTTCTGGC  
7261 CTTACAACCT AAGTCTTTTA AGCTGTTTCT TAGTTTGCTC ATCTCAAAAT TCGGAATAAG  
7321 GATAAACCT ATCTCTTAGA TTGTTGGATT AAATGAATTA ACATACTGGA AGCTCATGAA  
7381 ATGTGCTTGG CACACAGTAG TGCCTAATAA ACCATCTCTC TTATTCAGCC TGTTTTCTGA  
7441 TTTCAGAATC TACACTTGCT GAGCCAGGTT CTTTTCATTT CAAGGTGAGC AAAAGCATAC  
7501 AAGGAAGAGA TGGAGGTAGG AAGAGATTAA GCCCTAGGCC AAGGTCACAC ACCGATGGG  
7561 AGCTGGAATC AAAGGCAATT TGGTCAGTGA ATAAAAAGGA TTCCAAGGCC CATAAGGCAA  
7621 TTCTAACCTT AGGATCGAAA TTCTCGGACA TACAGGAAAT GCTGGGGGGG GAAAATCCGG  
7681 TCTTCTCAGC CCAAGAGCCA TGTGAAACCA GACCTTCAA TCTGATGATT CTCAGCCCAG  
7741 CTGCCCATTA GAATCGTTGT AATTTAAAAA TACCCTCGGA AAATTCTAAT ATGTGGCTAT  
7801 CAAAGGTGAT CATTTGCTTT TATGCCACTT TGTTTTCCACC CAAATGGGAC ATCCAACCCT  
7861 TTTCTTTGA GAGTAGTTGT AGGGAAGGA GGGGGTGGAG GGAGGGAAGA GCGGAAAAGG  
7921 CTGGATCCGC CCTGAGCCGG TGTCAATATC TGGGAAGTGG GAGGCGCGTC AGCAGTAAAC  
7981 AGCTTCTGCT AGGATTATTA TCTCCTGCGA CACACTCGGA TTTGAAGGCT CCAAACGAAA  
8041 CAATGCAAAA CGCTTCAGTG GAGTTCAGAG AGCGTTAGAC TAAACGACTG GGTCTGTTTG  
8101 GCCAGTCTGA GCAGCTGGGC GCAGATGCAT AGGCAAGACT TAGCCCGCCT AGACTTTTCT  
8161 GCCCACTTAA TTCCGATCAA AGCAGAAACC GGCCGGGCGC GGTGGCTCAC GCCTGTAATC  
8221 CCAGCACTTT GGTAGGCAGA GGCTGGCGGA TCACCTGAGG TCAGGAGTTC GAGACCAGCC  
8281 CGGCTAACCT GGTGAAACTC CGTTTCTACT GGTGGCGGGC GCTTGTATAT CCATCTACTA  
8341 GGGAGGCTGA GGCCGGAGAG TCGTCTGAAC CCGGGAGGCG GAGTTTGTAT GCAGTGAGCC  
8401 GAGATCGCGC CACTGCATT CAGCTTGGGC AACAGGAGCA AAACCTCCGT TCAAAAAAGC  
8461 AAGCAACAA ACAAAAAAAT GCAGAAACCG AGATCCGGA GAAACCTCG GCGAGATTCA  
8521 CAGAATCCAG GAAATAGGT CTCTAGAAAT TTGTCCATGG TCCAGATCT CCATTCTTG  
8581 TGGGTGGGGC AGCTGTTACC AGATCCCTAG AAGCAAAGGT TTTTTGGGG GACCGTGTCT  
8641 CACTGTTGCC CAGGCTGGAG GGCAGTGGCA CGATCTCGGC TTACTACAAC CTCGCCCTCC  
8701 CAGGCTCAAG CGACTCTCCT GCGTCAGCTT CAAGAGTAGC TGGGATTACA AGGTATGTGC  
8761 CACCACGCCC AACTTATTTT TTTATTTATT ATTTTATTT AGTAGAGAGG TGTTCACCA  
8821 GTTGGCCAG GTTAGTGTG AAGTCGTGAC CTCAGGTGAT CAGCCCCCTC GGCCTCCCAA  
8881 AGTGGTAGGA TTAGAGGGGT GAGCAGAAAG CAAAGGTTTT TGAGTGGCCA CAGCCCCAC  
8941 TCTATTTCTT TTTCTGCCTG TAATGGCAAC CTAGACGCTT GAGCTTCTTA AAATACAAGA  
9001 GTAAGTTGCA TGTGAGGCAC CGTCTACAT TAGGGACATT AGTCTGTTTT ACAGACACCT  
9061 TTCAACTCCC TGGTTAACTT TTAGGTAATA TACTCTGCAC TTTAGCAGGA ATGGGACCTA  
9121 TAACTCTCAC AGAATTAGGA AAGTGAGGCT GCCTACAGCC TAAATTGAGA AAAAAATAGA  
9181 CGGGGGACTA GTCGGAGGAC CAAACAAGGT TACCAACAGC TTAGAGTTTT GCCTTCAATT  
9241 TACATTTTTA AAGTAATCAC AACGAAGTGT TTAGATCACG AGGCATCCCT GCATGTAAAC  
9301 TGTTAGGCAC TAACTATGGT CGATCTTACA AAGCATTAA TAGAATATTT CTTTAGAGTA  
9361 TGATAGTACG TAACTGACCT ACTATTACAT ACAAACAGAC CAACCTTTAG TAACAGCGCT  
9421 CCCCCAAAAC CGAAAAGCAG TAATACGCTT TGCTCAAGGT TGGCATAAAA TTAACCTACC  
9481 TTAGTGCCTT TTTTCTTCT ACCTACAAGC AGTGAGGTTA GCTCTTCTT TGAAACGGTA  
9541 GGGGGGCTCT GAAAAGAGCC TTGGGTTTTG ATAGCGTTTC CGGGAGCTCA GATACCTGTC  
9601 AAATCACTTG CCCTTGGCCT TGTGGTGAAT CTCGGTCTTC TTAGGCAGAA GCACGGCCTG  
9661 GATGTTAGGA AGGACGCCGC CCTGAGCAAT GGTCACCCGG CCTAGCAGTT TGTGAGCTC

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9721 CTCGTCGTTG CGGATGGCCA GCTGCAAGTG GCGCGGGATG ATGCGAGTCT TCTTGTGTGTC  
9781 GCGAGCCGCG TTGCCGGCCA GCTCCAGGAT CTCGGCGGTC AGGTACTCTA ACACCGCCGC  
9841 CAGGTACACC GCGCGCCTG CCCCACCCG CTCTGCGTAG TTGCCTTTAC GGAGCAGGCG  
9901 GTGCACTCGG CCCACCGGGA ACTGGAGACC AGCGCGAGAA GAGCGGGATT TCGCTTTGGC  
9961 GCGAGCTTTG CCTCCTTGCT TACCACGTCC AGACATTGCA ATCAGACAAA AATCACCAAA  
10021 ACCAGCGGCC TAAGCTCACG AGAAAACAAA CAAAATCAAG AAATATGTAA AACATGGCCG  
10081 CTTTATAGG TAGTTCCTGG GGAGTAAATC CGACTTTTGG ATTGGTCGGT AGCAAATGCT  
10141 AGTCAGATAG CCAATAGAAA AGCTGTACTT TCATACCTCA TTTGCATAGC TCTGCCACG  
10201 GATGACAACT GTGCAGTTTG TCTTCCAATT AACTAAGAGG TACTCTCCAT CCCTCATTAG  
10261 CATAAAAGCC CTATAAGTAG CAGAAATCCG CTCTTTACTT TCGACACATT TCTGGTGTTT  
10321 TAAGATGCCT GAGCCAGCCA AGTCTGCTCC CGCCCCGAAG AAGGGCTCCA AGAAGGCAGT  
10381 GACCAAAGCG CAGAAGAAAG ATGGCAAGAA GCGCAAGCGC AGCCGCAAGG AGAGTTACTC  
10441 TGTGTACGTG TACAAGGTGC TGAACAGGT CCATCCCGAC ACTGGCATCT CTTCCAAGGC  
10501 CATGGGCATC ATGAATTCTT TCGTTAACGA CATATTTGAG CGCATCGCGG GCGAGGCTTC  
10561 CCGCCTGGCG CATTACAACA AGCGCTCGAC CATCACCTCC AGGGAGATCC AGACGGCCGT  
10621 GCGCCTGCTG CTTCCCGGAG AGCTGGCCAA GCACGCCGTG TCGGAGGGCA CCAAGGCCGT  
10681 CACCAAGTAC ACCAGCTCCA AGTAAACATT CCAAGTAAGC GTCTTAACAC CTAACCCCAA  
10741 AGGCTCTTTT AAGAGCCACC CAGATACCCA CTAAAAGAGC TGTGGCCAGA CGCCAAATTT  
10801 TATTTGGCGG CGGAGGGGTA TTAGAATATA GGAAGTGGAG AGGGGTGGGG ACAAGTGTG  
10861 CAGCTTAGAG AGGGACAAAG GGTCTGAAC CCGAAAGAAG CCAGCCATTA AAAATGGCTT  
10921 TGGGGTCAAT TCGTTGTGCT TAAATTTAAA ATGGAGACAA GCGGCCATTT TGCTAACTCG  
10981 GCGTTCCCGG AAGAAACCGC AGGCTCGCTT AGGTTTCAGA CCCAGCTGTC TGTCCCTGTC  
11041 TACGTCGCCA GGATCAACGG TTGCCGTAAT GTCATAATTT CGCCACCAGC TTCTAGCCAA  
11101 TAGGCTGTCC TGTCATTTTA AATATTAACC AATCGAGGGA AAGCTGTTTT GAGACTCTGA  
11161 TTTACATAGC GGACCGGAGT GGAACCTGG SCAGTAACTG CCTAAGGAAG GACTCCCCCT  
11221 CTGTTTTTCG GCGCACACC TTCGTAGTAT ACTGAAGGGT GTGTCTCCTG GGTTTCCAAAC  
11281 TGCCCCGGTA ATAGTCTTTT AACCTAATAT GCGTCAGTTT TGATAACAAC ACTAAGGCAG  
11341 TACAGAACTA AAGATGTAAG CACTGCGCCA GATGTTGCTT CATACATCTT ATTCTATTCA  
11401 ACTGGTTTAT TCAAGATTCA AATCAAATCA AATTTTGCTT GAATCCAGT GCTCAGTCAG  
11461 CCATAAATGG TGTGTTGCCT GATTGAACT TAAAATCTCC GTAGGGGGCT TGTAACATGC  
11521 AGACAAGTTT GAAAGTTGCT TTAGGAGAAG CCAACTCTTA ACTGCTGGGT AAATGACAA  
11581 GCCTTCGAAC ACTGAACTGA AGGCCAGTAA GGACTAGGCG CTGGGTGGGG GAGAATGAAG  
11641 AGGAGACGTC ATTAACCTTA GCACATACAC TGTATCTCCT AGAGGACTCT CCCTTCCTAG  
11701 ACAACTGCAG GCCGCTTGT GGCCTGGGAA ATTCCACATT CCCTTAAGTA TTTTACTCAT  
11761 GGTCTTTTCC AGGTAAAGAT TTAAAGATGA AGGGTTAGAC GTAGTCTACC TATCTTTTAA  
11821 TTCAAGTCTA GAACACGTTT TTAGCACCTA GAAGTTTGCT TTCTCCATTA AAAACCGGGA  
11881 ATATACAATA AATAAAATTA GTGTTAAAGC AGATTTTAC AAACCTAAAT ACCATGTAAT  
11941 TTAGGTTACA GTTATTTAAC ATAAGGACTG TGTGATCTTA AATCTGCAAT TTCTTTTACA  
12001 CCTGGGAAAT AACTAAGGC CTGTCTTTGG TGCCAGACAA GGCCTTATAC TTGAACACTG  
12061 CTGTGCAATC ACAGGCTGCC TTGCCTAGAT AACTTATCTG AGAAATTCTG ATGAGAAATG  
12121 AAATTTCCAG AGTCCCTCAC AAGTAAATTT TTTTTCTTT TTTTTTTTTT TTTTGGAGAC  
12181 GAAGTTTCTC TCTTGTTCCT CAGGCTGGAG TGCAATGGCG CGATCTTGGC TCACAGCAAC  
12241 CTCCGCCTCC CGGGTTCAAG CCATTCTCCT GCCTCAGCCT CCGGAGTAGC TGGGATTACA  
12301 GGCATGCGCC ACGACACCCT GGCTAATTTT GTATTTTATG TAGAGACGAG GTTCTCTCAT  
12361 GTCGGTCAGG CTGGTCTCGA ACTCCGGACA TCAGGTGATC TGCCCGCCTT GGCTCCCAA  
12421 AGTCCTGGAT TACAGGCTTG AGCCACCGCG CCGGGCCTAA ATGGTTTTTT TTTTTCTAT  
12481 GCCTCTAATG GACCTGGTCA CTTATTTCCA TTCAGACTGA CCGCTCTCCT ACCTGCCAAC  
12541 TAACTAATCA GTGTAACCAA AATCTGCAAA CAAAATTCAG TATTCTTTCC CCGCCTTTTC  
12601 CCCTTTCTCT TACATAGATT ATGTTTTTGC CTGTGTTAGA TGAAATAATT CTATTGCTTG  
12661 TTCTCTCTTC TGTACAAGTA CCCAGTAAGC AAATTATTAA CTTCTTGGTC ATTTATTTCT  
12721 GAATTTTCCA CCAAGACAGT GTTTATGTGA GTCATACAAAT AAGAACCAAC AGAAATGTGT  
12781 GTCTTGGAAG CAGGTTGTCT ATCCCTGGAC CCTTTGAGTT TTCTGTTTAC TTTCTTTGG  
12841 CTTTTGCATG CTAAAAGTTT ATCGTCCGCG TTTGTTTGT TTTGTTTATC TAATTGGACT  
12901 TGGCTGATTG GTTGCATATT GGTGGCAGTA GTAGAATTTG AATTCTGGTT TTCTGGTCAC

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12961 ATCATTAAAGT GATTAGTCAG TGGAGAGGAC AGGAAATCTG GTTTATTTAT TAACCTTTTT
13021 TTGGGGTGTT TTTGTTTGAA GATGTTGATA TTCTCTGTGA GGACACAGGG TTAGAGTTGG
13081 TGTTTTCTTT TCTGACTTTA CATGGGATTT GATGTTTTGT GCTTGTATGC CTCTTTCCAC
13141 CTTCCAAAC TTGCTTTTTT TGAGTCCAAA TAGTTGTCGA TATCTGCAA ACCAGTATTC
13201 CTGTGTTAAG ATGATATGAA TATAAATGG CTGCCCTGTT ATAACCTTTG ACTTTAAGAA
13261 AGTGTTAGGA CTAACAGGAG ACAAAGGAA AATCAAGGAA ACCGAATGTC TGGTCTCAAT
13321 AACTGCTATG GCAGAGGCTC TACAGCTTAT TATTAATTTT AGTAATTTCA CATTATTGCC
13381 CCTTCACGTT CTTTAAGTAA GGTTAGAGGA CAGAAGAAAC ATAATGTTGT TACAAATTGG
13441 ACTATTGAGT CAGGGAAAAA AAAGAGTGCT TTCAATATCT GAATAAAACA AAGATTTAAT
13501 ATTTTCTAAA CCTAACGAG TTTATTGTAA GGGATGTGAT GCTGGAAACT AGGAAACTAG
13561 AATTTTCTTC TAAACTGAGA ATCAGAATTA TTCATATTCT CAGCAGTGGT GCCACCTGAG
13621 GGACTTCTGA TCTTAATTAC ATACTTTTAT TTCTTTAACT GATCAACATG CTAAATAGAT
13681 AACCTATGGC TCTGTTTTTA CCCACTTTAA ATTCTGTTCT ATTAGCACGG TTAGCTTTCC
13741 TAATTGGCAA TAAGATTGAG ACTATCTTTT TTTTTTTTTT GAGACAGAAT TTTGCTCTGT
13801 GGCCCAAGCT GGGGTGCAGT GGCACAATCT CGGCTCACTG CAACCTCTGC CTCCAGGGTT
13861 CTAGCAATTT TCCTGCCTCA GCCTCCCGAG TAGCTGGGAT TACAGGTGCA CCACCACGCC
13921 TGGCTAATTT GTGCATTTTT AGTAGAGATG GGGTTTCGCC ATGTTGGCCA AACTGGTCTC
13981 GAACTCAGGT GATCCACCTC GGCCTCCCAA AGTGATGAGA TTACAGGCGT GAGCCACCGT
14041 GCCCAGAAAA GACTATCTTA TTTTATGAAT TTAAATAATT GTGAAATTAT CCACCTAAGG
14101 GAATTAATAA ATTATAATGT AATCTTAAAT TTAGTTGGC TTACATAAAG ACTTAAAATA
14161 CATCAATTTA AATAAAAACT CATTTGTCTA AAAAAAATC AAAAATTTTC CTTGTGCTTT
14221 AAATGTGCTA CCTCTTTAAG TTCTAATTAA GAGAAAAAAA GTTTAACTGT GAGTTTCATT
14281 AGTGGTCTTA GTTAACAGCT TAAAGTATTT TGTAACAAAA ATACTTCACA ATTTTAAAT
14341 AACTTAAAAA TATTAATACC TCTTTTATTA GGTTTTTTTA ATAAGGAAAA TATATAATAC
14401 ATCTAATCAA GATTTTTTTT GGACAAATTT GCTTAATAAT TTCATTTTAA AAATGGCTTC
14461 TTTATTCTTA TACTGTAAAA ATAATATTAG CAGAATATTA TAGTATACAC AAGTTTAGGG
14521 TTCATATTCT AAAAAACAAA AACAAAAGCT AATTTAACTT GCATTTACTA AATTTCTTCC
14581 ACTAGTTGTA CTGGTTACAT GAGTTAACAT CACTTTATTT ATTATTCTAA AATTGTAAAT
14641 TATTCATTGA ACCAAATTAA ATGATAATAG ATAATGTCAT TTTTAAAAAT GGAATTAAAT
14701 TTTATGTTAC TAATTATAAG GATTCAATGT GTGAGCTTAA GTACTGAGTT CACAGTGTAT
14761 GATAACTTTA AGAATTTAGG TGAATATTAT TAAATTGAGT AAATTAATTC TCAATCTTTG
14821 GATACCTGGA CAATTTCTAA ATTGGAGGGT ACAAATACA AATCACAAGA AACAGTGTAG
14881 TTTTATGCAA ATAACATTTT TACACAGTTT AGAATAACCA TTGATAAACA GATAAGAGAA
14941 CATATGATTG CCTTAGAATA GATACTGTTG CTTTCGCCAC TTTAGATTGT TAAATCACGT
15001 ACTGTATACG TGTGGGCGTA GAGGACCATG CAGGTTTTGG ATGACTGCCT CTGTTTTCGT
15061 CATGCCTATG CGGGAACACA ATTGCCTGCT TTGTTTAAAG GCTATGGTTA ATCCAAACAG
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15301 ATGATTTATA TTCATATCTT AATGTAATAA CCAATCTTCT CTGACAACAT TATAACAATG
15361 CTGGAACCTC CATTTTCAGT ACTTCAAACA ACAAATACTG CTTTTTACTT TCAGAGCAGA
15421 TGGATATGTG CTTCCCAGTG TAAACACATT TGGAACTCTA CTGAGAAATA CACTATCACT
15481 AAAAATACAG TTCTGAGATT CATTAAAAGA CCTCCAGAA TCTGGAAGTA GGAAGTTTCC
15541 TCTTCAAAGT CTACAGAGGA AGATGAGGTC TGAAATAGAC AGCTTCTTCC TTCTTTTACC
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15661 GATCTGGCCC TCCCAAGTAT TAAAAAACAA GCAAATAAAC AAATCTCAGT TATATTTTAC
15721 TAAGATATTG GCATGCTAAC TTTTTCAGG TTTGTAACAA GGACCTTTAT AACTTGACTA
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15901 TGACCAAACT GATCTTTGAG ACCTATTTCAT CTAAGACAAG CCAATTAAT TCTTGGAGAC
15961 AATTTGTACT TTAAGGAATT CTTATAATAT TTGTAATTAC CCTCATAACT TTTTTTTTTG
16021 CCCTACTTCT GTGCTTCTCT AATATGCAGA TTATTAATG TTGTTACAAA GCCATTGTCA
16081 AAAAAACAAA AAACAAAAAA CTAAACAAAC TCACATGGTT AGACTTGCTC CTTTATGAGA
16141 TATTTTACC AAAAATGGAG GAGTTGAAAA ACTCTGGTGC CAGAAATCGT GAAGACATGG

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16201 CCTACCTAAC ATGGAATGT TGGTTGTCAG TGGAAAATAC TACACAGAGA TAGCCATAGT
16261 GCTGCACAGC CAATCTTAAG TGTTTCTAGA GAATCACTAA TTGTTTCTAG AGAATCACTA
16321 ATTGTTTTCT TTTAACATTC TTGGTTTATA CAAGAAGAGA GTATCCATAC TAAACTCTTT
16381 TCTACTGAAA ATAATGTGCA AACATAACAT CCTATTCCTA GACAGTTTGT AGTTTTTTTC
16441 TCCCATTCTT ATTTTATAAA TCATCTTTTT AAAATACTTT GTTGAGTGAA ATCAGTCCAT
16501 TGCTTGATAT ACCTTGAGCA CAAGTAAATA GTATGCCAAA AATTAAATGT CTTTCAGTCA
16561 CAGTTTGACA AACTCAACTA CCTGAGCCT ATAGAGTGGT AATAATTGCC CTAATCATAA
16621 AGATGGGGTG AAGATTAAAT GAAATAGCAC CTATAGAACA CTAGTTCAG ACGTGGTATC
16681 ATGCTAGTAA AATGGCTGCA CAGCACTGCT CAATGATGAC AAAAAAGTAA GCTTCTGGAG
16741 ACAGACTCCA AGTTTGACTC CCAGATCACC ACATATAAGA TGTGGGACTC TGAGGCAGGT
16801 CATTTAATCT CTCTGTGCAT TAGTATCCTT CTCTATACCT TTACAGTGAT GGTAATAGCA
16861 CCTACCTTCT AGAAGTATGT GAAGATTAAA GATCCTTAAT GCATATAAAC CACTGTGTTT
16921 ACTGCTGTTT GACAAATTTT ATTTATAACC ATCTTTACGC TCCTAAAAGG ACTTGAAGCA
16981 GCTTATGACT GAAGACTTTG GTAGGAGTTG GCCTTCTATA AATTATAAGA ATTTCATAAA
17041 TTATTTGATA TGAAAATGCC AGTTGATCAT AGTATGTTTA CCGGGGTCCA ACAGGTTGAG
17101 AAAAAATACA CTTTTTTTCC CTGAACATAT GAAATTAGCT CTCTAGGCAT ATTCCTAAGG
17161 ACTTAAAGAA TGATAACTAT CATTTCTCTT AAATCTTCCA GATTTGGAAG GATATATATA
17221 TTCAGCACAT TGACAGACAA TCCCAGTAGT CCTAAATTAA AAGACATTAA AAATTAGTGA
17281 AACTTTTCCT ACCTTTAGCC TGTGTAATCC TGGATGACCA AGCATAAAAT TAAATTGAGT
17341 AGAGTATACC ACTGTAACAT TTCCTGAAAG GTATTCTAGG CTCTGAGTAA TTTCTTTGGG
17401 GTCTGAAGAT CAGTTTGACA TATCCTCAAG TATCATGAGT TCATTATAAT TAAGAAAAAG
17461 AGAGTAAATC TGGAGAATGA GCCACTTTCT TACTACTCCT TGACCTCAGT TCTTTTTTTC
17521 AGAGACAGGG TCTCACTTTG TTGCCCAGGC TGCCAGGCTG GAGTGTAGTG GCGCAATCGC
17581 ATCTCATGT AACCCTCACC TTCTGGGCTG AAGCCATCCT CCTGCCTCAG CATCCTGAGT
17641 ATCTGGAACC ACAGCAGGTG CACACCACCA TGCCAAGCTA ATTTTTTAAA AAGTTTTTTG
17701 TAGAGATGGG GTCTTACTAT GTTGCCCAGG CTGGTCTCAA ACTCCTGGGC TTAAGTGATC
17761 CTCCTGCCTC AGCCTCCCAA ATTGTTGGGA TTACTAGTGT GAGTCACTGT ACCCCGCCCC
17821 ACTTCAGTTC TGAGGAGGAA AAAATATGTA ATAATAATGG GACTTTGGTT TGCTGATTTA
17881 AAGATTCATG TAACCTTATC ATCCAATGCG CAATTTGTAG AATAATTAAT AGAGACATCT
17941 GGTCTCATGT TTCTACAGTT GCTCATGCCT TGATAGTAGA TCTCCTTGCT GCTGGCTCAG
18001 AAGGGTAAAA GAGCAGAAAT GATGGGGCTT CTCTCATCTT ATGAGGAAAT AGACCTATGT
18061 AGAGGAGGCT ACCTGTGGTA AAACCTTATC CTCATCACTT AAAATCTAG GCTTATTCTC
18121 TGACCATATC AAGTTTCAA ATGGTAAAAG AATTGGATTC AAGAGAAATA TGAATAAACT
18181 TTTGTTTCA CTTTTCTCCC TCCTCTCCCC CCATTCTCCC TTCCTTATT TTCTTGCTCT
18241 TAGTTTTCTT TTCACTTTTT TGTCTACTAT TATTTGCCCA AACTCAACTG TAGGCTAGAA
18301 CAAAAAATAA TTGAAAATTA AAATGTGCCC CTTTTGTTGT TAGACTTGCT TAAACAATTG
18361 GGGTAATGAA CCTTGGACAC TAGATTTTAA AACACACACA TTTGAGCTTC AGTGCAGTGA
18421 AATAAATATA TTTTAAACAA TTAATAAATA AAATTGCATG TTTAAAAAAT CTGCAGAGAA
18481 CAATACACGT TGTGAGATCT TGAATGGAAG GAAAACCTGCT AGCCTCAAGA GTGGATCAAA
18541 GATGCTCAGC AGGCAACAGA GTAAGAGCAT GTTGAGGGGT TTAGAGAGTG TGCTCAGGGT
18601 TCTAGGCTCT AAAAAACAG CAGTCCCCAC GGCCTGGCCT TCGTCGCTGT ATCTTCTTTA
18661 TGAAAAACAC TAAGTCTTTT TCCTCACTGG ATAAATTTTT ATCCTTCAAG TTTAGATCAA
18721 ATGGAACCTT AGGACACTGA CTAGGTTACA TTCATCTTTT AAGAGCGTAC AGACATTCAA
18781 GGGCTAGAGG ATGTGGGTTT ACTGCACAGG CTCATTATCC AACAGCTGTG CTACCTGGGA
18841 AACTTAACCT CTCTGTGCCT TAATTTCTCT ATCTATAACG CAGGGAGAAT GACAGTAGGT
18901 ATCTCATAAG GTTGTGGGAA CAACTAAATG CATTGGTATC TATTGTGTAA AGTGCTTAAA
18961 ACACTGCCTG GCACAGAGCA AACATCCAGT GAACCTTAGC CATCATCATT ATCATTGTTT
19021 TCAGAGTCAA ATACAATATC TCATATCTGA TAAATTACAG AAGTGAATCA ATCACTCTCT
19081 CTCTTTTCTC CAGGGGGAGA CAACAGCTTT TAGACATATC TTTCCAACA GTCGTCACTG
19141 CTGGACACTG TTTCACTTTG CAAATAAACC AATGAAAATG AGTGATCCTA GAAGAAGATA
19201 AATGGAGGTA TTTTGAACAA TCAAAGAAGG ACAAATGAAC ACCTGGCTGA GAAAAATTAG
19261 CTCTTTTTTTC TATGCATAAA ACTATTAAAA TATTCTTCAT AGAAATTTAT GACACAGGAA
19321 ACATAAAGAC AAAATTAAAA TAACTCCTAG TATCTCCTAT TCTTTTATA TGTATATTAT
19381 ATATACTCAT ATTCATATAT ACATATATCT CACATCATGT ATCATATATA AAATAAATTT

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19441 AGGTGTCATG ATATATATTT AGATAAATAT ACTTAGAAAC TTTTATATGG ATGTATAATT  
19501 TATGGATATA TTGATAATTA TGTATTTGTT ATTGACTACT TCAATTGATT CCCATTTTTTA  
19561 TGCATTATAT TATAGATTAT ATAGCTCACA CATCTTTGTA CATAAATCTT TGTTCAAATA  
19621 TTATTTCTTA AGGATAGACT TCATGAAGTG GAAATACTAA ATCAAAAGTG AAAAACATTT  
19681 TCTAAGGTTC TTAACATATA CATTGCCAAA TTGCTATTCA GGATCATACC AATTTATAAT  
19741 CCCAAAATAA TATGGAAATT CCTGTTTTAT AGCACTCATA TTTACATAAT ATTTTAAAAA  
19801 TCACTGTTAA CCTAATAGTC CTTCAAAAGA AAAAAAATTT GAAATTACAT TATTTTAATG  
19861 ACTCTATTAG TGAGGGTCAT TCTTCCCATG TTTCTTGTTA GCCATGACCC TATAAGAAAT  
19921 AAAGTCACT GCAAAATGAT AAACATGACA TCAATCATT CATGGGAAGG CACTATATAA  
19981 AGAATAATAC CTTAGGTTAA GGCCACATAA ATATTTATCA GGTGCCTTTT CTGCGGAGGA  
20041 CTCTGAAGGG ATACTAACT GCATTTAGCT GCATGCAACT GAAACTACTT TTACCTACAT  
20101 TGTCTCTTAT AAACATTATA ACTACTCTTT GAGAAAGTGT TTACTATGGA CTGAATTGTC  
20161 TCCCCATCCC CCCAAATTCA TATATTGAAG CCATAAACCC CAATATGACT CTATTCCTAG  
20221 ACAGGACTTA TAAGAGGTAA TTAAGGTTAA ATGAGGTCAT TAGGATGGGT TCCTAACTGG  
20281 ATAGGATTGG TGGCCTTATA AGAAGAGGAA GATTCTGCAC TTGGTCTTCC AAATTAATAA  
20341 ATTTATTTAA AAGAAAAAAA AAAAAGAGGA AGAGAGGGAG CTCTGCACAT ATACTGAGGA  
20401 AAGGCTATGT GAGCTCTCAC AGTGAGAAGG TAGCACTCTA CAAGCCAGCA AGAGAGCCCT  
20461 CAACAGAATC CAGCCATGCT ATACCCTGCT CTGAGACTTC CAGCCTCCAG AACTGTGATA  
20521 AAATTTTGTT GTTTAAACCA CACAATCTAT GGTATTTTTT TATGGCAGCC CAAGCCAACA  
20581 AAGACAGCAT CATTGCTGTC ACTTACAGAC AAGAAACTA AGACTAGGAG AGAGAAAAGT  
20641 TAACTTGTC CAAGGTCACA AAAGCCAGAA ACAAGTGAGG TGAGAAGTTG ACCTTGTTCT  
20701 CCTCAATCCA AGGCCAGGAC TCCTCCACTC CACATGTAGA TAGCCACCTC ACAGTCAACA  
20761 GCCAAATGTC CACACCCAG AGTCAGCATT AGACCAAGAT GTCTTACCAG GAGACAAATG  
20821 CCTCATCTTG AATAAATATG ATCTAACAACT TTACCCATGT AAAACATGA ATCTCATGAG  
20881 AAACAAAAAT GCAAAGTATG TAGAAAACTA TGTTTACCAC TTAAGTACA GTGATAAAAA  
20941 GCTTAATGAT ATCCTTATAG TCTTGGAGGG GTTTGTATAT GTGGTGAAC AGGTGCTCAC  
21001 GCACTGCTGA TAGACTGTAA ATTGGTCCTA GAGAGAAAAA TAAATAAAT GGAAGGAGAT  
21061 ATGCTGTATG TTTACTTTTT TTATGGAAC ATATGATATA CCTGGAAAT CGATTGACCA  
21121 TGCATCTATT TCTTCAATGG GTATGCACAG TTGAGCTGTT CCCATGCACC AGGCACTGTA  
21181 ATGGGACAAC TGCACATGAC AGTCAAAAT CTCACTCTCA TGAAGTCGAC ATGCTCATGG  
21241 AGAGGTGCTA CCCACTAAAC TAATATTTGT ATATCAATTA TGGATACATT GGGCCACATT  
21301 TACAGAAATT CACTTACAGT GGGTTACCAG AAGGGATTTT TTTTCTTGAT TGGCAAGAAG  
21361 GCTAGGCTGT TTTGTTGGGG GCTGGCAGGA GCTGTCTAGG CTGCCCAGT ATGCAGGTCT  
21421 CTTCTATCAT CCTGTGTTAA CCATCTTCCA TGTATCTTTC AACCTCATGG TCATCTGCAG  
21481 CATGTCTAGG GGTCAATCT ATGTTCCATG CAGGAAAAAA GGGTAAAGGG AAAGGGAAGT  
21541 AGGCATGTAC CATTTTAATG CACACCTTGG TTTTCAGAAA ATTTAAGAAG AAAGACTTTC  
21601 TGCTTTTCTC TGAATATTCT GTATCTGGA TTACAACGCA ACAGAAACGT CACCTTAAAT  
21661 TCTAATGTTT TTCTCTCCTT GCTTTCAAAA ACTGACTCAT TAACCTCCAC GTGGCTTGGA  
21721 AAAATTATTT CAGTCATCCA GTAATGAGCT GTTCATAGAA ATGTTTGGGA CATCAAGTCT  
21781 GTGTTGTTAG CATTATACAT GTTAAGCATT GAATAAAAA CAACATGATG TGGGTAAATT  
21841 TCTTTACTTA CATATAAGTA CTTATATACT TATAGCTGAA AAGAGAGGTT GAAATGTCAG  
21901 GTGGAACAGA AATAAGATTA CCTAGATGTT TCTCCTATGG GTGATTTTCA GCTATGCTGA  
21961 TCTTTCTTCT GGGTCAGGTA CTCCCAGAAC TTCTTAATTA AATGGTGGCC CTGATCTTAG  
22021 TTCTCTCTC CTCTTAGACA TTTTCCAGGA CTACAGAAGA TGTGCAGTTT ATAAATGAGT  
22081 AGCAGAAACC TACTGAACAA ATTATTCAGG CTCATCTGAA CAGAGAGGAC ACCTTCTCTG  
22141 CTATACTCTC TCAGTGATTT CCTGCTTGG GGGTCAATTA TTGTCTTGGA CATTGATTTA  
22201 AGCACATAAT AATTGTTGTC ATTGCTTATG TTGGGATTTT ATCTCCCAA ATAGATGGTA  
22261 AATTCTTTAG TTTAGAGACC AAGTAATACT TAAAAAAA TTTTGTGTGT GTGTGTGTGT  
22321 TTTTCTGTG TCTCTCAGCC CTGTAATAGC ATCGTACTTA CACTTGTTAG ATTTTLAGAG  
22381 ACAACTTTTA CAAAACATGG AATTATCTAC ATACCCTTTC TACAAAACAG ACAAATTAAT  
22441 TACTCAGTAG TTGAACCAA AAAAGCAGTT CAAATAAAAT ACTTGAAAAT GAAGAAATCA  
22501 TTTGAACAGA GTTAAAGTTA ATCGTAAAT AATGTCTGTA AAAATTATTG CCAATCAAAAT  
22561 ATAAAGTTCA AAAATAGTGC TTGAAAAGG AAGAATCATA TGAAAAGGGA CTACTCATT  
22621 TAAAAATGTT AGATATCAGG AAAAGCCAAG AAGTGAGTAT GGTAAGAGTG CTGTCAAGTG

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22681 AAACCCTGCT AATCTCACTG AACATGTAAA AATCTGTAGA TGCCTTTTATT TTATTCACCTC  
22741 ACACACATAT GTAGAAAGAG AAATATATGG TAAACATTAA AAAAACCCAA TTAGAATGTA  
22801 AAATTAATAC TTTAAAAAAT GGGCTGTATA CTTTCTTAT CACCGGAGAT AAGAATTTAT  
22861 TATTTTAAAA ATAAAGTTAT TTTCTCTGTG ACTGTTTCCA TGACTTTGCT ACTTAGAAGT  
22921 TAGAGATGCC AAAGTTTATC TAAGAAAATG TTTATGGAAA TATTATTTCA ATAATGAATG  
22981 TTTAGAAGAC TGAATTTCTT GACTGGGCGC AGTGGCTCAT GCCTGTAATC CCAGCACTTT  
23041 GAGAGGCTGA AGAAGGAGGA TCGCTTGAGT CCGGGAGTTC AAGAGCATCC TGGGCAACAC  
23101 AGCGAGACCC TGCAGCAAAG TAAAAAGAAA AAAGAATTGA AAAAGGAAGA CTGAATTTCC  
23161 TTTGGGCAAG TCATGTGACA TTCCTGTGCC TCAGTTTCTT CATCTATAAA GTTAATTCCT  
23221 ACATTTTGGG GGAAGGGAGA GAAAACTTA GGATAGTGAC TGGCACAGAA GAAGCACTAT  
23281 ATACTATATA TATGTGGATA TCATTTGTTT TTATGGTACC ATTTTAGCTA TCTAATGCAA  
23341 AATATGAATC TTTTTTTTCT GGGTCTTAAA TTATGGAATG TAAGAATTTT CTAAATTCTC  
23401 TAATTCTGTG TTAGTTTTAA AGCAATGGAG TAACGTATCT GTCAACTTGT AAATATAAGG  
23461 ATCAACCTGA TCCACAATTT GACCCCTAGC CACTAATATT TAATAGTACA ACACTCAGAA  
23521 ATTATCAAAG GTCAGAGAAG CCAACAAAT GTAAAAACAT ACAGGTGCTC AGAAAGATGC  
23581 ACCTGTAATC TCTCTAAGGA GAAATATTTT CCAAACTGAG TGACACGGTG CTTTAGTGAG  
23641 TTGTGGAATC AATCTCATGA TTTCCAACCT AGTGTCTTTT TAAAAATGAA CTAGTCCACA  
23701 GTAGAATATA CTAAAGTGCT GGTGCTTAAG ATAGTATTGT TTTCTGGAAA AAAAAAATAA  
23761 ATTTTTTTTT TTTGAGACAG GGTCTCGCTC TTGCCCAGGC TGAAGTGCAG TGGCACAATC  
23821 ATGCTCACTG CAGCCTTGAC CTCCTGGGCC CAAGTGATTC TCCCACCTCA GCCTTTTGAG  
23881 TAACTGGGAC CACAGGTACG TGCCACCACA CCCGGGTAAT TTTTAAATTG TAGAGACAGG  
23941 GTCTTGCTAT GTGCTTAGGC TGGCCTTGTG AACTCCTGGG CTCTAGTGAT CCACTAGCCT  
24001 CAGCCTCCCA AATTATGGG ATTATAGGCA TGAGCCACCC TACCTGGCCT GTTCCCTGAA  
24061 TTTTTTTTTT TTTCAGGTGT TTGTGCATAT GTGTGTGTGT ATGGGTATAA CAGAGAGACA  
24121 GAGAGAAAGA AACTTTTCTA TCTCACTTTG CAATCAGAAG TTTGAAGTCT TATCTTTTGG  
24181 CTTTGTGTTT AGAAATATTT CAAATGTAGA CTCTCTCCTT TACCACACTG TCCCCTTAGG  
24241 CAAGGTCTTT GCCATTCTTC TGAGACTATT GCAACAGACT CCCAACTTCT GACTGTGGGC  
24301 CCTTCTCAAA AATGATTGTT TATGCAATAA ATCTAAACCC AAGACAATA CAACAATACA  
24361 ACAAATTTCT TGCTTAAAAA CTTCCAATGT CTGCCGGGCG CGGCGGCTCA CGCATGTATT  
24421 CCCAGCACTT TGGAGGCAGA GCGGGGCAGA TCACTTGAGG TGGGAGTTC GAGACTAGCC  
24481 TGGCCAACAT GATGAAACCC CATCTCTACT AAAAATACAA AAAATTAGCC AGGCATGGTG  
24541 GTGGGCGCCT ATAATCCCAG CTAATTGGGA GGCTGAGGCA GGAGAATTGC CTGAACCTGG  
24601 GAGGTGGAGG TTGCACTGAG CCAAGATCAC ACCATTGCAC TCCAGCCTGG GCAACAAGAG  
24661 CAAAACCTCG TCTCAAACCA AACCAAAACA AAACCTCTAA TATCTACCAA ATGTTTCACA  
24721 CAAGTATTTG GGGATCTTCA CAAATGGCCC TTATGGAGTT TTCTTTGCT GAGACCCTAT  
24781 GCTCTGGCCA CACTAACTC ATTACGATC CCAGAAAGGC CTCAGCCTTT GTGAGCAAGC  
24841 TCTTATCTCC AGGCCTCTCA CAAAGACCTG TTCCAGTAGA AGCTCAGGGG AGCACACTGG  
24901 ACATTATTCC AACAACCCTT TCCCCACAGC TATGCAGCCA AATCTGCCAG CTCAGTTAAT  
24961 TAATTAAGCA ATTACAGAGT GAGGGTCTGC CCAGGCTGGA GTGCAGTAGC TCGACCTCA  
25021 AGCTCCTGGG CTCTAAGTGA TCCTCTTCAG TCTACCCAGA AGCTGGGACT GCAGGCATGT  
25081 GCCACCACAC CCAGCTAATT TTTTTTTTTT TCAGTAGGGA CCAGGCCAAC CTAGTCTTGA  
25141 ACTCCTGGCC TCCAGCCTTC CGAAGTGCTG TAATTACAGG CATGAATCAC TCGCCCCAGC  
25201 CAACCCGCCC AGTCTTGTTA GACATGGGTT CTGTAGTTTC TAGTAGGTTT TTGAGTCTAG  
25261 GGTTCCTACC TCATGTTTTA TAGTTAATTT AGGGGAGGGA CTGTGCTGTG TTATCTGGGG  
25321 ATGTAGGGGT GGGCAGGGGG ATAGAGGGGA CTTCAATTAA TGAAACCAGA AGCAAAACTC  
25381 AGTTGAGGAC ACCGGTCATG AGAGTGGCCT GATTATGGCC AATCTTACAT AATGTGTGAG  
25441 ATCTTGATAT TACCCCATCC TTGAGAGTCC TCTATAAAGC TACAGGGACT TGGGAGCACC  
25501 TTTAATTACA GACAACCCAT GTTCTGTGG ATTATGATT ATTAGATTGC ACATGCCTAA  
25561 ATAAAGACAT CCTCTGCAGT CTTTGTGACAA TTCTATAAGC ATCTTCTGAC TCCGCAATTA  
25621 GACAGCTAAG AGATCTGTGT TACTTCCCTC ACATATATAA ATAATTTTAA ATAAAAATCA  
25681 TGGCGTGAAT AATTTCTTTC CTCTACCGAT TTGAAGCTAT CCATTTGGAA GACCACTCTG  
25741 AAGAGATGAA ATAAGTCTTC TGCCAAAGAT TACTTATTAA TTTACAAGGA AAAGGGGAAG  
25801 TTTTGTTCCT CTCCGTGAAT TTGATTGAAA ATCGAGGGCT TTCTCGAATA GTTTTGGCAT  
25861 CCAGGGTCAT TTTTCATTAA AAAGAGAAAA GTCATGTCAA ATATGAATTT CCGCAGATTA

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25921 TTCAGCACTA GACCCTGGGA GATTCTGTAA AGAGGGGTTT TGTATACTC AACTTTTCCG  
25981 GGTAAAACAA ACACAAATAC TCCTCCTCCA AGGGGCGGGG GCGGTGCCTA GGTGATGCAC  
26041 CAATCACAGC GCGCCCTACC CTATATAAGG CCCCAGGGCC GCGCGGGTGT TTCATGCTTT  
26101 TCGCTGGTTA TTACATCTTG CGTTTCTCTG TTGTTATGTC TGAACCCGTG CCTGCAGCTT  
26161 CTGCCAGTGC TGGTGTAGCC GCTATGGAGA AACTTCCAAC CAAGAAGCGA GGGAGGAAGC  
26221 CGGCTGGCTT GATAAGTGCA AGTCGCAAAG TGCCGAACCT CTCTGTGTCC AAGTTGATCA  
26281 CCGAGGCCCT TTCAGTGTCA CAGGAACGAG TAGGTATGTC TTTGGTTGCG CTCAAGAAGG  
26341 CATTGGCCGC TGCTGGCTAC GACGTAGAGA AGAATAACAG CCGCATCAAA CTGTCCCTCA  
26401 AGAGCTTAGT GAACAAGGGA ATCCTGGTGC AAACCAGGGG TACTGGTGCT TCCGGTTTCT  
26461 TTAAGCTTAG TAAGAAGGTG ATTCCTAAAT CTACCAGAAG CAAGGCTAAA AAGTCAGTTT  
26521 CTGCCAAGAC CAAGAAGCTG GTTTTATCCA GGGACTCCAA GTCACCAAAG ACTGCTAAAA  
26581 CCAATAAGAG AGCCAAGAAG CCGAGAGCGA CAACTCCTAA AACTGTTAGG AGCGGGAGAA  
26641 AGGCTAAAGG AGCCAAGGGT AAGCAACAGC AGAAGAGCCC AGTGAAGGCA AGGGCTTCGA  
26701 AGTCAAAATT GACCCAACAT CATGAAGTTA ATGTTAGAAA GGCCACATCT AAGAAGTAAA  
26761 GAGCTTTCCG GGAGGCCAAT TTGGAAGAA CCAAAGGCT CTTTTAAGAG CCACCCACAT  
26821 TATTTTAAGA TGGCGTAACA CTGGAACAA GTTTCTGTGA CAGTTATCTA TAGGTTTAAG  
26881 TTGTGATGCA GCTGAGTTGA AAAGGCTTGA GATTGGAGAA TTAATTCAGG CCAGGCTTCA  
26941 AGACCATCCT GGGCAACATA GCCAGACTAC CATCTATACC AGGGGTCTCT ATTTCCCCGG  
27001 CCACCGACCG GTAACCGGTC CCTGTCCATG GCACGTTATG AATTGAGCCG CACAGCTGAG  
27061 GGGTGAGCGA ACATTAACCA ACTGAGCTCC ACCGCTCTGTC AGGTTAGCTG CAGCATTAGA  
27121 TAGATTCTCA TAAGCTCAAA CTGTATTGTG AATGGCACAT GCAAGGGATC TAGGTTTCAG  
27181 GCTCCTTGTG ACAATCTAAT GCCTGATGAT CTGAGGTTGG AGCAGTTTTA GTCCGGAAT  
27241 CATTGCTCCC AGCCCTGCA CCCCCTGGTC CGTGGTATAA TTGTCTTACA CAAAACGGTC  
27301 TCTTGCTGCA AAAAGGTTGG AGACTACTGG TTTTACAAAA AAGTAAATTA GTCAAGCATG  
27361 GTTGGCACGC TCCCTTAGTC CCTGCACCCA GGCGTTTAAG GATACAGTGA GCTATGATGG  
27421 TGCTACCTCA CTCCAGCCTG GGTGACAGCG AGTCAGACGT TGTCTCAAAA CTTAAAAAAA  
27481 AAAAAAGTTA AAACAGAAAA AGGGCTTCTT GTCAGAGACT GCCGTATATC TAGAGGTCCA  
27541 GGAATAAAA AGTCTGATGT CCAATCCTGA AAAGCTCGAT GGTGCACTAG AGGAGGCTTT  
27601 TACATGTAAG AGCATCTAAG TTCTGAAAT GCCAGTGTC GGGAGGGGAA GTGGAGAGCA  
27661 ATTTGGCATC CAAACATAAC TTGCTGATAC TTTTTTTTTT TTTAACACAA GTACTACATT  
27721 CTAGTCTTTC TGTGGTGTC TTTGTAACAT TGTTCCTTAA TATGCTATCC ACTGACTTCA  
27781 AGGGATCAAT AAATAGGAAT CAAGGTGTCC CAGAATATGG ATTAGGGGAG TTTTTTTTGT  
27841 GTTGTGTTG TTGTTGTTTT TCATCTATTC ATTATCCTGT AGCTGAAATT TAGAATTTTC  
27901 TTCCATTGTG TGTGACTGAT AGAAATAACA AATTTGTAGG TTATAGTTGT TGCAAGAATC  
27961 TGGAAATCGT GCTTGCTTAT TTCCGAAGTA CTATTAGGTA TATCAACAAA AACACACATA  
28021 TTACGGTCAA GTGGTTTGAT AATTATTTTA ATATTATTGG TCTAATACAA TTGTAACCTT  
28081 ATGAATTACT TTAAGTATCT TATTTATGAA AAGAATCTGT AAGTTTCATC AGACTACCAG  
28141 AGCATACCGA AGACTGAAAA ATTTTAAGAA TCCAAACCTT AATGGAAATG TTGGAGGCTG  
28201 CCCAATTAGG TTCTGAATTC CACCTTCCTG AATCACAAAC TTGTTTAAAC TCTCAGTCTG  
28261 AGGTAAACTA CGTTTCTCTT TAAACAGACA TAGTTTAAAT TTCCTTTGAT TTTTGATTTA  
28321 GTATTCTTAC TGATCATCAT AAATAACCAA TGCTAATGTT AGTCTACTTT GGACCATGGT  
28381 ATTTGAGAA ACTTTGAACA AAGTCCCCTG CAAAACATG CATTGCATTA TTTCACATAC  
28441 ATTTATGTTT TCCAGACGGT TCAATAGTAC CTCACCTTTC TGAACCTATT TGTATAGTTT  
28501 GGCATCTTTT TAAAAATTGT GTCCTATAAT GAAAGGTTGT AAACATTATG TTTTAAATTT  
28561 GTATAGATAA AATCAACCAC AGACCTTTCC TTGCTTGGAT GTAATTGCCA TTGTTTCCCA  
28621 ATGAGTTCGG AATTACTAGG ATTGTGCAAA AATATGCCTC ACTTGCCCTG CATAGCAGAG  
28681 AGCCATTTG CCTAAATGCT GTGCCCAGCA ATGGACTGTC ACCAGATTCT CATCACATAC  
28741 AGTGAGGATG AACAAC TAGC CTCTCCAGC AGCTGGCCCG TCTCTCAATA ATATGGGACT  
28801 CCCTCAAGAT GGCTTCTGTC ACCTTTGCTC CTCTAGCCTT GTATGTATAC AAGGCTAGCA  
28861 TGCCTGGCAT ACATAAGGTT AAAAACAAAA TCAATAAGTT ATGGTTCTTC CTCCAGTCTC  
28921 GGGGATTATT AGACCACTTT TTTGTTTTGT TTTGTTTTGG ATGGAGCCTC GCTCTGTCAC  
28981 CCAGGCTAGA GTGCAGTGGC ACAATCTCGG TTTACTGCAA CCTCTGCCTC CTGGGTTCAA  
29041 GCAGTCTCTT GGCTCAGCCT CCCACGTAGC TGGGATTACA GGTGCCCGCC ACCACGCCCG  
29101 GCTAATTTTT GTATTTTATG TAGACGGGGT TTCACCATCT TGGCCAGGCT GGTCTTGAAC

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29161 GCCAGACCTC GTGATCCACC CACCTTGGCC TACCAAACCTG CTGGGAATAC AGGCGTGAGC  
29221 CACCGCGCCC GGACTTAGAC CACTTTGTTT TGGCCAATAG GACAACAGCC ATAGAACCCT  
29281 CCGCAAATGA GAGCTTGTC CTAAAGATGC TTTATTTACA TAGCTGTGTG CCGCATGAGC  
29341 CAAAAGGTGA TAACCTTGT TCAACACGCG CCTCCAGCCC TTCGGTTAAG TCCAAAGTAC  
29401 CATTCTTAGA ATGCTCTAAA ATACATAATT TTTTTTTTTT TTTTTTTTTT TTTTTTTTGAG  
29461 GAGTCTCTCT CTGTCTCCCA GGCTGGAGGG GAGTGGCGCG ATCTCGGCTC ACTGCAATCT  
29521 CTGCTTCCGG GCTAGCTGGG CCTACAGGTG CAGACCACCA CGCCCGGCTA AGTTTTGTAT  
29581 TTTTTTTGGT AGAGGGGGTT TCACCATTTT GGCCAGGCTG GTCTCGGATT CTGTGATCTCA  
29641 AGTGATACAC TAGCTTTGGC CTCCCAAAGT GCTGGGATTA CAGTCGTGAG CCACTGCGCC  
29701 CAGCAAAATG CTTTTTGTGG AGCCAATCAC TTTATTAGCG CTTACCTCTC TATGCCACT  
29761 TTATGCTTTG AAATTTTGTC ACAGTGTGGC CGGTCATGGC AAACACAATT CATTCTTATG  
29821 CAGGATGTCA CGGTTATTTT TGTCATCCAA ACTCATTCTC GCAACGCATT TCAGTCTTTT  
29881 AAACGACTTT GTGAGCGGCC CTGAAAAGGG CCTTTGGGTT TTTTGTTTT TGTTTTTTGA  
29941 AGTTCTCAGG AGACCGCGTA TTCTTAGATT CAGCCGCCGA AGCCATACAG AGTGCGCCCC  
30001 TGACGTTTTA GGGCATATAC TACATCCATG GCTGTGACAG TTTGCGCTT GGCCTGCTCC  
30061 GTATAGGTGA CGGCGTCTCG AATAACGTTT TCTAAGAAAA CCTTAAGCAC ACCTCGAGTC  
30121 TCCTCATAGA TAAGACCGGA AATGCGCTTG ACGCCACCGC GCCGAGCCAA ACGGCGAATA  
30181 GCCGGTTTTG TAATGCCCTG GATGTTATCC CGGAGCACCT TACGATGGCG CTTAGCACCA  
30241 CCCTTCCCCA AGCCTTTTCC GCCTTTGCGG CGACCAGACA TGATTCCTAT CGCAGTGGAA  
30301 GGTATGAACT GAAACAGTTC CTAAATACA AACTTGGCGG ACCTGATTGA AAACAACATG  
30361 AGTTGGCGCG GTTTTTTTTT TTTTCAAAT TTGGTCACCA AGTGGGTGGA GCAAGAAAAA  
30421 CTGTTTCATT ATGGTTCATT GTTTGTATG GCCAGTGACA GCTTGCTCTT TGTGGGAGTG  
30481 GAAGGGTGTG TGCAAGTTGA ATGCGCTGTA TTCCTGTCAG CTTAATGACG CTAAGCATAG  
30541 CCCCATTCCA CATTTCTTTT TATTTCCACT TGCTAACTAA TAAATTACGG AATAGTTAT  
30601 TGGGGAACAT ACAAATAATG TTTAAAGGAG GTCAGATTTA TAGGTCAAGG GATTTACCCT  
30661 CCAATCATT TTAATATTTT TATTTAAACC AGGCATTTTG ATGGCCTTCT CTGTGCTGGA  
30721 CAAGGTATAA GTTTGGCTAT GAAGTTTCAC TCCTAAAGAC CCTATGTTTT GGAAGGCAA  
30781 AAAGGTAGCC AAATAATTGC AAATTAACAC CTCATAAGTG CAAACTTCTT CCTCGTCACT  
30841 TTCCCTATCT CGATTCAAAT ATTTGTTGAA TGACTCATT TTCTGCAAAA GTCTGAGAGA  
30901 GACAGGGAAT ATAACTTAA GTCTGGATAA TATGTTTTCC CGGGACGCTC TTCCTGGTCT  
30961 GCTGTGCCCTG TTTGCTGTGC CTGAAATTC AAACACTCTT CCCTTCCCTC CGTTTTTAAT  
31021 CCCCTTTCAA CTTGCTACAG CTTTAGGAA AAGAACATTC GTTTGTACA GTTGGGGATT  
31081 AATTGAAGTG TAGGGCTAAT ACTTGATTAA GGTCAATTACA AAATCTACAG GGTCTTCTC  
31141 TGGGAGGTTT TTGTGATAAG ATTATTGGTG TTAATAAAG GCTAATCCCC TTGAAAAATA  
31201 AATAGAATAG CAGAATTGGG TCTGAATGTG GTTTGAAGAA AGGGACTTCT CAATTCAAAA  
31261 TTTTATTCTT AGCTTCCTGC GGGAGCTTTC CAGAATGCCC ATAAGATCCA CTTTTGTTTA  
31321 AAAACAAAA ACAACCCAC CCACCCTCT CTGGTTAATA AATGAATTC TATTGGGAAT  
31381 ATTTAGAATG GGGCTGTGGC CTGTGAGAGA CATTATATAG TAACCTCAGA CTTGCTCACA  
31441 TGAAGAGAAG AAATCCAGGA ATGGAGAAAA AAGACCCAGG AAAGGCCAGA ATGCTCTACA  
31501 TGTCATATTG TTTGTATCAC TTCTGAAATA ATTGATTACA TTCTTCTGCC CCAAATTGAG  
31561 TTCTTAGGTT CTTCCACTCA CTGTCCACAT GCCACAACAC AGACCTTATA ACTAGAGACT  
31621 TAGCTAGGAA GAAATGTCAA ACATTACAGA GAAAAAATGC AGAGTCTGAG ATCATAAGTA  
31681 AAACCTGAA ATCTCAACAT GCCTTTTAAT TCATGAAAAT AAAAAATATA GCAGCATATG  
31741 CAATATGACA ATTCTCTGAA AACATACATC ATGTGAACTA CCCTGGAACA CATCTCGCCA  
31801 AGTGCCATCT TCATTTTAAC CAGAGGTCTA GGATGCCTTT CCTTTATTTT GCCTATTATA  
31861 TCATTTATAA AACCCCATTT TTATTTTGAT ATTTTATTTA CTTTCTATTT CCTGCTCCTA  
31921 ATATCTCCTT TCTAACTTT TCTCAATGAC AGTGACTCAA AAACAATGAA TGTCAGAACA  
31981 AATATTTAAA GGATCTGTAC ATGTAGATAT ATATATTTAA AATGGATTCT TCCACTCTGC  
32041 GAAGAATTCA GGCATACTCA ATCTTATGGT TAGGGAGAGA TTAGGCTCAC TCGCCTAATC  
32101 TGTATGGCTT CTCGTTGCTT TTCCATTCA CCTTCTCTC ACCCATCAGA TCAAACACTC  
32161 TCATTGAACA AGAGACCTAA GCCCTTCAGA TTAACACTCT GCAAACAAGT TGTGGTTGAG  
32221 AGGATACATG AAGCATTCAA ACAAATAAAT CTATGATATT AATCAGAGGT TAATCTATGA  
32281 TATTAATCAG AGGTTAATGC AGTGGCTCAC GGCTGTAATC CCAGCACTTC AGGAGGCTGA  
32341 GTTGGGAGAA TCGCTTGAGC TCAGGAGTTC AAGACCATT TGGGCAACAT AGCAAGTCTT

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32401 CATCTCTACT TAAAAAATAA TAACCAGAGG TGTTATGAAA ATATAAATTG TCCAGAACTA
32461 CCCTCCACAA ACTAACTCTC TCAGAATATT CGATATGAGG AATGAAATAT GGTGTGTGTG
32521 TGTGTGTGTG TGTGTGTATG TGTGTGTGTG TGTGTGTGTA TGCACCTATA TATGGCACCT
32581 ATATATTCAA CAAACAATTC TGATAATTGG CCAGGGTTGA GAATGACTAG CAGCCCAGCA
32641 TACACTATCA GTTTTAAGTA TATAATTGCG CTTTAGTAAA ATGTAAAGAA ATCCCAGAGT
32701 AGAAATACTT TTAAGCTATA TTACAGGTGA GAAATGCGAT AAGTATAGTC TCACCCAAC
32761 TAGACTATGG GGGCTTTATA ATGTCACAAAC AGTTGTTTCC AGGCATTTGG GGACATCACC
32821 ACTGGTCTTG GGCAAGAAAC TCCTCTAGCC AATGGCTGAT TTATCTCACT CCCATCTAAG
32881 GCTTCACTGC ATTTCTCTTT TTCAGCAACC TAACTTATTT AAAAATATCC ATTTTCTGAT
32941 TCATTTTTTT CTGAATTAAA CTGTCAGTAC CATTGGCACA CCTTTGGTTC CGTAGCATA
33001 CTGTGTCTCT GCTGTGTTTT TTTTTTACCT CCACTCCTTA CTTTTCTAGA AAAAAATCTC
33061 TGCTTTTTCT TTTCAAGTTA AATTATTTCA CAAAAGTTT TCTTGACTTG CACTTCCTAG
33121 GCTTGCTGTC CTTGTGTGGG CACGCTCCCA TAAACACTAT TAATACACTT CGATTTGTTA
33181 AAAATAAAGA TATCTGGACA GAAAATTTCT TTTCTTTTTT TAAGATTTTA AAATTTTAA
33241 TGTTTATTTT TTTCTTAGAC TGGAGTACAG TGGCACCATG ATGGCTCATG GTAGCCTACA
33301 CTTCCCCGGG CTCAAGTGAT CCTCCCACCT CAGCCTCCCA AGTAGCTGGG ACTACAGGTG
33361 TGCACAACCA CACCTGACTA ATTTTGTTTA TTTGTTTGTT TTGTTTTTTG AGATGGAGTT
33421 TCGCTCTTGT TGCCAGGCT GGAGTGAAT GGCGGGATCT CGGCTCACC GCAACCTCTAC
33481 CTCCCAGGTT CAAGCAATC TCCTGCCTCA GCCTCCCGAG TAGCTGGGAT TACAGGCATG
33541 CATCACCACG CCCAGCTAAT TTTGTATTTT TAGTAGAGAC GGGGTTTCTC CATGTTGAGG
33601 CTGGTCTGGA ACTCCTGACC TCAGGTGATC TGCCCGCCTC GGCTCCCAA AGTGCTGGGA
33661 TTACAGGCGT GAGCCACCAC GCTCGGCCAC TAATTTTGTA TATTTTGTA AGATGGGCTT
33721 TCCCTGTGTT GTCCAGGCTG GTCTTGAATT CCTGGGCTTA AGTGATCTGC CCACCTTGTC
33781 CTCCCAAAAT GCTAGGATTA CTGGCTGAG CCACCAGGTC TGGCTGGAAA GATAATTTCT
33841 AACATTATCC TCTCTTAAAC ATTTGTTTCA AAAATTTTAC AAACATGAGA GTAATTAAT
33901 TTGATTTTCA AAATCCCTT GAATACTTTC TTAATAGCAC ACAGAAAGCA CAAAGTATTT
33961 TACATTTGTT TTAATGATGA AATTGTGAAC CCAAACCTAC ACAAAGAAAA ACCCGTAACA
34021 TTATACCCAT ACTTAAACA GATGCCCTCA TATACATAGT AAAACTCTTG GGGGCAGTAG
34081 TGAAGTTGGT TATTTACTGT TTTATGAAAG TGCCATTCAG CCGGGTGCAG TGGCTCATGA
34141 CTGTAATCCC AGCACTTTGG GAGGTCGAGG CAGGCTGATC ACGAGGTCAG GAGTTCAAGA
34201 CCAGCCTGAC CAAAATGATG AAACCTGTG TCTACTAAAA ATACAAACAT TAGCTGGGCG
34261 TGGTGGTGTG TGCCTGTAGT CCCAGCTACT CAGGAGGCTG GGGCAGGAGA ATCGCTTGAA
34321 CCTGGGAGGC GGAGATTGCA GTGAGCCGAG ATCGCACCAC CGCACTCCAG CCTGGGAGAC
34381 AGGGCGAGCT CCGTCTCGAA AAAAAAAGTGC CGTCATAGTG ACTCAGTTTT
34441 AAGGAATAAA TCAAGGATAT TTAATCAAT AGACTACAGT TAGCTAACGT GACTTGCACT
34501 GAAAGTTATA CGAATATTGG TACTTATTC CCTGCCCCTG AAGTATGAAT TAAAGACTCC
34561 AAAATTCTTT TTAGAATCTT CAGAGTAAAA GCTAGAATTT GATTTTTTTA AATAATAAAA
34621 AAATACTTTG TATCTAAATC TGGTGATAAA AATAACTTGG TGGATGATGC TTCAAGGCTA
34681 TCCATCCCCA AATTTCTCCC TGAATGATAA AGAGAATAAA TGAATATGTC AATTCAAAAG
34741 TTAGAAATTT GGCCGGGCAC GGTGGCTCAC TCCTGATAAT CCTTTCGGAC GCTGAGGTGG
34801 GTGGATCGCA TGAGTCCGG AGTTCAAGAC CAACCTGGGC AACATAGCCA GAACCCGTTT
34861 CAATAAATAA TAGAAAAAAA TGAGCCAGGC GTGGTGGTCC CAGCTACTCA GTAGGCTGAG
34921 GTGGGAGGAT CACTTGAGCT CAGGAGGTCG AGACTGCAGT GAGCCGTGAT CGCAGTACTG
34981 CACACCAGCC TTGGTGTGAG ACTGAGACCC TGTCTCAACA ACAACAAAAC AAGTTAGAAA
35041 TTTGGCTGGG CGCGGTAGCT CACGCTGTA ATCCCAGCAC TTTGGGAGGC CAAAAGGGC
35101 GGATCATTTG AGGTCAAGAG TTCGAGACCA GCCTGGCCAA CATGGTGAAA CTCCATCTCT
35161 ACTAAAAATA CAAAAAAAT TAGCCGTGCA TGGTGGCATG CGCCTGTAGT CTCAGCCACT
35221 TGGGAGGCTG AGGCAGGAAA ATTGCTTGAA CCCAGGAGGC AGAGGTTGCA GTGAGCCGAG
35281 ATCATGCCAC TGCATTCCAG CCTGGGTGAT AGAGTGAGAC TCCATCTCGA GAAAAAATA
35341 AAAATTCTGT ATGAACTGAA CAAATATTC TTAATTTTA AAATACATCT GAAAGATATT
35401 TCAAAATATT TAGGAAAAAA ATTAGGGGA TCAGGCAAAAT TCTGAGATT CTTTTTCCCT
35461 GCAGCAACAA TTAGGAGTGC TGCTGTTCTT AAAAAATGG TAACTGTTGC CACACCGTAT
35521 GTTTCCTTGG CTCAGACATA AGGTTGTGTA GTTGTATTTC CAGAAATAGCT AGAATAAAAA
35581 TCCAGCACAT CATTTCTTTC AGCAAGTTAA CTAACCTCTC TGTGCCTTGG TTTTATAACA

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35641 GCAACATAAG CATAACAGAA TAGCAGCAAT AGCTCCTACC TACCTCATAA GATTCTTTGG  
35701 AGGAATTAAA TTAAGATTCA GAACACAGCC TAATATCTAG TAAGTAATAA TAATTGGCTA  
35761 AAAAAATTTT CTTAAGATTA TATATATTCA TGGGGTACAA GTACAATTTT GCTACATTAA  
35821 TATATTGCAT TGTGGTGAAA TCAGGGCCTT CAATCCATCC CGGAAAAAAA AAGTTTTTGA  
35881 AAAGATTTCT GCCATGGAAG ACTTTTAATG TACAAATTCA TCCATCCAAG AAATAGAAAA  
35941 TATATAAGTA TCAACTCCAA ATCCACCATA TCTATCTCTT CTACACCTTA AACAATTACT  
36001 CAGAAATAGA ATGCTTGAGA TACCAGAATG CATGCATATC AAGTAATAAA TGCATGCAGG  
36061 ATGTCAACGC ATCCTAGGCT TTCAAATAAA ATTGTCATAC AAAATACTTT AATATTGTAG  
36121 TAACATTCTA CATGTTAGAG TGTAGAAGTT AATCGCTGAT GCAAAAAAGG AAAAGAACAC  
36181 ATTATACCCA AAGCCTACAG AGAGAATCAC AATTACAAAT ATCAGCCTGC ATGTGAAAAT  
36241 CTTTAATTTG AAAGTCAGAA ATATTTAAAT GATAGTCATT GTTAAATCAG ATTGTGGTTT  
36301 GAAAAAAGT TAGTTTAAAA CTGAGTTTAT GAAAAATTTG GGGATTTTAT AGACAGTGTT  
36361 TTGTTTTTAA ATGTGTGTGA GTTTGTGAAG AATGTTTTAT AAAATACTGA CAGTATTATA  
36421 AGATGACATT ATTATAATAC AACATAAGAA TTTTGGCCTG TACCTCTCAG CAGTCTCAA  
36481 TCACCTGCTG TACTTGACTC AATGATTATC AGAGTGGTTT GTTTTCCTTC TGTGTGTTT  
36541 CCAGTTCAGG CAGCTCAGCA ATGGCCTGTG ATTCCAGCAA TTCAAATAGC TGGTAAGTAG  
36601 TTTCTTGTTT GTTTTCTCAA ATTTTCAGGG GCTTTTCTCT ACAAGTGATT TCCAGTGCAC  
36661 GCCCTCCAC CCATTCTTTA TTCCTTTACC TTCAGGAAAA CCCTCAGCGC TGCATCTCTG  
36721 GTCACCGGAC CACCGTGGTA CATTTACCTA TGGCCACCAG GTGTCACCCT TCTCTTACT  
36781 ACCATGGTTT GTGAATGGTT TTGCCAGAGG TGAATAAGAA TTTAAAATGC AGGTCTTTGA  
36841 TTTTTCAAAT GTAGTTGACC TTAAGAATTT ATGAATAAAG CCAGAAAAAT TAAGCTTAAA  
36901 AAACACCGAA AGAAAATGAG GACTTAAAT TTCTATTAAA AAAATTAACA GGCCACAGTT  
36961 GCTGATGTTT AGTAAATGTG TTAGTGAAT GTGTTACTGT GAAGACTGGG GTGTTTCTTG  
37021 AAATCTCAGC CCAGGTGAAA TAAAACCAAT ATAAAACAAA TGCTTACCTA ATAAATTAAT  
37081 TGTAACATAT TCCTTATGAG GTAGAAGAGT AAGTGAAGCC TTATAGCAGT CTGCTTTTCA  
37141 TATAGTAAGA TATTAAGAGA GAAATAATTT GTCATATGCT TTCAGAATGG TTTGCTGGTA  
37201 AAATAACCAA TGTCTTACAA CTTAGACGAC AATGTCCCTA GAGTGAAGAA ACACGATTAA  
37261 TTCGGCTACC ACAGTTGAAT GAAAATATTC CGTAAGACAA AATGTAAAGA AATTAGAAGC  
37321 AAAATAAATG TCTCCAAAAT GACAAAGCGA TTAAGTATAT ACACAAGATG AACAAGAAGT  
37381 TCAATAAAAT CATGCAGTAT ACAATACAAT ATACATTTAT TAAAGTATAT GCATTTTTAA  
37441 TGCAACAATA ATACTAACAG GTAATAGACA AGTTGTTAAT AGTTTTTCAC TGGCTAATTA  
37501 AATAACAGCT TTAATTGTAT TCATTTTATA GCTTTTCTAC AATGAGCGTA AATCACATTT  
37561 ACTTTTTTCT ACATAACTTT TCTAACCAAA AAAAAAGAAA ATGGTTTTAA AGAAGAGATG  
37621 AGATATCTTT GCTAAAATTT AATGCCTAAA GAAGAACTT CTGAGCTGTA TATGGTATCC  
37681 TGAAGCACCT GCCCTTCAAG ACAGAATGCT TGTACCACAT TTATGCAGCC AAGTGCATGT  
37741 AGTAACATAA AGTAAACACA TGCCATCTGG ATATATATAT TAAGACTCTT TTGACGGCTG  
37801 GGCAGGGTGG CTCACACCTG TAATCTCAGC ACTTTGGGAG GCCGAGGCAG GCGGATCAGG  
37861 AGGTCAGGAG AGTTCGAGAC CAGCCTGGCC AACATGGTGA AACCTGTCTT CTACTAAAAA  
37921 TACAAAAATT AGCCGGGCAT GGTGGTGAC GCCTGTAATC CCAGCTACTT GGGAGGCTGA  
37981 GACAGGAGAA TCGCTTGAAC CTGGGAGGCA GAGGTTACAG TGAGCCGAGA TCATGCCATT  
38041 GCACTCCAGC CTGGGCAATA GAGTCTCAA AAAAAAAGAA AGACTCTTTT GAACATGGTG  
38101 AACTGATTTT CCAGAACTTA GCAATTCCTG AATGTCCTGG TTAGATTTTT TTTTTAATGT  
38161 GCACCGGAAC CCCAGTGGCT CCATGGAAGG ACCTGGGCAT CCTTAAGCC ACTTGGTGCC  
38221 TTCCATTATA CCATCTCAA ATGAGAGAGC TTACTCCACT TCATTGAGGG AAATACCACC  
38281 AGAGTTCTGA CTCCAGAGGC ACTGGCCTAG GGAGGACACC GTGTGTGAAG CCCAGCAGGG  
38341 CCACTAGCTG TCCCCACCAA TTACAGTCCT TCGTAGGGT CCAAAGAAAT GAATGCCAAA  
38401 GAGAGCAACA GAGGAGCAAG GGAGTCACAT TCCAGGACCT TCCTTCAGGG ACTTTTAAAG  
38461 GAAACATGAC AGCTGAGGAT CAGTTGGTTG TTTTCTGCTG TTCCCTTCA TGTGATTCAA  
38521 GCTCACTCAG AAGAAACACA ATGAGACAAG AGAAGAGCCA TCTCCTTCTT TCTCTATTTA  
38581 TTCTAGGCAT CTAACTACT GAATGTAGTG GTGTCTGAGA TGTATCAAAC GGTGAGATTG  
38641 ACTGAGTTTG AAACCTGTTT CTATCACTGA CAAACTATGA GATACTCTAT ACTTCACTTT  
38701 CTTTTTTTTT TCATTTTTTT ATTTTATTTT TTATTTTTTT GAGATGGAGT CTCACTCTGT  
38761 CACCTAGGCT GGAGTGCAGT GGCGCAAAT CGGCTCACTG CAAGCTCTGC CTCCTGGGTT  
38821 CATGCCATTG TCCTGCCTCA GCCTCCGAG TAGCTGGGAC TACAGGCGTC TGCCACCACG

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38881 CCCAGCTAAT TTTTGTATT TTTATTAGAG ATGGGGTTTC ACCATGTTAG CCAGGATGGT  
38941 CTCGATCTCC TGACCTCGTG ATCCACCCGC TTTGGCCTCC CAAAGTGCTG GGATTACAGG  
39001 CGTGAGCCAC CGTGCCCGGC CTACTTCACT TTCTTCATTT AAAAAAGAAA TGGGGATAAT  
39061 AGTACCTATC TCATAGAATT ATTGTAAGAA GTGCATGCAG TAATGCATGT AAGTAGGTGC  
39121 TCAGAAGAGT CGGACACGAA GTAAGTGCTT TTATCATCCT TATCATAATT TTCATTATCA  
39181 GAACAAGGAG AGACCAGGTA GAAAATTATT GTGATTCTTC AGGTCTGGAA TACTAGAGTA  
39241 GCATCCCAAA TGAAGGCACC ATTAACTTT GCAAATCTGT ATGACACCTT CATGCCAATT  
39301 AGAAAAACA CCTCTTCACA ACCCCTTTCA AGATATTTGC CTCCTACCTG CTAAAAACAC  
39361 CCATCATACT ACCCACAGAT AGCCATGATG CTTTTTCTGG GACAGGTGCC TCTTCCATTC  
39421 GTGCAGTGTA CAGCCTTCAT AGCTGTGCAA CTCACATCAC AATCAGATGG AAGAATCCCC  
39481 AAGGCTTGGT GACAGATGAG TTAGTGGGTA ACACAGAGAG AGGATTCAAA GGAAAAGTTG  
39541 AACGGGTCCA GAAAATGCAT AGATACATGT GTAAAAATCT GGTAAGGTTA TGACTAGCCA  
39601 CGTCCCAGGG TTCAAAGCTT TTCTCAGATG TTTAAATGAA TCATGTAAGT CCCCCAAATT  
39661 TAAGGAGTCC TCTTCCAAA ATAGGAAATG AAATGACATA GGTGTATGTC TCTGAGGTGA  
39721 CGGAGGAAAT GAAGGAAGCC TCTAGATGCA GCTTGAGGTT CATGAGAGAC AGTTCAGGG  
39781 GAGAGGTCAC AGCTAGGGAT CACCGGCATG CAGGAECTCA GAAACCTAAA TGGGGAAATC  
39841 TTTTGTAGGA AATGAACAGA GAAGGCTAAA ATCAAGGAGT TCGTCAGGCA ATTTCTATGT  
39901 TTAGGTTCAA CTCTCTCCTG AAACATGAAG AGCTCATAAA TGCCTCCCT CTTTGAGTCT  
39961 CTAGTTTTGT CTCCTTCCCA CAGTGAGTCT GCAGGCTGCG TGTCACTCAC GTTCAGCTAA  
40021 GACGTAGTGC CCCATGGCTC CTCCTGTGGA GACAAGAGAC CCAGGAAAGA GGCATCACAA  
40081 ACCTAGGCAC CATCTTGCTT CTCTCTCTT CTTATTTTC CTCATTCACC CATCTCAATT  
40141 TAGACCTGGG CACTATTGGA TTTCAAGAAC CATTATCTCT CATCTGGAAA TGCTTATTGG  
40201 CTTTCTAACT GGTCTCCTCA CCTCTCATCT AACTTCTTAA CAACACATTC ACCATAAAG  
40261 GGAGATCGTG GTCCTCCTT CTTAGGATCC TTCAATGACA CCCCAGTGAT CATAACCCAA  
40321 TATCCCAAAA GACCCTTGGA CTCTGTATGA GCTGGCTTCT TTCTGATTCT CTTTTCCCTA  
40381 CACCACAGAT GTTCAGGGGG TAGAAATGCA TAATTGGTGA GTGATAGCTA CGCAAECTCA  
40441 GGGTTAAGGT ACAGTAATTA TTTCTAATCT CCCAGTATGC CTTATACTCT CCTACTTGGC  
40501 ATGGTTGCTC CGTCTGTGTA GACCTCCCAT CATCTTCAAC CTCACCTAAT GGAATCCAGC  
40561 TTCTCCTTCA AGATCCAGAA GGCTATCTTG ATCCCCAGCT GAATGTGATC ATTCTTTCCT  
40621 TTGACACCCT AAGCATTGTC TTCCTGCCTG CTTTAGGACC TCATGGGGTC TTCTTTAACT  
40681 ACATTTACTT GCTATCAATT TCATTCCCTA CCAGATTGG GTTCTGAGAA TAGCCACAGT  
40741 GACTTCTCAA CCTCAAAGCC CTTGTAATAC CTTAAACAGC TCTTGCAAAA TAGTAGTGC  
40801 TCTGAAGATG TTTGTTGAAT TAGAGACTTT CATTCTGGGG AGAACCATA TTTTCTGTCT  
40861 CCCAGGGAGC TGCTGGTGTC CCCAAAGAAT ATAAATGAGA AAAATGCTTC CCATGGATGC  
40921 CAGATCCCCT CTGCCCTCT TCCCCTGTG CCCTGGGGCA GAGGTACTAA GAGACTTCCC  
40981 CCTTGTTCCT ACTCACTTGA ACCCTGCCTC TTCCTTAATA TTATGAACAA AATTCCAATG  
41041 AACAGATGA CGACAAAAC AGCAATTCCA CTGATGACTC CAATGACTAG GGTGCCAGAC  
41101 GGTGAGGGCT CTAAACAGA AAAAGCAAGT TAAAGCCTTT GATTGCCACC CTCAGCCCAC  
41161 CCCCTAACAA AGAGCAGATC CTCATCTCAC TGCCATAATT ACCTCCTCAG GCACTCCTCT  
41221 CAACCCCAA TAGATTTTCT CAGCTCCTGG CTCTCATCAG TCACATAACC CAGATCACAA  
41281 TGAGGGGCTG ATCCAGGCCT GGTGCTCCA CCTGGCAGT ATATCTCTGC TCTTCCCCAG  
41341 GGGGTACAGC CAAGGTTATC CAGCCCTGGT AGGTCCCATC CCCATTGGGC AATACGTCTT  
41401 TAGGTTGCAA CTCCTTGGA TCCATTGGCT GCTTATCCTT CAGCCACTTC ATGGTGATGT  
41461 TCTGGGGGTA GTAGTTCAAG GCCCAGACCC GTAGAGTGGT CACTGAAGAG GTCACATGAT  
41521 GTGTACCTT CACCAAAGGA GGCCTTGAC AGGAAAGAGG AAGGATGAGG AGAGGGGATC  
41581 TGTTTACCCT TGCCAGGAAG ACTGGAACCT TCACCTCCTT CTATAGGTTG GAGGAAGGAA  
41641 ATACCCTTTT CAGAAAAAA CAAGCTACAG GAGAGACACC ATTTTGTGTC CTAAGATTGG  
41701 ACTCTAACAC AGTGTCACTT GGAGAGCAGT CAGATCAGCT TGTTCTCCTC ACATGTAAAT  
41761 ATACATATCT GTTACCCATG TTCTTTGTTT TGATAGATAA AATTGCCCTT TATGTGCATT  
41821 GAAAATGATT GAATACAGAT GGTGAGTTTC ACCTGGGTCA ACCTAGGAGG CATTGTTATA  
41881 AGAAGCGGAC TTGTAAGATA GGTAGCTTCA GTGATTATTG CTATGTTCTA TGAAAGAAAC  
41941 TTTTAACCTA AAGGATTCTT CTACTCTGAT AAGTGGCCTC ACTTGATATT TTGTCCTGGT  
42001 ATTCATATGA TAGCTGAGAT CTCTGAATTC TCTTTTTTTT TTTTTTTTTT TTTTTAAGAT  
42061 GGAGTCTCAC TCTGCTGCCT AGGCTGGAGT GCAGTGGCGC GATCTTGGCT CAGTGCAACT

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42121 TCCGCTTCCC AGGTTCAAGC GATGCTCCTG CCTCAGCCTT CCAATTAGCT GGGACTACAG  
42181 GTGCGCATGA CTGTGACCAG CTAATTTTTG TATTTTTTTA GAGACGGGTT TCACCATGTT  
42241 GGTCAGGCTG GTCTCAAACCT CCTGACCTTG TGACCACCCG CCTCGGCCCTC CCAAAGTGCT  
42301 GGGATTACAG GGGTGAGCCA CCGTGCCCGG CCTTGACATT TCTGAATTTT TAACAGGTAT  
42361 AAATATACAA AAGATTATTG GTTAAATAAA AAGCAAGGGC CATAGACACT TCCCTTTGAG  
42421 CCATATGCAT GGAGAAAAGA AATTAAACCC ATGACTTGTG GCTGTCTCAT ACATCTCAAT  
42481 TATAAGGTAG AGACTCTAGG ATTGAGAAAG TCCCTTCCCA GAATTTGGAG AGGCACACAG  
42541 CCTCAGCCAC CTCTGAAACT CCAACCAGGG ATTCCGTGCC CTGCAACCTC CTCCACTCTG  
42601 CCACTAGAGT ATAGGGGCGAG AAGTGTGTTT CCACCATAACC TTGTTGGTCC AAAACACCTC  
42661 TCCCCAGCTC CAGCAACTGC TGCAGCTGTG CAGGGCAGTC CCTCTCCAGG TAGGCCCTGT  
42721 TCTGCCTGGC CCGAATCTTG TGCCTTTCCC ACTCCAGCTT GGTGGGCCAG GCCCTGGGTT  
42781 CTGCTGCTCT CCAATCCAGT GTGTCAGGGC AGAATTCAAG GTGGTCTGTC CCATCATACC  
42841 CGTACTTCCA GTAGCCCTCG GTACTGTTGT CTTCTTGCAT TTCACAGCCC AGGATGACCT  
42901 GCAGGGTGTG GGAATCTGGA AAAATCCCCA GCCTTGTTAA CTGCAACCAA AGGAATAGGT  
42961 CCCTATTTCC ACCATCCCCA AGGACCAAAT GATCTCAGGA AGCAAATTCC TTCCCTCTTC  
43021 CCTGCTCCCA CAAGACCTCA GACTTCCAGC TGTTCCTTC AAGATGCATG AAAAGATGAA  
43081 AAGCTCTGAC AACCTCAGGA AGGTGAGGCC CCCTCTCCAC ATACCTTGC TGTGGTTGTG  
43141 ATTTTCCATA ATAGTCCAGA AGTCAACAGT GAACATGTGA TCCCACCTT TCAGACTCTG  
43201 ACTCAGCTGC AGCCACATCT GGCTTGAAAT TCTACTGGAA ACCCATGGAG TTCGGGGCTC  
43261 CACACGGCGA CTCTCATGAT CATAGAACAC GAACAGCTGG TCATCCACGT AGCCCAAAGC  
43321 TTCAAACAAG GAAAGACCAA GGTCCTGCTC TGAGGCACCC ATGAAGAGGT AGTGCAGAGA  
43381 GTGTGAACCT GGAGACAGAG CAACAGGCCT TAACCATGTG TAGTAGGAGG GGAGCAGGAT  
43441 GTTGAGGCTC CACACACCTG CATCAACTCA TACCATCAGC TGTGTCTGGT CCTCATTTTG  
43501 TGAAGGGTGA GTTGAGTCC TGTCTTTCTT CCATATGACA GTCCTGGGTG CTCTTTCCTT  
43561 GTGTGCTTTT CTCTGCCACA CGTGGCTGCC ACCCCCTCAC TGCCCCCAGA TCCTATTCCA  
43621 ATACTCATGA TTAGACAGAC TCCACTAAAG CTGGTGGATT CTAGAAAATG TTAAGGTGTG  
43681 TCTAGCCATG GTAGTTGAAC TCAGGAGTTG GTGCTCAGGG GTGCTCAGGG CCAAATTAGC CCAAATCCTG  
43741 AGGAATAATT CCTTCAGTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTGAGA CAGAGTCTCA  
43801 CTCTATCACC CAGGCTGGAG TGCAGTGGCA CAATCTCAGC TCACTGCAAC CTGCACCTCC  
43861 TGGGTTCAAG GGATTCTCCT ACCTAAGCCT CCTGAAAACC TGGGACTATA GCGGTGCGCC  
43921 ACCACACCAG GCTAATTTTT GTATTTTTAG TAGACATGGG GTTTCACCAT GTTGGCCAAG  
43981 CTTGTCTCAA ACTCCTGACC TCAAATGATC TACCTGCCTC AGCCACCAAA GTGCTGGGAT  
44041 TACAGAAAGT AGCCACCGTG CCCAGCCTTG GTCCTGAATT CTTACACTGA ACTGCCTATG  
44101 TGGCCTCACC ACTTGGAAGC CTGACTGGAA TCTCAAACCT AACATGTCCA AATGCAGATC  
44161 CTTGATTTAC CCCAAACTGC TTTTCTCTCT GCCTTCACCA TCTCAGAAAT GGCATTGCCA  
44221 ATTACCCAC TGCTCAGGCC AATAAAATTA AAATAAAGAA CAAAGTCAAC TTTAATCTTT  
44281 CTCTTTTTCA GGGGGTCAGG GGAGACAGGG TCTTGCTCTG TCACCTAGGC TGAAGTACAG  
44341 TGGCACAGTC ATGGCTCACT GCAGCCTCAA CTTCTTGGGC TCAAGCAATA CCCTCCACCT  
44401 CAGCCTCCCG AGTAGCTAGG ATCAGAGGTG CATGCCACCA CACCCAGCTA ATTTTGTAT  
44461 TTTTTGTAGA GAAGGGGTTT TGCTGTGTTG CCCAGGCTGG TCTTGAATC CTGAGCTCAG  
44521 GAATCTGCTC TCCTTGGCCT CCTCCTTGGC ATGAGCTACT ACACCCAGCC AATTCTTCTC  
44581 TTTCTCTCAC ACAACATAGA ATCCTTCAGC AACTTCCTTC AGAATATATT CAGGAGACAA  
44641 TGGTTTGTCA CTCCCTTTTC TGTTCACCC CAGCCCACTC CACTACCTCT TGCCTGGACT  
44701 GTGTAACAGC TTCCTGGCTG GGCTCCCTGC TTTTACTGTT GCTCCCTTCA TTCTGCTTTC  
44761 CACATAGCAG CCAGAGCAAT CTTTTAAAAG CCTGTGACAG ATCACTGTTA CTCCTTGGCT  
44821 AGAATTCACA CCACAGCCTA CAGGCGCCTG CACAACCTTG TTTGTGGCTC CTCTTCTGAG  
44881 CCCATTACCT ACTTCTTGGC CTCTACTCCC CAGCACTACT TGTTTATTTT TTTCAACCCG  
44941 AGCTTCTTAA CCAGGAGTTT GTCTACTAGG TGACATGTGG CAAAGTTTAG AGACATTTTT  
45001 GGTGTGCAAG ACTGGGGGAG TGCTCCTAGC ACCTAGTGAG TAGGGAGGAC AGGATACTGC  
45061 TAGACATCCT ACATGCAGAT GGTAGTCCCC CTTCCCACCC CCACGCCGCC CCCCCCCCCC  
45121 ACACACACAC ACATGAGTAG TGCTGAGAAA ACCCGCTTTT TAATCCAAC TGCCAGGCCC  
45181 ACTCAGTTTG CCTGGGAAAT ACTGCTCCCA GTCAATATCA TTCTTATTTT CTTCATGTCT  
45241 CTGCTCAAGT GTCAGCCCCA GAGTGACTTG CCCTGACTTC TCTGCTTCTC ACAACACCCA  
45301 TGATTTCCTG ATGTTGTATA TCTTCTGCT CATTGTGCTA TTGTCATCTC TCCCACTAGA

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45361 ATGCAAAATA TCAAAGGGTA AAGACTTGTT TCCCTGCTCT CTCCCTTGGG GCTTGAACAG  
 45421 TGCAACACAT GGCTGGGACT CATTTACACT TGTAACAAT GAATATTTCT GCTCAACATG  
 45481 AAATTTTATT ATTCAACCTC TAATGCAGTG TGATGTTTAA GAATCATAGC TATGAAGTGG  
 45541 AGACATGAGC TCTGCCACCA AAGCCCATGT TACCATTGAA TAAATTTGCC AGGAAGCAGG  
 45601 CCGTGCCATG CCTCATTCTT GTCATGTGTA AAATGTGGAT ACACGTAGTA CCAAAACTCA  
 45661 AAGTGCTGTG CTGAGGCCGG CGTGTGACCC ACAGAACACT GTGCTACACT ACAGGGCAAA  
 45721 ATCACTGTCA ACTAAGATTA GAAGCAGCTG TAGTACTTGA AATAACATCA GAAAACCAGA  
 45781 TTATTTATGT TCTTTGTAACT CTGAAAAGAG TTATATAATC TGAATTCAG TTAACCTCTA  
 45841 GTAAATATAA CGTATTATTA GCTCCTACCT CCCTATGCCT AGTGAAAATC AAATAAGATC  
 45901 AGATATGAAT GTAACCTAGA AGTGAGTGCA TTGCTTACAT GTTCATTATC AGTACTTTGT  
 45961 AGAGAGGCCT CTTAATTACA CAGCACATTG CAAATCAATA AAGCCTAGCC GAAAAGAGAA  
 46021 TTGTTCAAGT CAAACGTTCA AAATAACAT ATACTTAATT TTCCAGGCAA AAGAACAATT  
 46081 GCCAAGAGTG GGGAAAAGCC CGAGGTAGGC CTCTCTCAGG AGCCTCCAC CCTAGAGACC  
 46141 TCCACCCAG GTCTCACCAG AAGTGGGTGG AATGGTGAAG AATTGAGATC CCCAACGCCA  
 46201 CTCTTTTCGG CCCCCACCGC CCAACGCATT CGTTCAGAGG TGGAAACCCG GTGCGGATCC  
 46261 TGCTGTGGGT TTGCTCAGCC TTCTCGGCAA GCACTCAGGG AAGAACTTCC TGTTTGGAGA  
 46321 TGAAGTGGGA AAAAAGTGA CAGCTGACAT TGGAAATAA CCCGAGTTCC AGGTTCAAGG  
 46381 AGCCCCAGGC TTAGCTCAGC TCAAGTGAGG AACTACGAGA TTTATTTAAA AGCATTCTAG  
 46441 TTGGGGGAAG GGAGTGGGCG GTTCCAAAAG TCACTCCGCA GAGCCGGGAC AGCCGGGGGA  
 46501 GGGGCGAGGT CCTGGGGCGA GGGACCCCTA TCTGCAGTTC AGTGGTAGGC ACTCCCTCAC  
 46561 GGGGTCTGGA CGCAGAAAGT AGGGAGAGGG GCTTGCAGGAT AGGGTTGAGC AGGTCTCTCA  
 46621 AAGTTAGCAA ACTCCCAAGC GCAAAGAAAA AGCTAGTTTC GATTTTTCCTA CCCCCGCCGC  
 46681 GCCCCTAGTT CGCCCCGAGC CCTCGGACTC ACGCAGCAAG CGCCCCGCA GGACCGCGGT  
 46741 CTGCAAAAGC ATCAGGAGGA GAAGCGCCGG CCTGGCTCGC GGGCCCATTT CCCAGCTCT  
 46801 GGCCGACGT CCCCCTTAAA TCTCCGCTTC TTTTGGGGGG CGGGGAAACG GGGATGGCTC  
 46861 CAGAAGTCAC CCTACAGCTA TTGCCTAGGC TCAGGAGATG CCCAGTAAAA CTCTCTGGTG  
 46921 AAAAGCAACA GGTCTTTTCA AACTTTAGTT CTCTCTCTCC TACAGCAGAA GGTACCTGCT  
 46981 TGTGAAACAC TAGGTGATCC AGTGTCCTCC TTGGTTTTTA AATCCTGAAG GGGTGTGTGT  
 47041 GATTGGGGAA AGTAGCTTCG CAATGTTCTG ATCTGAACTT TAGATATTTA AATATTTATG  
 47101 ATTTTCAAAA TTCAATCATA CATTAAAAA TTTTATCTCA ACCTTAGACC AACTTATGTC  
 47161 TTATTTGACT TAGAAATATA AAGCTTTTTC ATTTTGTTTT TTGATTCAAA TTAATTAAGT  
 47221 CATAACATTA ACCAATTAGA TCCTACTGAA ACACCTTCCA CAGCCTTCAT AATTGAATTA  
 47281 TCTGACAAGT GTTTCACAAA CTTTACAGTA TTGGGATTAT CTGGAGAATG ATTAACATA  
 47341 TTGAGGCCTG CTCCTAACCC CAGACACACT GATTTAATGG GTAATTGTGA GGTAGTTAGA  
 47401 CATTAGCAGT TGGGAGGGGA TGACAGAAGA GAGCGGAAAG GCTGTCACTA AGACAGCCAC  
 47461 TGGCCACCT AAATTCAGGC CCAAGACTAC CCTAATGCCA CCCTAAGGGA TGGAGTTTAT  
 47521 GATAAAGTCT GTGGCCAAAA TATCCTGGAG AAAGAGAAAG GAGGGTACAG GTGGAAATTC  
 47581 CCTAAGGTGG CACATGCCCA ACAACACAAA AGCCTGTCTT CAAGTTTACC CCAAGTTTAT  
 47641 CATGCCATCA TTATAATAGA ATTTACATAC AGTTTTGCCC CCCCATCCCT GGGAGGCTTT  
 47701 TCTTAACAAA TTATAGGTAA GACCATGCAC AGTTTAATTT TAGATTGTAT AGCTATACAC  
 47761 TTCAATCAAA TAACATCATC CTGTCACTCA GATACAGCCC AAACCTCAAC TCCTCCCCAC  
 47821 AAACCCCAT AAGACACCTT GAGCTCTGTA AAGAAGTGCT GAGTTCACTT CGCAGAAATA  
 47881 AGCCCGCTGT CCTCAGAGT GTATTATTGT GCTTCAATAA ACTTTGCTTT AAGCTTGCAT  
 47941 TTTGGTGTGA GTTTGTAGTT CTTTGCTCAC TATCACAAGA ACTGAGATTG CTGGTTCAGA  
 48001 GCTCCGGCTA TAATAATCTC CTCGGTTAAA GGATCCATCC CAATGCATAA TTCCCAGTAA  
 48061 CAGTATGGGA TGCCACCTGG GCAATGGGAT TTTAAAAGCT TTCCTTCTCC CTCAACGAAG  
 48121 TTTGGGAATT ATTGCCTTAG ACATTTCAAA CAATATTAAT AAATTTAATA CACCTGATTT  
 48181 GCTCCAAACC TTTACATATC TAGCAAATTC AACAGGCATT ATTTTGTAA GCATGTATGC  
 48241 AAATTTTGGC AATTCAAGAA AATCAAACAG GATATCAGGG CCTCGACTGT AGGCAAACAG  
 48301 ATACAATAAC ATTGGAACA TGTAAGATAT TGATGATGGG CACATTGGGG CTGATAGTAC  
 48361 TATTCCTTTT TTTCAATTTT TGGTAAGATA TAATTAGCAT ACCATATAAT TCATCTATGT  
 48421 AAAATGCAAA AATTGGCCCG GCTCAGTGGC TCACGCTTGT AATCCCAGCA CTTTGGGCGG  
 48481 CCGAGGAAGG CAGATCACCT GAGATCAGGG GTTCGAGACC AGCCTGGCCA ACATGGTGAA  
 48541 ACCCCGCTCT TACTAAAAAT ACAAAAATTA GCCGGGCGTG ATAGCAGGCA ACTGTAATCC

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48601 CAGCTACATT AGAGGCTGAG GCAGGAGAAT CGCTTGAACC CGGGAGGCGT AGGTTGCAGT
48661 GAGCTAAGAT CGTGCCATCA CACTCCAGCA TGGGAGACAA GAGCAAGACT TCATCTCAAA
48721 AAAAAAAAT TAGCTGGGTG TGGTGGCATG CACCTGTAAT TCCAGCTACT CGGGAAGCTG
48781 AGACAGGAGA ATCGCTTGAA CCTGGGAGGC GGAGGTTGTG GTGAGCCGAG ATCATGCCAT
48841 TGCCTCCAG CCTGGGCAAC AAGAGCGAAA CTCCGTCTCA AAAATAAAAT AAATAAAATA
48901 AAATGCAAAA ATTAATGGAT TTTAGTATAT TTACAGAGAT GTGCAACCAT TACCAAAATT
48961 TTACATTTCT ATCTCCCCAA AAAGAAACCA TGTTCCCTTA ATTCAGTACC CTTAATTCAT
49021 CGCCTCCAG ATTCTCCAT TCTCCTCCTC CTCCCTCCC AGCCCTAGAC AATCTTTAAT
49081 CTACTTTCTT TCTATTGGA ACATTAGTA TACATAGAGG CATATAATAT ATTGCTTTGC
49141 CGTGACTGGC TTCTTTCATT TAGCATAATG TTTTATGTA TGTTTTTCAT GGACCAATAA
49201 TATCTATTAT AAGGACATAC CACAACATAT TTTATTATT CATTCACTAG CCGATGGACA
49261 TTGGTTTGT TCTACTTTAT GGCTATTGGG AATAGTGCTG TTATAAACAT TTATGTACAA
49321 GTTTTTTGT AGACTTATGT TTTGATTCT TTTGGTTATA TATCTAGAAG TGGGTTTGCT
49381 GGGTCATATG GTAACACTGT TTAACCTTT GAGGAATTGC CACATTCTTT TCCAAAGTAA
49441 GCATTTTATC CTCCTATCAG CAGTGTATGA GAGTCTGAT TTCTCTCCAT CTTTGCCTGG
49501 GTTTTTGAAT CAGGGCCCCA GATAGAACAA AAATGTGGTT ATTCAGTTGT TCCACCATCA
49561 CTTGTTGAGA AGACTCTTTT TTCATTGAAG TGTTTGGCA CCCTTATCAA AAATCAATCT
49621 ACCATAAATG TGAGAGTTTA TTTCTGGAGT CTCAATTTTA TCCCATTATG CTATAATCTA
49681 TAATCCTATC TTTTTTTTT TTTGACAGAG CCTCACTCTA TTGCCAGGT TGGAGTGCAG
49741 TGGCCCAATC CCGGCCACTG GCTCCTCCTC CCAGGTTCAA GCAATCTCC TGCCTCAGCC
49801 TCCCAAGCAG CTGGGATTAC AGGTACCTGC CACCATGCCT GGTTAATTTT TGTATTTTAA
49861 GTAGAGACGG GGTTCACCA TGTTGGTCAG GCTGGTCTGG AACTCCTGAC CTCAGGTGAT
49921 CTGCCCACCT CAGCCTCCCA AAGTGTCTGG ATTACAGGCA TGAGCCACCA CACCCAGACT
49981 ATAATCCTAT CTTTATGTCA GGACTACACT GTCTTGATTA CTATAGCTTT TTAGTAAATT
50041 GAATTCAAGA AGTTTCTCAA CTTCAAATTT GATCTTTTTT TGGAAGACTA TATTAGCTAT
50101 TCTCAGTCTG CTGAATTTCC CTAGGAATTT TAGGATCTAT TATCAATGTC TATTCTATTT
50161 TTGTATATGT TTTAATATTT TCATAAGAAA CTTTTTTCAT TTAACCTTTT TTTTTTAAGA
50221 AAAATAGTGA AAATCAGAAC ACTGGGGGTC AGGCGCATT AACAGGCAGA AGAAGAATAA
50281 AAACCTGTCA TATAAACAAA AAAGAAATGA CCAATCACAT TGTGGAAGCC ATGGAGTGGT
50341 TATAGGTGCC AAAGGCTGCA GAGAAATGGT GTCAGATATA CCTGAAAATT GTCCATTGTA
50401 TTTGGCCATT AAGAGACTTA GAAGACTTAA GCCATAGATT GCTCAGTGAG ACCCCGAGGG
50461 CAAATGGTCT GAAGGTGAAT AGATCACTTC ACCTTTAAGA GAGCAGGTAG GAAGCTATAA
50521 ATCCAAGATT AAAAAGTTGA CTGAATCTTT AAGGAAGAAA CTCTAATCTT GAGCCACCCT
50581 ATCCTGGCTC CACCTTCTGC TGCAAGCAAA CAGAAATGCT GAAATTCAAC ACTCACAAAG
50641 GCTGGTAAGC TGGAAATGAC AAAAATTACT CCTGGGAAAG TCAGATTTAG AATTAGGCCA
50701 TATTTGTTGG GGTTCAGATT TTCATGTACA CTTGGGAAAG GGTTTAGCTT ATAGGCACAT
50761 GCATGAAGGG AACTGGTATA GGGCTGTGTT CATAAGGTCA AGAGTTGAAG GCCAGGCATG
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50881 CAGGAATTCA AGACCAGCCT GGGAAACATA GGGAGATGCT GTCTTCACAA AACAATTAAA
50941 AAATAAAAT AGTCAGGTGT GGTGGCACAC ACTTGTGGTC CCAGCCACTC AGGAGGTTGG
51001 GAAGATCACT TAAGCCTGGG ACATTGAGGC TGTAGTCAGC CATGATAGTG CTAATGCACA
51061 CCAGTCTAGG TGACAGAATG AGACCCTGTC TCCAAAAAAA GAGCTGTATC CACATCCCAG
51121 GAAAGTGGTT GAAGATCTAC TTTTCTCTGT AAACCTAATA AAGAATAGAG TGACAAATGT
51181 GTGTTGTGGA AAGAAATGGG GTGAGAGCTA CGTAGATGCA AAACAATACA TCCCCACATA
51241 CCACTTGTTA ATCATCCTTT TCCACCCACT TATGGGATGA ATTGCATCTC CCAAAAGAT
51301 ACTCTGTCTT AACCCTCAGT AGCTGTGAAC CTGACCTTAT CTGGAATACG GTGAGTTCAC
51361 TGGTTAAGAA GAGATTATAG TGGAATAGGG TGAGTCCTCC AACCAATGAC TGGGGTCCCTC
51421 ACAGACACAG AGGGATGATG GCCAGGTAGA GATGGAGGCA GAGATTGGAG TTATGCTGCC
51481 ACAAACCAAA CACAGGAAGC TGCTAGAAGT GGAAACAGGC AAGAAAGAAT CCTTCCCCAG
51541 AGGCTACAGA GGGATCTTGG CCCTGATAAT ACCTTGATCT CAACTGGCCT ACGTAACTGT
51601 GAGAGAATAA ATTTCTTTTG TTCTAAGCCA CCCAGTTGAT AGTACTTTGT TACGGACGCC
51661 CTAAGGAAC TGATATACAT TTCTTTTACT GTCATAGAAG TTTTGAATCT TTTAAGTAGG
51721 TCTGTACCCT TCCTCCAGT GTCAACACAT GGAATTCCTC TCCTTGTGCC TTGAAAAGTG
51781 AAAGGTGTTT GAACTGGTAA TGAAAGAAAT CTCAGCATGA GGCCAGATGC TGTACCTCAC

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51841 ACCTGTAATC TCAGCACTTC GGGAGGATGA GGC GGCGCAGA TCACTTGAGG TCAGGAGTTC  
51901 TAGACTACTC TGGCCAACAT GGTGAAACCC CATCTCTACT AAAAACAAAA AATGTTATCC  
51961 TAGCCGGGCA TGGTGCCGTG AGTCCCAGCT ACTCAGGAGG CTGAGGCAGG AGAATTGCTT  
52021 GAACCCGGGA GGTGGAGGTT GCAGTGAAGT GAGATCACGC CACTGCAGTC TAGCCTTGCT  
52081 GAGAGAGCAA GACTTGGTCT TAAAAAAGAG AAAAGAAAAA TGAAATTTCG GCATTATAGA  
52141 ATAAAAATGT TTCCCTTCC CCCCAACTT TAAAAAAGCA GAAGTCTGCA TCATAAAATG  
52201 GTCTTTGCCA ATGTTATTTT TATTATAACA AAGGAATCTT GCAAGGCTAC CAGATCTCAG  
52261 CAATTGTCAC TATGTTCTGT AAAAATCACT TCCTAAAATG TCTGAATTGA CTGCTTGTCT  
52321 CATTTATTTG TTTCTCGTGT CATACTGCAA TGGATATCTG TCTTGTTAGT ATAAATATTT  
52381 GTGCATTTTG TTGTTGTAA AACAGCTTTT TTGGCCTGTC TTCTTCCACC TATGAGGTAA  
52441 TATAAACTC ATGTTTAAACA CTTATTTTGT TAGCAGGACA AGCTACAGAC AAAACCCCTC  
52501 AGACACTGAG TTAAAGAAGG AAGGGCTTTA TTCAGCTGGG AGCTTTGGCA AGACTCACAT  
52561 CTCAAAAAC CGAGCTCCCT GAGTGAGCAA TTCCTGTCCC TTTTAAGGGC TTGCAACTCT  
52621 AAGGGGGTCT GTGTGAGAGG GTCATGATCG ACTGAGCAAG TGGGGGTATG TGACTGGCAG  
52681 CTGCATGCAC CAGTAATCAG AACAGAACAG GGATTTTCAC AGTGTTTTTC CACACAATGT  
52741 CTGGAATCTA TAGATAACAT AACCGGTTAG GTCGGGGGTC AATCTTTAAC CAGACCCAGG  
52801 GTGCAACACC AGGCTGTCTG CCTGTGGATT TCATTTCTGC CTTTTAGCTT TTACTTTTTTC  
52861 TTTCTTTGGA GGCAGAAATT GGGCATAAGA CAATATGAGG GGTGGTCGCC TCACTTATTC  
52921 ACCCCCTTTG AGAATCTCAC TCATTAGTGG GAGTTCTCAC TTTTATTCTC ACTACCTATG  
52981 TCTTCTTGAA AGACAGATTG ATAATGATTG ATATAGTACA CTTGTGCTGA AGCATTTTGG  
53041 TGAGCTAAGG TAGTGATGAA GCTTTTATC ATTTGGAGAA GTACAGGTAG CAAACAAGGA  
53101 AGCAGTAAGC AGGTTTCTAT TAATATTATA ACTCCTATTA TAAGAGTTTT AAATCTTCTT  
53161 AGCACTCGGA ACCATTTTTC AAACATGGCC CCAGAAACAA ATCCATACCA CACCTACATG  
53221 GGCACATGTG CCACCTTTGT CATATTTCTA ACTATGTCTT CAACTACTTG CCCTTAATCA  
53281 TCTATGTGTA GACAGCAATT AGTAAGGTTA AATTTCTTAC AGACCCCTCC TTCAGTTGCT  
53341 AGCAAGTAGT CGAGAGCCAA TCCATTTTGA TAGATAGCAT TTTGCATCTG AGTTTCTTGC  
53401 CAGGCCACAG TAGTCAGGGC TCTGCTGGTC TTATTAGTAA TTATTCTAA GACAGCTTGT  
53461 AACCGTATGA TTCAGTTGAG CATGTAAATG GGGGTCCCAT ATCCCCACAA GCCGTCTTGT  
53521 GCCCAAGTAG CAGGCCCATTA ATATTGTATG ATTCTCTCAG GGGGCCATTC ATTATTTTTTC  
53581 CAATTTTCTA TAGCTATGCT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTGCGG  
53641 GAAGCATATA CAGGGAAGCC CAGGAGTTTG CCTGTCTTTA TGGGCAGTAG GAAGAAAGAT  
53701 GGTTTAGTAG TGTCAATAAC ACAACTACCT GCCCACTGGT CAGGTAATTT GGCATAAGCT  
53761 GTATGCCAC ATATCCAGTA TAATCCAGTG GGGGCTGTCC AGTCCCGGTG GGACTCTGGG  
53821 TGGGTCCACA CAGTTTGCAA CTTTGGGAAT TTAATAAATA GATTTTCTT AGTGTGGTTT  
53881 GAACTCCACT AGGTGGCTGT TTTTATAGTA CTATTATACA GTTTTGGCCC AAGGCAGCTG  
53941 AGTCTTCCA CAGGAAGGGT GAAGTCCTTC CCCACTTTTG CTATACAGTA TTGTCTAATG  
54001 ATTGAGGCTT TTAGGACCCA GAAGTTATCA GGGTGAGTCT TTTGAGCTGG GAATTTATCA  
54061 GGAAGTGGGT CTGTAGGTAC TAATCTCGT GCTTCCCATG GCCATTGATC TCCCATTACA  
54121 GTTCCTCCAC ATACATACAT AACATGAAGT GACATTGAGA GACTGGGCTA CATGCTCAGC  
54181 TAATTGCAAA AACAAATTTT TTGTTTTTCC TGGAAATTTCT AGTACTGGCA CATTAGTTT  
54241 ATCATAAGAA GGTTTGAAAT ACTGGCTCAG GGGAGCATTT ATAACTTCT CCTCAAACCA  
54301 CCATATTTAC TCAAGGATCC AGTCCAGCCC CAACTATTTT TAAGGTTACA CGATCCCCTT  
54361 TTTTCCAGTG AGAATCAAGG GGGTTGGTTA TTAAGTTTCT TAAGGGGTTA CACTGACCAC  
54421 TGGTACAGGA AGGGCCACTT TTCCCTTTCT GAAGGTGGAC AGGATTCTTT TTATTTTTTA  
54481 ACCAAGTTGC CTAAATGACA CAAGACCAGT ATCTACATTT ATTTCCACGC AGTCTTAATT  
54541 CATGACAAGC GTACTTATTT TCTGCCATAT AGCCTCTTTC CTAATGAACA GAACCACATC  
54601 CTATTTCTAA CTTATTACTA TTAATGACAG CACAGGCATC AAATTTCAAG GTGACTTGT  
54661 TGGGCATTCC TTTTCTTCT GTTTTGGCTA ACACCTTACT CGTATCGTTT ATGAACCCCC  
54721 ACCAGTCTC AGTCTCAAT CTTATTTCAA AAAGTGTGGT CGTGGGAGGC TCAGATGGGT  
54781 CATAACACAC ATCAGGTTGG TCATTTCTTG GGCTACCTAC CTTGTATAGA ATAGCATTAT  
54841 ACAAACAAGT TATTTTGA GA GTCTTTGTAC ACTTATAATA ACCATAAAAT AATAAGACTG  
54901 TAGCAACTTT TTGTCCTACC TCAGTGACTT GATGTATACA CTGGGAACAG CCCTCAGTCT  
54961 GAGGAAGGTT AGTTGAAGTC TTTACTGTGC AAGTCCAAAT TTTAAGGAAA ATGAGTCCCT  
55021 TGATGAGTTT TCTCATGTTT CGGCCATGCA TGGACCAGTC AGCTTCCGGG TGTGACTGGA

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55081 GCAGGGCTTG TTGTCTTCTT CAGTCACCTT GCAGGCGTTG GCGAAGCTGC CACGTACAGC
55141 TCACAGTCTA CTGATGTTCA AGGATGGTCT TGGAAAGTTGG GCCCACTAGA ATTAAGTGAG
55201 TCCAATACCT CTAAGTCACT ACTTTCAACT GGGCTTTCTG ATACCAGGAG CAAGGTGGCA
55261 GGTTTTAGGG TGTTGCAAAT TTCAATGGTT ATGCAGGGAT TTTCACATAG CAAACTTTGG
55321 TACTTGGTTA ATCTAGCATT TGTTAGCCAA TGATGTATTT ATTAAAGTCA CCACAGCATG
55381 GAGGGCCTTT AAGTTTAGGT TTTGTCCAAG AGTTAGCTTA TCTGCCTCTT GTGCTAGCAG
55441 GGCTGTTGCT GCCAAGGCTC TTAAGCATGG AGGCCAAGCC TTAGAACTC CATCTAGTTG
55501 TTTGGAGGCC CAGCCTCGGC CAGGGCCCCA CAGTCTGGGT CAAAAGTCCA ACCGCCATTT
55561 TTTCTCTTTC TGACACATAG AGTGTAAGG GTTTTGTCTG GTCAGGTAGC CCCAGGGCTG
55621 GGGCCGACAT GAGTTTTTCT TTTAACTCAT GAAAACTCA TTGCTGTTGG TTGTAATAGA
55681 TGTAATTTAT CCAATCTACA TTTTATTAA CTGTCACCCA CCAAAATATT GACTCAAATC
55741 CTGCAGCTAT TTGATTTTGG GATTTAAATG GATCTGCTAT TCCCTGTGGG ACTCCAATTG
55801 CATCTAAATA GATGTGAGAG TTGAAAGACA CATAAGGGTC TTCTCTTGGT TTACGATGTC
55861 TTATTTTCTC TCCCTCTGGT TGATGAAATG CTAGGGTGAA AGGGATAGCC AATTGGACTA
55921 AAGTACAAGT GCCGCTCCAG TTATTTGGCA GAGTGCCCAG TAAAGGTCCA CCACAATACC
55981 ACCACACATC CGCTTGGGGA TGAACAAAGG CTGACTGATT GAGAAGCTCC TGAAAATTCT
56041 TAAGCTCACT GCATCCCTTC AGGTCTCCAA GGAATGCTAA GTTTCCTCCC TGTCATGAGA
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56161 CAGGGTGCTG GACTTTGGGA TATAGCAGAG AGAGCTTGGC ACGACTTATT ACTCCAGGCT
56221 GTAGAATCCT GGAACACAGT TACCATGCAG CCCATGCCTG GTCACACAGG GGACCACCTT
56281 AGTGGAAAGG GGATAATCTG GCCCTCTGGC CTGCCATGTG CACAAGCATA ACAATTGGTT
56341 TTGTTTAATG TGTGGACAGA ATATTTGATC CATTCCAAGT GGGCATTTGC ATCTTGGTAT
56401 CCTGCTTAAT TATCAAAGTT TGTTTAAAGT CTTTAACTTC TATGACCTTC TAGTAAATG
56461 AATGTATGAT TTTAGGAAAT TACAAAAACC GGTGGGGGCA GTCCATCCTT GCTCTTTAGT
56521 GGTCCACACA ACATTGACC AACTATGGCA TAAAAGCTCT ACATCGGGGG GCAAGACTCC
56581 TCGTTGACAC TGGGGTCTTT ATTGAAATCT CTCTGGAATA AATGGTCTCA GTTTACTAAG
56641 GCTCAGTCTG AGGAGAGTCA GGAGGGACAG AGGTACTTTT CTGAAGTACA GAGATGTCTT
56701 CGACTTGGCA AGTCCCCACA GGGTATAACA AGGCAAGCAT TAAATCAAT AGTTTGAGGC
56761 AAAATTGACT TGGTTATGTT AATAACTAGA TGGTCAGAAA TAGAGTGAGG GAAGAAGAAA
56821 GAGTAAATAGA ATAGATGAAG GAGTTAAAT TTTCTTAGCT TTAGTTTGGT AGGGTTTTCC
56881 CCTGGGACTA TGGCCCATGA CTCTGGAGGG GGTGGCACTT TCTTGACTCG GGTGTGATGA
56941 GTCCATCCCT TTTTCACCGT ATGAACAACA GTCTCGGTGG TTAGCAGCAC AAGGTAGGGT
57001 CCTTCCTAGG CTGGCTCAAG TTTTCCTTCT TTCCACCCTT TGATGAGAAC ATGATCTTCA
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57541 TCACAGAAAA ACTGTATGAT ACCCCTTAAC TTTAGCCAAT ATGTTTAGAC ACAGAATTTT
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58081 CAAGATTAGA AGTTACTATA ATACATGTTA CACTGTTAAC TTTTAGCAAA CTTTACTTTT
58141 GTTGAAGAAC TTGTAAAGTT GGGATTTCOA TTATCCTTTG CTATTAATAA GACCTTATTT
58201 AGTCCAAAT AACTTAGAAT TGGTATAGAT GGCTTTTTTT TTTTTTAAAT TACCTGGGAG
58261 GAACCATCTA TCCTCCTGTC CTGAAGGGAG TTCCTCCTAG GTCTGGTCTG AGCTTTGTAT

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58321 GGTAATTAAG ATTTAGATCC CCTGTTAGGA AACCTGCCGG GTTAAGAGAA TTTTCAGTGG  
58381 TTAATGTAA ATCATCTTCT TTTTCTTTT TTCCTTAGGA TACTTCTGAA CCGGTGAGGT  
58441 GTGCTCAAA TGAGGTTTCC TGTAAGAGTT ATTTTTTTAC TTTCTTCTGT TAGCAAAGCA  
58501 GTTGCCGCTA CAGATTGAAT GCATTTGGGC CATCCGCGGG TTAAGGTTT AAGGATTTT  
58561 GATAGGAAGG CCTTAATGCT TTTGGAATAT GCCCTGACAA CAAAGTGCCA GTTCCTTCCC  
58621 GGTGTTTCA GCCTGCGTTG ATCCTCCACG AGGCGCTGCC ACGTGCTGCT CTGGTGAGGC  
58681 GTTCCACCGG GGCAATTGCC TACCTGGGAG CGCTCTCCAG ATCTGTGTCT CTCAAAGTGG  
58741 CTGGAGTTCC CCGTAGGGAT GCTCCACAGG GCAGGCCTAA GTCGCCTAAG GGGCTGCCTT  
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58861 CCTTTTAAGG GCTTACAACCT CTAAGGGGGT CTGCATGAGA GGGTCGTGAT TGATTGAGCA  
58921 AGCAGCGGGT ACGTGACTGG GGCTGCATGC ATCAGTAATC AGAACAGAAC AGAACAGCAC  
58981 AGGGATTTTC ACAATGCTTT TCCATACAA GTCTGGAATC TATAGATAAC ATAACCTGTT  
59041 AGGTCAAAGG TCGATCTTTA ACCAGACCCA GGGTGCGGTG CCGGGCTGTT TGCCTGTGGA  
59101 TTTCAATTTCT CCCTTTTAAT TTTTACTTTT TCTTCTTTG GAGGCAGAAA TTGGGCATAA  
59161 GACAAATATGA GGGGTGGTCT CCTCCCTTAA TTTAAACAAA ATTTTCAAAG TCCTACCCCA  
59221 AGTAAATTGG CAAATATTAA TAAAGTTATG GCATAGAAAA TAAAAATGAT TGTAAGAGGC  
59281 GTAAAGATAT TTCTGTGGGG AAAACATTTG TTCATTAGTT ATCAGTTAAA ATTCTGTGAA  
59341 AAATAACCAC TAGAGACCTT AAAGTACCCA GGGGCTAATA ATAAGAAGGG AGGAACACCC  
59401 TCTCACTCCC CACCGTTACC TGCCACAGAG GGAAGAGGAA GAGGGTGACT CCAGGAGAGC  
59461 TGTGGTCTCC CCTCCCCATA TGTCCACATA TACCTGACCT CCCCTCCCCA AAATATATAC  
59521 CCAATATCTC TCCCATATAT ACATATTTAT CTGACCTCTC CACATATGTA TACCTAAACT  
59581 TTCTCTATAT ATCCACATAT ACCTAACCTC CTCACACACA TATAGCTGAC CTCCAGTGGA  
59641 GGAAAAATGGG GAAGAGAGAA GAGATTATCA AAGGATAAAT CTAGGTCATA CTCAGAAATG  
59701 TGAAAAACAA AAACACACA CAGAAAAAAA AAACACACAC AAAAAAGAAA TTGATAAATT  
59761 TGTTTGTGTC AAAATTAAGA ATTCCGGTTC AATGAAGGAT CCCATGGATA AAGTTAAGAC  
59821 ACTGCTGTAA GGATGGTAGA GAATTAATG TCTGAATCAG ACGAAAGGAT GAGTAATTAG  
59881 AATGCACAAG GCCAAGAAGA ACAAACAGA AACTCCACAT AAAAAATGTA TGAGGCCGGG  
59941 CGCGGTGGCT CATGCCAGTA ATCCAGCGC TTTGGGAGGC CAGGGCGGGC CGATCAGGAG  
60001 TTTGAGACCA GGCTGGCCAA CATTGTGAAA CCCCATCTCT AAAAAAATA CAAAAATTA  
60061 GCGGGGCGTG GTGGTGGGTG CCTATAATCC CAGCTACTTG GGAGGCTGAG GCAGGAGAA  
60121 CACTTAAACT CAGGAGGCAG AGGTTGCAGT GAGCTGAGAT CACACCATTG CACTCCAGCC  
60181 TGGGTGACAG TGTGAGACTC TGTTCAAAA AAAAAAATA TTATATATAT ATATATATAT  
60241 ATATATATAT ATATATATAT ATATGAAATA AATGAACAAG AAATTTAGAT ACAGGAAAT  
60301 CCAAAGCACT TGGTAATGAA AGAAGGTAA AGTGATGTGT CCTTTTGCAT TTAAGAGAGA  
60361 GCATTAACAA ATTAGAGAGC TGAATAATGC TCAGTATTGG TGTGGATATG GAGACTCAGG  
60421 AATCCTCATA CACTGCTGAT GGGAGTGCC ACTCCCTGGG AATATTTTCC AAATATCATC  
60481 TCAACATAT CCCATAAAGG TGACAGGAAA GTGTGGGCTG ACTGATATCC TTCCTGAGA  
60541 GAGGTGGAGG TAAATGAAG TCACTGCACA ATATAGAGTT GGAAGCAATG GATTAGATGT  
60601 CCACATAGTT ACGTGAAGA ATCCGTAAGA TACACACACA CACACACACA CACACACACC  
60661 TTTGTGTATA TTGTTCTTGG CAGGTAGGCA TGGAGGTTTA GAGGCTTTCT ACATCACACC  
60721 TACTGCACAC AGTAAATGGC CAGGCTGAGC ACTGACTTCC ATGAAGGGAG ATTGAAGGTA  
60781 AGAGATTGAA GATTGTTCCC TGCTCTGGGA CCCTGCAACT GAATATGCAG AAAAAAGTAC  
60841 ACCCGCCAC CCCGCTTCCC ATCTTTCCTA CCTGATTAGA ATAGCTTTTT CAGAAAACGT  
60901 TGGCCAGGGG TTGTGGCTCA CACCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCGGGCAG  
60961 ATCATCTGAG GTCAGAAAGT CCAGACCAGC CTGGCCAACA TGGCGAAACC CCATCTCTAC  
61021 TAAAAATATA AAAAATTAGC AGGGCATGGT GGCACACACC TGTCTATCCA GCTACTCGGG  
61081 AGCCTGAGGC AGGAGACTCA CTTGAAGCAC AGTGATGGAG GTTGAAGTTA GCTGAGATCT  
61141 TGCCACTGCA CTCCAGCCTG GGCAACAGAG TGACACTTTG TCTCAACAAC AACACAAAAA  
61201 CCCACAAAA CTTTAAATCT ACCTATGGCC AAATGCCTGC TAAATGAGC ACCCAAGAGG  
61261 CAGTGTTTCA GAAAGTCAGA TGAATACCTT AAAATTAGAT GCAATGTTGG CTGGTCACAG  
61321 TGGCTCAGGC CCTGTAATCC CAATCCTTCT TGGGAGGCCG AGGCGACAGA TCGCTTAAGC  
61381 TCAGGAGATC GAGACCAGTC TGGACAACAT GGTGAGACCG TGTCTCTACA AAAACGTACA  
61441 AAAATGAGCT GGGAGTGGTG GCGCGCACCT GTAGTCCAG CTACTCAGGA AGCTGAGGTG  
61501 GGAGGATCTC TTGAACCCAG AAGGCGGAGA CTGCAGTGAG CAGAGATCAT GCCACTACAC

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61561 CCCAGCCTGG ATGATAGAGC CAGACCCCCA TCTCCAGAAA AAAAAAATAA AGAGAGAGAG  
61621 AGATGCAATA TTTAGGGTTC AACAAGACTG AATTTCTGAC TCCTTTCCCT ACCTCTCCAG  
61681 CATGTTAGAT TCTGGGTCTT TCATCCTAAC CCCCTGTTCA TGCCATAGCC ACCCTGTGGT  
61741 ACCAACTTTG GAAGCCTGGA TCTTCATCCC CTCATGATAA TGAGTGTCCC ATCAGGTCTC  
61801 CATGCTCAGC TTGGCAAGAG TATCTGTCTT CTCCTCATGG GACGGTCACA TTCACCCAGC  
61861 ACTGACAGGT TCCATTCCCA CTAGGGTGGC ACCCTATATG GTCTGAGTCC AGGCCTTCCT  
61921 GGTCCCTCAG TAATCTCAGC ATGGTAGCAC AATCGAAAAG GGCTAGGCAC GGCAGCACCA  
61981 TTTCCCAACA AGAGGTCTGA TGGCTCATCA CATAGACTGA AGGAGATTCT GAAGAGCAGA  
62041 GGTGGAATGA AGAATGAATC GTGGGCTCTG CTCTTCCTAG GCCTGTCTTC CTCTCTCCCG  
62101 AGATGTTAGC TAACTCATGA GAGCCAGAAA CCAACTGCAG GCTGGCCTCA GGCACCTAGG  
62161 TAGTGCTTCA GCCTCAGCAG TCCACATTCT AGGAACCCTC ATAATATGGG TTGAAGTATG  
62221 CATTCCCACA AAAATAAAGT TGTGTAAGTC CTAACCACCA GTACTGAAAT GGGAAAAGTT  
62281 CCCTTGTCCT GCTCGCATGG CATGTGATAG GAGTGTGGCT AATTTCTTCA GTGCCTGGCT  
62341 GCTCAAACCT CTAGGGGAAC ATTAAGACGG GCAGGTTGTG GGTCTCCAAC CCCATGACCC  
62401 CACCACAGTG TCTAGGGTTG AATGTTTACA GCTCCTGAAG CCACAGTGGG TGTGTGTTAC  
62461 AGGGTGCTCT TTTAGTTTGG CCATTTATAG GCAGCTGGTG TTAACCAACT CAATTAGACC  
62521 GTCTACCTTG TCCCAAGGAC AGAAGAAGGC TTTCTGTATC CCAGGTTCTT GCCTTGGTGT  
62581 ACCGGAATAA ATCAGACCAC ACCTGGGCTT AGAGAAAGAG TGCAAGGTTT TATTAAGTGG  
62641 AGGTAGCTCT CAGCAGTTGG GCAAAGCCAA AAGTGGATGG AGTGGGAAAG TTTTCCCTTG  
62701 GAGTCAGCCA CTCAGTGGCC CAGGCTCTCC TCCAACCACC CCAGTCAAAT TCCGCCTCAT  
62761 TTTGCCAGGC AAACGTTTGT TGTGTGCTCT TCTGCCAGTG TGCTCCCTG GACGTCCAGC  
62821 TATTGCTGTC TTGTGGCAGG CCAGGGGAGG TCTTGGGAAA TGCAACATT GGGCAGGAAA  
62881 ACAAAAATGC CTGTCTCAC CGTGGTCCCT GGGCACAGGC CTGGGGGTGG AGCCCTAGCC  
62941 GGGGACCAGC CCCTTCCCTT CCCCCTTCC ATATCATTTA AAGGGACCAT GCCCTTCCCT  
63001 TCCCAGCACT TTCCCTCTCC TGTATCAGGA CCTGTGAATG TGGCCTTATT TGGAAATAGG  
63061 GTCTTTGCAC TTCATCAGTT AAGATAAGAG TGGGCTCTAA CCCAACATAA AGGGTGTCTT  
63121 TATAAAAAGG AGAAATGTCA TACACAGAGA CTGACACCTA TAGAGAGAAA ATGTGGTGAG  
63181 TAGACACAGG GAGAAATCACC ATTCAAGTCA AGCAATGAGT CTGGGGATAC CAGAAGCTGG  
63241 GAGAGAAACC TGGAACAGAT TATCCCTCAT TGCCTTCAGA AGGAATCAAA CCTGATGATA  
63301 CTTTGATTTT AGACTTCCAG CTTCAGGAC TGTGTGACGA TAAATATCTG TTGTTAAGCC  
63361 AACGAGTTTG AGGTACTTTG TTA CTGTCAGC CCCAGAAAAC TAATACAGTA GGTACTATGG  
63421 ACTGAATTGA CTCCCCGTCG CAAAATTCAT ATGTTGAAAC CCTAACCCCT AGTGTGATGG  
63481 TACTTGGAGC TGGGGCGTTT GGGAGTTCAT TATATTAGA CAACTCATC AGGATGTGTC  
63541 TCTCATGATG AAATTCATGC CCTTATTAAA AGAGACAACA GGCCAGGTGC AGTGCTCAT  
63601 GCCTGTAATC CCAGCACTTT GGGAGGCTGA GGTGGATGGA TCACCTGAGG TTGGGATTTT  
63661 GAGACCAGCC TGGCCAACAT GGTAAAACCC CATGTCTACT AAAAAATCAA AATTGGCCA  
63721 GGTGTGGTGG TGCACGCTTG TACTCCCAGC TACCTGGGAG GCTGAGGCAG GAGAAATCCCT  
63781 TGAAACCAGG AGGTGGAAGT TGCACTGAGA TCACACCACT GTACTCTAGC CTGGGTGATA  
63841 GAGACTCCAT CTCAAAAAA AAAAAAATAA AGACAATAGA GCCAGGTGCT GCAGCTGATG  
63901 CCTGTAATTC CAACACTATG AGAGGCTGAA GCAGGAGGCT CGCTTTAGCC CAGGAGTTCA  
63961 AGACCAGCTT GGACAAAATA GTGAGACCCC CAACTTCTAA AAATTTAAAA AATGAACTGG  
64021 GTGTGGTGGT ACACATCTGA GGCTCCAGCT ACTCTGGAGG CTGAGGTGGG AGGATTGCTT  
64081 GAGCCCAGGA GGAGGCTGCA GTGAGCCATT GCTGTCCAGC CTGGGCTACA CGAGAACCTG  
64141 TCTCGGGAAA AGGAGAAAAC AGTGAGACCT CTTTTTCTCT CTTCTTCTC TCCACTGCCT  
64201 AAGCCCTACA AGCACAAAAA GGACACCACA TGAGCACATA GTGAGAATGC TGCTGCCACC  
64261 AACAAAGTCAG GAAGAGAGCG TTCACCTAGA AACTGAATTG GCCAGCACCT GGATCTTGGA  
64321 CTTCTGAGCT TCCAGAACTG TGAGAAAGTT ATTTTTTTTT TAGCGACTAA GTCTATAGTA  
64381 TTTTATTACA GCAGCTCAAG GTAACATAA TAGTAGAAGG GATGAATTAT GGAGATCACA  
64441 AGTCCACGCC TCCAGAAAAA GACTTCCCTA AAAATTAGTC TGAGCAAAAT TCGAATGATG  
64501 AATTATTTTT AAGAATTTTT AAGGGATCTG ACAAGTTTGC AAGAGCTAGA GAATGCTTTA  
64561 CAACGTGATA ATAGAATGCT CTGTGATGAC AGAAATCTTT CCACACTGTT CAAACTAGC  
64621 TACTGGCCAC TTGTGACTAT TGTGCACTTG AAATGTGACT GGTGTCTGAG GAGCAGAATG  
64681 TTTAATTTTA CTTAATTTTA ATTCATTACA ATAGCTACAT GTAGCTAGGG GCTACTGGAT  
64741 TGAACAGCAC AGCTCGAGTC TTTTAGAGGG AGACAGGACT CACCAAGATG GATGCTGGTG

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64801   GCCAAGCAGC AATGGCAGGT AGTACACACA CAAGAGGCAG ATGATACAAC ACATCCTTCC
64861   CAAACCTGGA GATAAGCTCA CCCCAACAATC CCGCCGCTGA AATAGAGTTG ATGTTACCAA
64921   TGTGCATTTT TATGTCCTTT TCCATACAGA AAGATCATTC AGCAAGTACT ATGGTACTTA
64981   AAAACAACA TCAATTCAT TATTATGACA AAATTAAATT AATAGCTCTT CCTTAACTT
65041   TTAAATTCAA TTTACAATGC TTACTATTGG CATTTATTAA TCTACCAATT TTTTCCCAT
65101   GAACCCATAG AACAAATAAT CTACCAAATT TTTAACATT CATTTTGGCA AGGCTTTTGC
65161   AATTTGACGA ACTTTAAGAA GAAAACCTTAT AAATTGCAAT TTTTAAATCT GACATACTGG
65221   ACTTTTAAAG TATCCAATTG ACTAATGAAC AAAACTGCTC CAAATTTTTT AATTCTTAAA
65281   AATCTTAAGA CAATACTTAA TATGGCAAAT CTTAACTTCT TAAACTTTGT AAGAATGCTA
65341   ATCAACTTAG ATTGGTATAA AGTTGAGTTA AAAATCACAG GATACATCAT CTCAGCTATA
65401   AGTTTTTCATG AGTTGAGTTT TTACAATCAC TTGAAATGCT TAGAATAGGA AATACGTATA
65461   AATTATTTAA CATAAAATAT TGTTACAAA CCTCTGGAGT GTCAGTTTCT CTGGCCAGAC
65521   TTTATGCTGC AGCACCTTTG CCTGAGTTCT TGTCTGTCAT CCAGGAAGAA TTAGGTACAG
65581   AGGCAAGAGT CAAGAAGATT AGTTTCCAA TAGTTCAGCT CACCTAGTTA ACTCCTGTTT
65641   ACAATCTTCA AAGTTATCAG AAACCTGCAA TTGAGGGTTA TAATCCATT TTTGCAGAGT
65701   TTCAAAACAA GACAACATTT GTCTATGAAT GTTAAATGT CCTAGGGTAG TCACAGTCAA
65761   AAACACAATT GACAAAGAAA TTTAGTCACC TCTGTGATTT ACAATAGCCT AACACAATA
65821   CTCTAATTAT AACTGATGAC ACAAACCTCAG ATATCAGAAC TCTAGAAATC CCCTATAATT
65881   TTGGAACACA CATTCACAGT TTTCACTGAA ATATGACCTG AAGATCAAAT ATCACCTTAT
65941   TTCAACAATC CTATATAACT AAACGTGTCA AATGATCCTG TTTACCTCTC CTTTGATAC
66001   TCCAGGGGCC CTCTGTAGCA TCCAAAAGTT AGGGGTTAGC AAAGACAATT TTGAAGCTGT
66061   AAAGGCTCAA AACACTTAAT GAACCTCTAG TCATATCTGT TCTCTACTCA CTAAATGCTA
66121   GTAGCACCTC TCAGTTGTGG CTAAGCTGGG AGGATCTCTT GAGCCTAGAA GTTTGGGGAC
66181   GCAGTGAGCT ATGATTATGC CACTGCATC CAGCCTGGGC AACCAATGCT AATCCTGTCT
66241   CAAAAACAAA AACAAAAAAC AAATTGCCTA TGCTGTGGTT ATCTCACAAT TAATAAAAAG
66301   GAAAAAATAA GTATGCAGTC TTTGTAGGTC CTTGGGGTTT GTTGGAACTC AGAAAAAAT
66361   ACCCCAAAAT AAAGACCGCA GAAGCCAAAG TTTTCTCTG ATCTTCTCCT GCCCTCCTGT
66421   CTCTGAGTCC CATCTCCTCC GGAGTCTAGC CATAGAAATG AGAATTCCTC TTCCTCAAGT
66481   TAGGTCATAG AAATCAAAAC ACCTTTTCCC CAGAGCCCAG CCATAAAACC TAAAAATATT
66541   ACTCTAATT TCCCTCTGTT TTTCTGTGTA AAAACTGGCC ATAAAGAAAT TATCTGAAGT
66601   ACCTTATTTG ATCATAGATC ACCAGACCGC ATTCCAGAGA GGATCCAGAA GGAAGGAATG
66661   CTGCACAGAG AGGCGAAGAA GAATCTAGC AGACAGGCCT TGCTGGGTTT CCCTACTCTG
66721   TTTATTAGCA ATCCTATTTT TACACGGCG CCCATACTTT GTTGAATCTA AAAAATAAAA
66781   ATGGACAATT TCCCCTGTAC ATGTTAATAC ACATTAATAA ATTGGATATA AATTGGATAA
66841   TTTATTAATA TACACATTAA TAAATTGGAT GCAGCCGGGT GCAATGGCTC ACGCCTGTAA
66901   TCCCAGCACT TTGGGAGCTG AGGCGGGCAG ACCACGAGGT CAAGACCACC CTAGCCGAAA
66961   TGGTGAAACC CCGTCTCTAT TAAAAATACA AAAGTTAGCT GGGCGTGGTG GCACATGCCT
67021   GTAGTCCCAG CTAAGGCGGA GGCTGAGGCA GGAGAATTGC TTGAAGTCCG GAGGCGGAGG
67081   TTGCAGTGAG CCGAGATTGC GCCACTGCAC TCCAGCCTGG TGACAGAGTG AGACTCCGTC
67141   TAAAAATAAT AATAATAATA ATAATAATAA TAATAATAAT AATAAATTGG ATGCATTTTA
67201   TCCTATTAAT CTTCCTCTTG TCGGTGGTTT TCAGCGACTC TTCAGAGGCC AAAGAGTAAG
67261   TTTTCCCTTA GCCCTACAG GTTCTTATGT TTAATTTGTT ACTCTCATTT AAGACATAAT
67321   TAAAGTGGCT TCTCCATGAA GATTATTTCT GCATCCATTA TTTGGTAAGA TTGGCCGTTT
67381   TCTCCTTTGA TCTCTACTTC AACTGACCC ACATAAAACA TCACTGCCTG TTTTTTGTGTT
67441   GTTGTGTTT GGAGACGGAG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG TGGTGTGATC
67501   TCCGCTCACT GCAAGCTCCG CCTCCCGGAT TCACGCCATT CTCCTGCCTC AGCCTCCTGA
67561   GCAGCTGGGA CTACAGGCAC CCACCACCA GCGCGGCTAA TTTTGTATT TTTAGTAGAT
67621   ACGGGGTTTC ACTTTGTTAA CCAGGATGGT CTCGATCTCC TGACCTCGTG ATCGGCCCCG
67681   CTCAGCCTCC CAAAGTGCTG GGATTACAG AGTGAGCCAC TGCGGCCGGC CCCGTTTTTT
67741   TTTTGGGTTT TTGCATGTCT TCTCCCTTTT ACTGTAAACT ATTTCCACTA CCAAGCTAGT
67801   TATCATTTCT ACTGCTTAAT AATTGTTTTT GGGAAAGTGAA TGCATCAACC CACATGAATT
67861   TCTTGTCTAT TTGACAATTT ATTCTCTTTA GGAATAGTAT TAACTCCTAA GGTCTGGGA
67921   GCCAGTCTCT GTACTTGGCT GCTCCAGGGT CCTACTTCAG TTTCCAGCT TCTCAGTACT
67981   GTCAGTGTCA ATTGTGGGTA ATAATTATTT TTGTCCACCA AAAGACTCTG TATGTGAATG

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68041 AGTTTTGAAA TCTGCTGAGT AATACAGTGT CAACCCAGTT AATGATTTGC CGGGCGGCTT
68101 GATCAGGGGC TGTCCAAC TA CCGGCATTTT GATTTGGAGC GTCATCTAGT GTCTGAAAGC
68161 ACAAACAACA TCCTACATTG TAAATGCCTT TGGCTACAGA GATTGAAACC AAAGCAAACC
68221 TATGTTTTGA ATTGTTATTC TTCAGCAGTT CTGCTAGCTT TGAAAAATCT AAAAGTTAAA
68281 AAAAAGCTTT ATATTTTCATT TTCTGCCTAA ACTCTTTAAA ATTGCTAGTT GACAATTAGA
68341 TATTTTCAAT TTAATGAAAT TTTTTTTTAG TTCACAGATT AATACACAAT GGGGGAGGGT
68401 TCTTATCTG TTGGACTTTT ACATAACCTC CACTTTAGTG CAGTCTGCTT TATGGGGTCT
68461 TGTTTGAGGT GTGTGTGTGT TTAAGGGAAT GTGGTTTACA ATCAAAATAT TGGGTTGCTC
68521 TTAGGCACAT TGTAAGTCA CACACCTGTA TTCTTATTGA TACATAATGA TTAATAACAT
68581 TATTATTACA GCCTGATCAC CATCATTATT GATATATCTA AATAATGAAT TTTATAATTT
68641 TGCTTCCTGT CAGGCAAGAG CCAATTTTCAG TGCTACCATG TTTGTATAGC AGTATTTATG
68701 TCTGTCATCC TCAGTCATTT TACTTCACTT GTTCTTAGCC AAACGGCCGA GAAGCGATGG
68761 TCATTTTACT TCAAAAATGA AAAGAATTAA TATTTTACG TTTCCCTTAA AGACCCTATG
68821 TTTAACCTCC ACTCCTGGGT AAAATGGTCT AGTCCCTCCT TTTTCATATCA TCTCTGATAT
68881 CTTTTGCACA GCCACTATTA CCTACCGTTT TCTAGATCCC TATTCTTCAA ACACCACCAT
68941 GAAGGTAGAG CCTGTCTGAA TTATTTTCTT GTCCCCGAA CTCAGTACAT TGTGAGGCTT
69001 CTTGAAGATG TTGATCAGTT GTTTGTGGAG TGAATGAATC AGCTAGCATG ATTTTCTTAG
69061 ACCACTGAGA CAAGTGTCTA AGACACTTGT TCCTTCCCAT GTTCTTGCCT GCCTGTGCAA
69121 TCCATGCAGT CTCATGGCTT CCCAGTGCCT CAGAATTATC CCCTGTCAA CAGGCATTAT
69181 AATTTCTGTC CACTGAAAAG GACAAAAAAC TAAGTGTATA GCTAGAAGTT AAAAATTACC
69241 GGCCAGGTAC TGTGGCTCAC TCCTGTATT CCAACATTTT GGGAGGCTGA GCGGGGCGA
69301 TCACCTGAGG TCAGGAATTC GATACCAGGC TGGCTAACAT GCGGACCCCG TCTCTATCAA
69361 AAATGTAATA GTTAGCCAGG TGTGGTGGCT CGCACCTGTG GCCCAGCTA CTCAGGAGGC
69421 TGAGGCAGGA GGATCGTTG AGCCCTGGAG GTTGAGGCTG CAGAAAAATA GGAATATACT
69481 CTCTTCAAG AGTTCGTGGT TTTGACTGCC ACCTAGCGTA CATCAGAAAA ACCCGATGAC
69541 ATAGGAAATG CCTGTGACAG AGGGGTAAGG TGAGAGAGGT TGATGAAGAA TGTATTGAAG
69601 GAGTGAAAC GCTTCCATCC CTCTACTTAC TAAATATATT AGTTAAGTAG TTGGGGCATA
69661 TTTTAATTCA TGCATTTTGT AGATAGAAAA ACAAAAGTTT TATTCTGTTT GATTTAGTTG
69721 ATACTTTAAT ATGTGTGTGT TTAGGATGCA TGATTATATA TCAGTCTGCA GCACTTCTTG
69781 GAGAAGTCTG AATTCCTATT CTCCATTTC TATTGGCAA CGTGAGAATG ATTACAATGG
69841 TGGTTGTCTC ATAGAATGCA GGGAGTCAGA ATGAAAATAG TCCATATAAT GCCTGGTGCA
69901 GAGGAAGGGT TCAGTTAACT GTCTGTATTA ATATTACTGA TAACAGTCAT GACAAACAAA
69961 AGCTTAACAA CAACACCACC AACAACAGTT GCAGAATTGA GCCACCAAT TGCACACAAG
70021 ATTGTAGGTA GGATGTTTTA GAAAAGTTAT TATTTAATAT ATGTATATAT TTTTGTACTT
70081 AAAATATGTC AGAGGTTGTT CTAAGAACTA TTTAAATGTT AACTCCTTAA TCCTCATAAT
70141 GACCCATGAA ACAGGTAGGC TTATTATTGT CTCTTTACAT GTGAGAACAC TGAGACACGA
70201 AAAGGTTTAT TAACTACCCC AAAGTCACAC AGCTGGTAAA ACGGCAAAAT TGAATTTGAA
70261 CTCAGACATT CCAGGTTCCA AGACAGTCTA ATTATTCTTT TGAATAATAT ACTAAGCTGC
70321 CTCTGTATTT TTCCTTGATT ACTTTGTAAA AGTATGAGGA AAATATAAGT GCTTCAAGTA
70381 ACCATGAAAA ATATAACAA TCTATGTATC AACTGAAGCA TAATTACAAA TCCTTTGATA
70441 AGCAAACATA ATAAAAATTT GATATCAATC AAAACTTTCA TGTAAATGTA GCAGGTTGAG
70501 ATGAATTCTA TAGTAAAAAA GTGCAGAGTG CTGGAATACC ATGCTCCTAA TATATTGGCT
70561 AGGCACACCT GCCTGCTATC AAAGGTATGC ACACACCTTG GATACAGAAA GTTGGGACTG
70621 GGTAGTTATG TGAGTGTCTA CAGAATTCTT TCCCCTTGG GAAAGAATTG TCCATCATAA
70681 GCTTGGATGA TGGACAAGGA GTGAGCTCCC AGAACAGTGA TGTGGGGATA CATCCTCACA
70741 TCACAGTGAG AATGAGTGTT CTAGACTGTT TACACACCTA CCACTCCTAA ATGCACACAT
70801 ATAATTGCTT GCACACACAC ACATACACAC TCATCTCTTC TCTGGTGGTC CAGCTCTATC
70861 TCTTATCATT AGGCTTCTTG GGGCTAGTAC CTAGGGCCTG TATCCTTTCA GAGGCAGCTA
70921 AGGGAAGCAC ACATAATTAG AAAGAATGAA CCAGCTTGTT GGATTTGGTC TCTTCGCATC
70981 CAGCCCTCCA AGTTAAGGAG AGTACCATT TTTTAGGGT CACCAAAGGA AAAAAAATA
71041 AAAGAAAGAA ACAGAAGGAT ATCATACAGC AAGGATCTAA TGCAAATATG CCTCAAATGA
71101 GAGGCTACTG TGTGCTGATC CCAATCCCAG GAACTGTATG CACATTATCT AATTTAATCC
71161 TCACTGTATT TCTGGGAGTA TTATTCCCAT TTTACAGAGA AGGAACTTGG CAGGGTAACC
71221 AAGCTCATGA ATGAGAGAAC TGGGATTAAA TATAAAGCTT CCTTGCTCCA GAACTGCTGT

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71281 CTTTCTGCTC TTCCACACTA CCAGCTCAGC TGTGCTCTCT ACATGCAGGC AGTTTTACAA  
71341 GTTTCAGATT AGCCTGGGAC TTCCAGGGTT TTGAATGGGT TAGGGAATGG GGAACTTTTG  
71401 GGTTTACTTT CCATTTTTTC TTCATACATA TGTAATATAT AACATAAATC TATGGTATAT  
71461 ATGATAAATA TATGGCTACA TATGAACAT ATAATCACAT ATATGCATTA TAAATAAATA  
71521 TTAATTTTAT AATATTTTAA AGGTTATCAA ATAAATATTA ATATAAATAA TTAATAAATT  
71581 AATACTCAGC TTTGTTTTCC AAAGTGATAA ATGCCTATAT TTAGCAAAAT ATTTTTTGGA  
71641 GGCCTGATAG TTTTtaggag TGTAAGAAG TCCTGATATC TAAATGTTA AGAACCACATA  
71701 TTTTAGGCTG TTGTCTTCTG TCTTATTTTC CCAGCTAGAC TGGTAAATAC TTGAAGGCAA  
71761 ACGTTTAGCC AGCACATTAA CATTTTATGT TTTTATTCTT TTGTGCTCTC AGTGGCTGTG  
71821 TCTTTTCTAT CGATTTCTCA CACTGTATGA TGGTTATATT TGTCTGTATC TGTCCCACCA  
71881 GGTATAAGTT CTTGAGAGGA CACACTGCTA GGCTGATCTT AGTTTTTATT ATTTCTCCTG  
71941 GTGTCCTGTG CTTAACAAGT GCTCATTAAG TGTGTAAAAA CACAGCACAG TAAAAAACTA  
72001 GACATTAAAA AATAATGTCA ACCAATCTAT TGAAATTTGC ATTTCCATGT TTCTTCCAAT  
72061 ATAGTCATTG TGTCAAGTTA TGTACTTATT CTGATGAAGA CTATTGCCTA ATATACGTTT  
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72181 CATATCCTCA CAATTGACAA ATTCTTATCC TTTGAGGGTA GGTTTGACTT TCTGAAATGC  
72241 TTTGACATCA TTTGAAAGAA GCTTGAAGAA TAAGATAGCT GTTAATGACC CAGTTTCTCA  
72301 TGTCATTAT ACAATTATAA TGGCAATTTT AAAATGTTAG GTAAATATAT TTTGCAATAT  
72361 ATTGTTCTT TTGTAATACT CTCTATGTAT TTATTATAT TTTTAAATTT TATATTTATG  
72421 TATTTATTTT TCTGGACAGA GTCTTGTCTT GTTGCCAGG TTAGAGTGAA GTGTTGTGAT  
72481 CATAGCTCTC TGCAACTTCA AACTGCTTGG CAAAAGTGAT CCTCCTGCCT CAGCCTCATG  
72541 AGTAGAGTAG CGGGAACCTAC AGGCGCATGC CACTGCACCC AGCTAATCAC TATTTATTAT  
72601 GCTCCTACTG TGTGCTTAG TATATTTCT GTTGTCTTCT GCAACCCATT TTGAGGGCGT  
72661 GTTAGGGAAT ACAGATGCAG TAACTTTCGT CTCAGCCCTT GAGGTGAGGA AATATTATTAGC  
72721 CTCAGGTTTA ATCTAATTGT TGGCCATTG CCTTCAAAGA TTGAAATATG AGCAAACTG  
72781 TGGCTCTGGG TTATATGTTA AAAAAAGTT TATGGGGCTG AAGCCAGGCA ACAGACAAGA  
72841 GCCCTACAA TCTTATTTAG GCTGAAAATA TCCTGGAGTC CCTGTATTGT TGGTCTCAAG  
72901 CAGATAGCAA CACTAACCT TACTCTTGA GGCAGGCACT GCCAGTGGG TGGCTGTTAT  
72961 TATTAGCTTC ATTAATTGGT GAGTCAGGAA AAAACAGCTT TAAATCATTC AAAGTCTCTG  
73021 CCTATACAGG ATTTAGTAAT ATTAGGTTAG CTACATCCAA AAGATGACAG AACCTACTC  
73081 TAAGGCTGGG CTGGTGGTT CACACCTATA ATCTCAAAC TTTGGGAGGC TGAGGCAGGA  
73141 GGATCACTTG GTGCCAAGAG TTTGAGACCA GCCTGAGCAA CATAGTGAGA CCCCTGTCTC  
73201 TATCAAAAC AAAGAACTCT AATTGGCATA GTAGAAGGAA AAAGTGAAAG AAAAACCCAGC  
73261 TGTCACCCTC ATTCCTTACA CCTGTCTTAA CAACTCCTCT CACTATCCTT TGAATATATC  
73321 TTGGCTGTTT GAGTCTCTCT CTAGCCCAT TACTGCTGTT TGGACTTGAC ATTTTGTCTC  
73381 GCATTTTTAA CTTTTCTACC AGGGTTTCCA GACCTGAAG AGTGTGGCAT GAAACAAAC  
73441 TAGTCAACCT ATAATATTTA TGATGTGTGT GTAAATAAAA GAATACACAA TATATTGCAT  
73501 TACAATATTT TAAGTGCTC CTCAATTTGT TTGTGGCTTT CTTGAGGACA TCAGTTTGG  
73561 GTGGGACGAC CACATCCTTA ATCTGAACCT TCCCTTGGAG GTCATTCTTT TTTTTTGAA  
73621 ATAGAGTCTC GCTCTGTAC CCAGGCTGGA GTGCAGTGCC GCAATCTCAG CTCACGCAA  
73681 CGTCCGCCTC CTGGGTCAA GTGATTCTCC TGCTCAGC TTCCAAGTAG CTGGGATTAC  
73741 AGATGCACGC CACCATGCCG AGCTAATTTT TGTATTTTGA GAAGAGACGG AATTTCAACA  
73801 TGTGGTCTAG GCTGGTCTTA AACTCCTGAC CTCATGATCT GCCCACCTCA GCCTCTTAAA  
73861 GTGCTGGGAT TACAGGCGTG AGCCACCCCG CCCGGCCAGA GGTCAATCTA ATAGACTTTT  
73921 TTTTGTGTTG TGCTCACAGG CTGTGTTCAAT CTTATTTCAA AATTTGAGAA ATACAGTTTC  
73981 CATGGAACAC CAACCAGATA TCAGGTGCT ATGGAGTTGA TAGTCAAAAG CTTTGTATCT  
74041 TCCAGTTTTT CAGAAATGGCT TCTAAAGGTT CTGATTGAGA GCTCTTAGGC GAAATTGAAC  
74101 AACCAAGTGT CAAAGTACAA CATTCAGGAA GTTAAAAACA TGACTGACAT ATATGTACTA  
74161 TATATAGTGA GCTTGTGTAT GTGTCAATGA ATGATTAAAT TCATTAATGA AGGAGGAAGC  
74221 AGAATCACAA TTAGGTCAAA GGAAGATACG GGAGAATAAA ATATGTATTT GGTGAGGAA  
74281 AGGATGTATA CTGGAAGAGG AAGGGAAAAT CAGATATAAA GTTGTTTAAT GACTTATTAG  
74341 GCAATACAAT AATAACTTTT AGGGTCATTT TTTCTATATT AAGAATTCAT TTCCATCTCT  
74401 ATGACAAAAT CCTTATTAAT TTATTAACT TCTACAAGTG AATGTTTACT TTTAGATAGT  
74461 CTGGACCCAA TAAATGTAA ACATTAAGTC AGAGTTACTT TCACGTAGGA CAGTGTGTCT

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74521 CAATAAGGTA CCACTAGCTA CACGTGATCA TTGACCATTG GACTATAGC TAGACTGATT
74581 TAAAATGTTC TAAAAGTGTA AAATACACAC CAGGTTCTGA AGATTATATCA TTTAAAAAAG
74641 AATGTCAACT GTCTTTTTTT TTAGCTTATT TATTATATGT TGAAGTGATA ATAGTTTAGA
74701 TATATTAAGT TAAATAAAAT ATCTTAAAT TAATTTTACT TGTTCCTTTT CATTCCTTCA
74761 ATGTGACCAC TAGAAATCTG GAAAGTATTT ATGTGATTCA CATTCATTTT TACTGTCTAG
74821 TATTGCCTTA CATCATCAGG TACCCCATAA GTAGGCTTTT TAGATAATTC TCTAATATAG
74881 CTTGGAAGGA TATGGAGAAA TATTTTTCG TTGCTTTTAA GTTTTGCATA ACTTTTTCAA
74941 CACACTTTAT AAAGGATCTA GAAAAGGGT GGTACATGT TTCTCTGTCT TCTGGCCTCC
75001 ACCATGTTGC CAGGAGGTTG GGGACAAGAT TCTGGGTGGC TGGATGTCCT AATGGCTTGA
75061 GGTCTGGACT TGAGATTTGC ATATAAAGAG ATGTGATTAG ATTGAGTCGA CTAGAAAAAT
75121 CATATTAGAG AACTGAATCA CAGCGATTAA ATTTACATGT CGATTATATA ACCAGGACAC
75181 CAATTTATAG TGAAAGAAGG TCCAGTTACC TGGTAATCAA GACGTTTCAT AGCTATTTTC
75241 ATGATGGATA TACTTAGCTG AGTTTAAAT GAGAAGGGGG TTCATTGCAC ATAGAATAAG
75301 ATCTAAGTGA AATGTTTATT TTATTTTTT TTTTGTGACA TGGAGTCTTG CTCTGTTGCC
75361 CAGGCTGGAG TGCAATGAGG CAATCTCGGC TTCTGGAGTG CAATGAGGCA ATCTCGGCTT
75421 CTGGAGTGCA ACGAGGCAAT CTCGGCTCAC TGCAACCTCC ACCTCCCGGG TTCAAATGAT
75481 TCTCCTGCCT CAGTTTCCTG AGTAGCTGGG ATTAGAGTTG CCTGCCACCA CGCCAGGCTA
75541 ATTTTTGTAT TTTTTTTAGT AGAGATGGGG TTTCACCATG CTGGCCAGGC TGGTCTCGAA
75601 CTCCTGACCT CAGGCGATCT GCCCGCCTCA GCCTCCCAA GTGCTAGGAT TACAGGCGTG
75661 AGCCACCAAG CCTGGCCTAA GTGACATGTT CTTATATTGT TCCTTTCTTT CTTTTTTTTT
75721 GAGCTAGTGC TCACCCTGTT GCACAGGCTG GAGTGCAGTG GCGTCATTTT GGCTCATTGC
75781 AACCTCTGCT TCCCGGGTTC AAGCGATTCC CTGCTCAG CCTCCTGAGT GCCACCAACC
75841 CCAGCTAATT TTTGTACTTT TAGTAGAGAT GGTGTTTAC CATGTCGGCT AGGCTGATCT
75901 CAAACTCCTG GCCTCAGGTG ATCCGCCCCC GAGTCTCCCA AAGTGCTAGG ATTACAGGCG
75961 TGGGCCACGG GGCCAGCCT TATATTATTT CTTTACTAC AATATATTAG TATGATGCAG
76021 GTGCTTCAAT TGTTTATACA CTTTCCATAA TTTTGTATAA TTCTTATACC CTGTCACTCT
76081 GAGGAATAGC CGGTCTAAGT GTTTTCCAC CACTGCTAAT TCATCCATCA CTAATCTCAT
76141 TAGACTGTTA ATCCCAGAG GACATAAGCA CACAAGCAGA CAATGTTTAC AAATGTTGGA
76201 CAAATGTTAT TTAATAAAC AATGGGGTCA CCCTTAGTCT AAAAGATGTT TCACTTTTCA
76261 TTTGTCAATG AACTCTTATT TGTAGGTTCC CTTTGTGACT TCCCAATC TAAGGCTGTT
76321 CTCTTTAACA CATATTTTCA TGAAACATA TATTTGAGCA GAAATTGTTG GGGAGTTGTA
76381 ATATTACCTT TGTCCTTAAA TATGAATCTA TAATTATATC AAATATATGG GCAGACAATT
76441 TACTTTGCCT TTAATCTCAA GAAAAAATA GCAATTACTT GGGGTCCGAG AGTAAAAATA
76501 GAAGTAGTGA ACCTTAAAGT AGCAAACCTT AGAACAGAAT AGTTTCAGAG GGGATGAGAA
76561 GAGGTGATTT TTCAGCTCAT CAACAACAGA TCTTATAATA AATTACATGT TCTGGTACTT
76621 TTCTTGTCTT TCTGTGTTAA ATTTTGCTAT TTAATAAAT AAATTTCAA TACATTGTTT
76681 ATCTTAAAG TCAAGAGTGT GTTTTATTAA AGTCAGTTGC TTTATTTGCA ACTCAAAGA
76741 TATATTTGAG TTCCCAACTG GAGATTGTCC TATATGGTAA CTTGCGTAAG GTATGGTTAC
76801 TGAAAGTAAC CTACAATTTT CATGGGCTGA AATTCAATTC TATATTGCAG CGTACAAAAA
76861 TAAATAAATA AAAAATGCTT GTTTTCTTTG AAAACATATT ATCTCAGTGC CTCTAACTGC
76921 CAAATCTATT GGCTTTTTTG CAGGCTTAAG GGCTCTCCCT TGTTCCCTTA TGATCTCTAT
76981 CTTGAGGGCC AGACCTCCTG CCTTACACAA CTCAGAGGGG GACCTCAGAG CTCTTTAAAA
77041 AGAGCCCAAT TTCTCGCTG TAGAGAAGTG AAAAGGATGC CCCACCCCA TCTATGAAAA
77101 GAGGGATTG ATAGTTTCAA TGTCTTCAA TCAAAGATTT AAGTCTGTAG CCCCCACCA
77161 CCCCAGACCC TAGCAAGGCT CATGAACCCC CTCCCATCCC GCCCTAATTG CTTTGGACTG
77221 GCCGTGGAAT CCTTGTCCCA GTCCACAGTT CCTGTGCGAC TGCACGAAGA ATTCACAGAG
77281 GACCTGTGTT ACTTCCCTTG TGAAGAAAC GAATTATCAT GAAAATTTAG GTGGAAACCA
77341 TTTGCTTTT TTCTTCAAAA ATAAGGGAAG CATGTGCCCA ACCACCCCTG GGAAAAAGAA
77401 CCTTCAGGGG CAAAGGAGCG AACAGGTAAT TTATAAGAAA AACAGAAAGT GGTCTCTGAC
77461 TGCCCCAGAC TTCCTTCGGA GTTGGGGGAA TTGGGGACGC CTGGACGCGT TGTTTTTTGTG
77521 TTTGTGGAAG AAATAAATGA AGAGCATGAA GCGGAGGCT TCTGAGATCC TTTCTTGACC
77581 AAACCAAGT GATTTGGTGC GGGGAATTTT AATATTTTTC CCCTTTGTG AGGTGGAACA
77641 AACACAACCT GGGAGCAGCG CAGCGGCTCA GAGCCTGCCA GCCAGGCGGG CGACCAGAGC
77701 ACCAATCAGA GCGCGCCTGC GCTCTATATA TACAGCGGCC CTGCCAGGC GCTGCTTCAT

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77761 CGGCGCTTTG CCACTTGTAC CCGAGTTTTT GATTCTCAAC ATGTCCGAGA CTGCTCCTGC  
77821 CGCTCCCGCT GCCGCGCCTC CTGCGGAGAA GGCCCCGTGA AAGAAGAGG CGGCCAAAAA  
77881 GGCTGGGGGT ACGCCTCGTA AGGCGTCTGG TCCCCCGGTG TCAGAGCTCA TCACCAAGGC  
77941 TGTGCCCCGC TCTAAAGAGC GTAGCGGAGT TTCTCTGGCT GCTCTGAAAA AAGCGTTGGC  
78001 TGCCGCCGGC TATGATGTGG AGAAAAACAA CAGCCGTATC AAACCTGGTC TCAAGAGCCT  
78061 GGTGAGCAAG GGCACCTCTG TGCAAAAGAA AGGCACCGGT GCTTCTGGCT CCTTTAAACT  
78121 CAACAAGAAG GCAGCCTCCG GGAAGCCAA GCCCAAGGTT AAAAAGGCGG GCGGAACCAA  
78181 ACCTAAGAAG CCAGTTGGGG CAGCCAAGAA GCCCAAGAAG GCGGCTGGCG GCGCAACTCC  
78241 GAAGAAGAGC GCTAAGAAAA CACCGAAGAA AGCGAAGAAG CCGGCCCGCG CCACTGTAAC  
78301 CAAGAAAGTG GCTAAGAGCC CAAAGAAAGC CAAGGTTGCG AAGCCCAAGA AAGCTGCCAA  
78361 AAGTGCTGCT AAGGCTGTGA AGCCCAAGGC CGCTAAGCCC AAGGTTGTCA AGCCTAAGAA  
78421 GGCGGCGCCC AAGAAGAAAT AGGCGAACGC CTACTTCTAA AACCCAAAAG GCTCTTTTCA  
78481 GAGCCACCAC TGATCTCAAT AAAAGAGCTG GATAATTCTT TACTATCTG CCTTTTCTTG  
78541 TTCTGCCCTG TTACTTAAGG TTAGTCGTAT GGGAGTTACT GAGGTATCAG ACGAATTGGG  
78601 TGACGGGGTT GGAGAGTGGC CGTGGTGAGG TTACAGCATT TAAACCTTTA TTGCGGCTTC  
78661 TAGGTCCCTG ACCGGAGGCT TTTCTCGCTG GCGGATGGTT TTGGGATGGC AGTCCCGCCC  
78721 CAGGCCTGTG AACGGCAGAA AAGACCGCAA AACAAGAGCC AGTTTCTTAG TCTAAAGGGA  
78781 TGTCCGATT GGAATAAAAA ATTTTCAAAA GTCCCGCCCT GCTCCCGGGT TGGTCCGTTT  
78841 TTCTAGTACA TGACTTTCAT TCTGTATTTA ATTGGATGGT GGAAGACGTT GCTTATTCTG  
78901 TGTTTTTTGC TTTACTGTGA CTTAAAGTT TTGCCTCTTT TCTCTTTATA TTAATGTCTG  
78961 GGATTTCCGA CGCTTTCCAT GTTGTGGTA GTCAGTTGA TGTCTCCTGG AGGTAGTGGC  
79021 AACATCCAGC CCTGGGAGGA GAGTGCCTGC AGGTACCTTT GTCCTACATT CCTCTGCTGT  
79081 TAATTCTCA TTCCTGTGGC AACGAAGGAA TGCATTAA AAACAGCCAC AACACGGCA  
79141 ATAGCCCTTC CTCCACCCAA GGCAATCGTG GACCTAGGGA GTTTTTGTG CCACATAACA  
79201 TGTAGCCTTC CGCTAACTG ACAGGTTTGA GCGTATCGAT TTTGAGCGTA TCGAAAGCAC  
79261 AACTTTTAGC CAGCCATTTT GTCCTCGCAT GACTACGGTT GCTTATCCTG TTTAGACAGA  
79321 CAGCAACATT TAAAAATCGA AGTTCCTTTA AACGTATTTT GTTTGGCAGT CCAAATGTTT  
79381 CTATGCAGAA AACAGTATTT GTACTATTAA CTATGAAGAG TGTATGGATA AATGGGAGAC  
79441 ATTTCTAATA AAGGCCTTCG TTAATGGTTC CCTCTGTTTG ACATCCATGG TGCTTCTGAA  
79501 TACAGAAAGC CTAGCGTCTT ATATTCGCTT CTTTTAAAT CTGGTGGGCA CATTTTGGTG  
79561 AGACCTAAAT TATGGGACT GGGGCTTCTG GAGATAAGCT GCTCAATTAT TCTACCATCT  
79621 CCACAATGAT TAATATAGTG AGTTGATTTG TTAGTGATAG TGACCACGGA TTCATCCCAA  
79681 GAAAGAGAAA GGGGAGGGAG GCAAGCAGAG AGACAGGAAG ACAGAGGAG GGAAGAAGGA  
79741 GAAAACATTC TCCCATGGTT TAAGTAATTT TGTGTGTGTA ATTTTACATT ACAACACGGT  
79801 TTAACATGGT GAACCTCTA TTTTGGTGTA AGGTTTAAAC TATGGACATA TTTTCCCAA  
79861 GACCATTTAT GAACTTTCAT TTCTGCTTCC CCCTTCTTCC TCCCGTGCCA CCCTCCACGC  
79921 TCCTATCAAT TTTGCTGTT TTGTCATAGG CTAATACGCT ATAATTTTAT GGACAGTTGG  
79981 ACTGTCTTAG GTTCTCAGG TTTCTATTTT GTTCCCTTAG TCATTTCCAC AATTCTTAAG  
80041 GTAGAATTGT ATTGTTTTAA ACATTGTGTT GTGTGCTATC CTCAATGCTG AGATGATTAT  
80101 GTGACAAATG GCAAGTGTTT AACTAATACC TAAATCTGTA GTATCTTATC AAGCCTAATG  
80161 CTACTTCACA ATGCCTACTC CATTACGCTC ACTTTATCTC ATTACTGGCA TTCTGTCTATC  
80221 TCACATCATC ACAAGTAAAA CGGTAAGCTA TTTTGAGAGA GATCACAGTC ATATAATTTA  
80281 TATTTATATT TATTTATTTA TTTATGAGAC GGAGTTTCCC TCTGTACCC AGGCTGGAGT  
80341 GCTGTGGCAG GTTCTCGGCT CACTGCAACC TCCGCCTCAC GGGTTCAAGC GATTCTCCTG  
80401 CCTCCGCCTC CCGAGTAGCT GAGATTACAG GGGCCTGCCA CCATGCCCCG CTAATTTTGT  
80461 TATTTTTAGT AGAGACGGGG TTTCACTAAG TTGGCCAGGC TGGTCTCGAA CTCCTGACCT  
80521 CAGGTTATCC GCCCACCTCA TCCTGCCAAA GTGCTTAGAT TACAGGCGTG AACCACCGTT  
80581 CACAGACTCA AATCATTTTT ATTACAGTAT ATTGTTATAA TTGTTGTTTT ATTATCAGTT  
80641 ATTGCTAATC TCTTACAGTG CCTGATTTAT AAATTAATTT CATCATTTGC ATGTGTATAT  
80701 AGAAAAAAAC AGTGATATA CGGTTAGTA CTATCTGTGG TTTCAGGCAT CCACTGGGGG  
80761 TGCAGTTTAT TAAACATGCA TTTACATTAG TCTCCCTTTT GGGAGACTAA TTAACCTGAGA  
80821 TGTGTAAACG TGACTTTAAT AGCAGATAGA GCTAATTTTC TCTCATTACT CTTCTTTTTC  
80881 AGAATTTTCC TGGTTATTCC ATTTTATTAT TTTCCATATG TATATTAAGA TCTCTCCAC  
80941 CTCTCTCTGT TTCTCCATCT CAACATCAAA CAATTAAGAA AAAAAAAG GCTGGGCGCG

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81001	GTGGCTCACG	CCTATAATCC	CAGCTCTTTG	GGAGGCCTAG	GCGGGTGGAT	CACGAGGTCA
81061	GGAGTTCAAG	ACCAGCCTCG	CCAAGATGGT	GAAATCCCGT	CTCTACTAAA	AGTATAAAAA
81121	TTAGCCAACC	ATGGTGGCAG	GCGCCTGTAA	TCCCGGCTAC	TCGGGAGGCT	GAGGCAGAGA
81181	ATTGCTTGAA	CCTGGGAGGC	GGAGGTTGCA	GTGAGGCGAG	ACCTTGCACT	CCAGCCTGGG
81241	TGACACAGCG	AGACTCCGTC	ATAAAAAAAA	AAAGCCGGAA	GCAGTGGCTC	ACGCCTGTAA
81301	TTCCAGCACT	TTGGGAGGCT	GAGTCAGGCA	GATTACCTGA	GGTCAGGAGT	TCAGGACCAG
81361	CCTGGCCATG	AAAATACAGC	CTGGCCATGA	AAACACACAA	TAAATTAGCT	GGGCGTGGTG
81421	TCACACACCT	GTAATCCTAG	CTACTCGGGA	GGCTGAGACA	GGAGAATCAC	TTGAACCCAG
81481	GAGGCAGAGG	TTGCAGTGAG	TTAAGATGAC	GCCACTGCAC	TCCATCTGGG	CGACAGAGCC
81541	AGACTCTCTC	TCAAAAAACT	AAATAAATAA	AAATAAAGTT	ATGGTACATT	GAACCTCTGT
81601	GTTCCCTTCT	CCCTTAGATA	CTTTCATGGC	TACCCATTTA	ATTGATGTTT	TTATCATCTC
81661	CAAGAGTTAG	TCAGGAGAGG	AATCAACCCA	AGCAAAAATA	GCTGATTTTC	TAATTTTCCT
81721	TCAATGCCCT	TTGGGGTCTT	AATCCATTTG	ATTTATGTAC	TTTCAATTAA	TCCTAACCTC
81781	GAATGTCTTC	TGCAACATG	TTTCCACAGA	TGAAACTCGT	CAAATGAAAC	ACATTCCTTT
81841	AATTTATAGA	GTTAAAAATT	AGAAAAATTT	TCAATTCTAT	TTGGCCTTTA	GATTCACTCT
81901	TGCATATGTT	TTCTCAATTT	TGTTCTAGCT	CTTTAGTTTT	GTTTTATTCC	ATCACAATTG
81961	TTACATAGC	TTACTGGCTT	AGGTCTAATG	AACCATTTCAT	TTGGAAATTA	AAATTGGCCA
82021	TTTTAAGATG	AAAAAGATTC	TTGCCTCAAT	TTTACTTAGT	TTTTGAAACT	GTCAATGAGG
82081	ACACATGTTT	TTCTGTACTC	TTAGATTCAC	TAAGTAGTGT	CTTGCAAATT	TAAGTGACAA
82141	AGGACAGATT	AACATGCGAA	AAAAAGAGCA	TGCAATTTTA	TTAGTATATT	ACATGCACAG
82201	AGTTCCCAAA	GAAAAAATAA	TTGAAACCTT	AAAAACGCGG	TTAGACTCAC	AGACTTATAC
82261	ACCATTCCAA	CAAAGGAAAG	GGAGTTTGCA	CTTCATGGGA	TGACGAATTT	GGGAATGTGA
82321	CAAGGAAATA	AATACATGGG	CAATAAAAC	CATGGAAGAT	AAAATGAAAG	ATAGAAATAA
82381	TTGTAGTAAG	GTTTGTTTTT	GCAGAGTCAT	CTCAGTGCCA	ACCTTCCATA	TCTAGTGATA
82441	AGAATTGCTC	TCTTTTTCCT	GGTATAGCAG	TTGGGGACAC	TTTTACAAGG	GAAATTTCTG
82501	TCACCTTCAC	AAAGGGAAAT	TTGGGTAAAG	AGAAGACAGA	GACCTCTTCC	TACACCTGTT
82561	GATTTTCAAT	TGCCTTCAGC	TGAAAATAAC	TTTTATGCCA	AAGTAGAATA	ATTTGGGGGT
82621	GACATCCTGA	TATCTTCAA	AACCTATATT	TAATTTTACA	TTAGTAATTA	TATCATTTTT
82681	GATTTTTTAA	TTAGTTTTAT	AAAATAATTT	TGAAAAACGG	TAATAATATT	CAAATAATTC
82741	CAGAAACACT	GCTGATAAGC	CAAAAACATC	AATGAATATT	GCATAAACAA	CTGATAATTC
82801	AACCATGAAA	ATTTATGACA	TTGTTCTTGT	GTGATAAAAC	TATGAGTAAC	ATAAAAACTA
82861	GAGGCTACTT	GTAATGCATT	ATTCCAAACT	TCTGTTTTTT	TATTTATTTA	TTTATTTATT
82921	TTGAGACATA	GTCTCTCTCT	GTCACCCAGG	TTGGAGTGCA	ATGGCGTGAT	CTTGGTTTAC
82981	TGCAGCCTCC	ACTTCCCCGG	TTCGAAGCAAT	TCTCCTGCCT	CAGCCTCCTG	AGTAACTGGG
83041	ATTACAGGCA	CCTGACACCA	AACCCGGCTA	ATTTTTTTGT	ATTTTATAGT	GAGACGGGGT
83101	TTCCGCATGT	TTGCCAGGCT	AGTCTCGAAC	TCTTGACCTC	AGTGATCCAC	CTACCTCGGC
83161	CTCCCAAAGT	GCTAGGATTA	CAGGCGTGAG	CCACCATGCC	CGGCGCATT	TTCCAACTT
83221	TCATACACAG	TGCTATCATG	GCTACAAATT	GAAGTATCAT	ATTATACACT	CCTAGGCAAA
83281	GCTCTGGATA	TTTTGGCTAT	ATAAGCCTGA	GGGAAATGTA	GTAAGGACAT	TGTGGTTGAA
83341	ATTCATACCA	GAGATGAACA	GGCCCAGTGC	AAGACAGAAT	TACATCACTA	AAGGATATCA
83401	GAAGAGAATA	GGGATTTAGG	GTACAGTGCC	AACAACAGTT	TTGGGAACCT	GCATTTTTTG
83461	AGCACTTATT	TACAATATGC	CAAGCACTGT	TGCTGATTAC	TCTATATTTA	TTTTCAAACA
83521	CATTCTTGTC	ACAGCACTTT	GAGATAAGTG	CCATTGTCAT	TCCCATTCCA	GGGTGAAGGA
83581	CTAAAGCTTG	GTGTCATTAA	GGATGTAGCT	AGTTAGCTGT	GTGTGTGTGT	GTGTGTGTGT
83641	GTGCATTTTT	TTTTAAATTT	AAAGTCAATA	AATTTTTTAT	TGAAGAATTT	CACATCAAGG
83701	TAAACTTTGT	TCCTCTAAAG	AGCTGGAGTC	AAAATGTATC	TTCAAAGAT	TCATCTTCAA
83761	GTTAGCCCTT	CTTAATAGAA	CTGATGCTTA	ATCCACAGTT	GTCAGCCAC	AGTTCTTTTA
83821	TTTTGACTTT	TTTTTTTTTT	TTTTTTTGAG	ACGGAGTCTC	TCACTGTCAC	CCAGGCTGCT
83881	GGGCAGTGGC	GTGATCTCGG	CTCGCTGCAA	CCTCTGCCTC	CCGGGTTCAA	GTGATTCTCC
83941	TGCCTCAGCC	TCCTTAGTAG	CTGGGACCAC	AGGCGCATGC	CATCGTGCTC	GGCTAATTTT
84001	TGTATTTTTA	TTAGAGACAG	GTTTTCATA	TGTTGGCCAG	GCTGATCTCA	AACCTCTGAC
84061	CTCATGATCC	GCCTGCCTTG	GCCTCTCAAA	GTGCTGGGAT	TACAGGTGTG	AGCCACTGCA
84121	CCCGGCCCTA	TTTTGCCTTC	TTTAATCTCC	ATTTGAACAT	ACACATACTG	ATGAAAACTA
84181	CAACATTCTT	CACCAAAAAT	CTTTGGGATT	TAATTTCTTC	AACCACTTTA	CTTTGGGGTC

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84241 ATTTTAAGAT TAGGTGTATC TGCCTGGTTC TCAATTTGAC ACCCTTTCTC TCTAAACATG  
84301 AATGAGTTCC AATCATATTT ATTCTTAAGC TATCACACTC AAATATACTA CAGATCTGTG  
84361 GAATATGCCA AAAGTTAAGG TGAAAAATTA AATTATTAGG TATTTCATAG TTTTGCTAGT  
84421 TTTTGATCTG TGAGTGAATA TAACTATCCT CTATGTCCTG GCACTGTTCC TCAGAAACAT  
84481 AGGGTCCACA TATGTAATTT TAAATTTTTT AATAGGCACA TTTTAAAAAG TGAAAAAGA  
84541 AATCTATTTT AATGATTTGA ATCCAGTGTA ACCAAAAATT GTTTCACAA GGTATCTAAT  
84601 ATTAAAAATAT TGAGTTTTTA CTTTGTATT TTTAGATTCT TTTGAAATCT GGTGTGTATT  
84661 TTACACTTAA AGCACATCAC AGTTTGGAGT AGCCACATTT CCAATGCTTA ATACTCACAT  
84721 ATGGTTAGTG GCAACTATCT TGGACAGGAC AGCTTTTATA CTCTGGGAAG ACACAAGCAA  
84781 ATACTTGCTC TGCAGCAGAA TCCAGATGTT TTCCAAGAAA ACACTTTTTC TGACCTGTTC  
84841 CTGAAACCCA GGTAGTGTCT CTAATACTTT ATATTTTATT GGTTTGTCTT ATTGTAACCA  
84901 CCCAACGGGC TCTCCTTGTC CACTTCCTAG ACAGAGCTGA TTTATCAAGA CAGGGGAATT  
84961 GCAATAAGGA GCCAGCGCTA CAGGAGACTA GAGTTTTATT ATTACTCAAA TCAGTCTCCT  
85021 TGAGAATTTG GGGACCAAAG TTTTAAAGGA TAATTTGATT GTAGGGGACC AGTGAGTCGG  
85081 GAGTGCTGCT TGGTTGGGTC AGAGATGAAA TTATAGGGAG CCTAAGCTGT CCTCTGTGTC  
85141 TAAATCAGTT CCTGGGAGTG GTGGGGTGGG GGACTCAAGA CCAGATAATC CAGTTTATCT  
85201 ATATGGGTGG TGCCAGCTAA TCCATTGTGT TCAGGGTCTG CAAAATAGCT CAAGCATGTA  
85261 TCTTAGGTTT TAAAATAGTG ATTTTATCCC CAGGAGCAAT TTGAGGTTTA GAATCTTGTA  
85321 GCTTCCAGCT GCATGACTCC TAAACCATAA TTTATAATCT TGTGGCTAAT TTGTTAGTCC  
85381 TGCAAAAGCA GTCTGGTCCC CAGGCAGGAA AGGGGTTTGT TTCTGAAAGG GCTGTTATTG  
85441 TTTTTGTTTA AAAGCAAAAG TATAAACTAA GCTCCTCCA AAGTTAGTTA ATCCCAAAC  
85501 CAGGAATGAA AAGGACAGCT TGGAGTTTAG ACGTTAGATG GAGTCGGTTA GGTAAGATCT  
85561 CTTTCACTGT AATAATTTTC TCAGTTATGA TTTTGC AAA GGCAGTTTCA CTGTCCACTT  
85621 CACCTCACAT CAGGCCTCTG ACTAGAGATG TCCAACAATA CTTAGGCCAG GACACCACCA  
85681 TGTCTCCTTA TCCACCCTGA GGGAGTCCAA TTCTGAAAC AAAGGAAACT ATATATGATA  
85741 GTATGAAACT ATATATGAGA AGGAAATTAT ATATGATAAT CAATTTTAGG GTTATCTTAT  
85801 TGATTAGAAG ATATTAAAGT GTGACACTGC CTGGCAATGA TATCTGCTGG TAGTAAGAAT  
85861 TTGGCGAATT TAGTGAAATT CCTGAGGCTG AACCTCCACT TCTGTAAAAT GGAGACAGTG  
85921 AGATAATTTG CCTTACAATG CTGAAGTAAG AATTTTACAC AATAATTCAG ACCAACCCT  
85981 TCATGTGGTA CTTGGCCCCG GGAAGACTAT CAATGACAGT TAGTTTATAG TTTTACTAT  
86041 TAATGAATCC TTTGTTTCAT TGTATTTCCT TTCTACACGT TGGCCTCTCT AAAAGAAGGT  
86101 AATATTCAT ACAAATAAAG TTAACACAGC TTGCAGAGTT GTCCCGGGA ACTCACTTAA  
86161 CCACTGAAGT GTTCAAATTG CTTAAGTTTG ACTTTATATT CTCCTGACTA ACCTTTCTCC  
86221 TTCTGGTATT TCTTCTGAGA ACAGCACCAC CATCCAAAGC ATCATGCAAA CAGTGGTCAT  
86281 CCCAGACCAG TAATTCTCAA CTCACAGGGT GCTCCTGCAG AGATGTATTT GAATAGAGTG  
86341 GTAGGATGCT GAAGAAGGCC ACGTAAATTT TGGCCAGTGA TCTGGGGCAG ATTTATCCTG  
86401 AAGCTAATGA AACACAAGTG TAAGGGCCTG TACTTCCAAG GTGCAGAGAG GGGCCCTACA  
86461 AATGTGTTAG TTTGTCTCTC TCTCTCTCTC TGATTTTAAA ATTTGCAGTA TTAAGGTACT  
86521 TTAATCACGG ATGGTTCAGG CTGCTATTTT CACTCAATCC TCCTTTTTAT TAAAATCACC  
86581 ATTGTCTGAT TATGTTAGAA TCCTGATGAA AATATTTGGA ATTTGAGTAA GAGAAAGTTT  
86641 AGTTGAAGAT GTATCTAGTA TGGGGATAAT AAGTTACGTG ATTTGCATAT GTGATCATGT  
86701 GTACTTCATT CGTTGCCAGC CAATCTGACG TAAGAATGGC TTCAAGGAGG CCGGGCGCGG  
86761 TGGCTCACGC CTGTAATCCT AGCATTGTTG GAGGCCGAGA CCGGGCGGATC ACGAGGTCAG  
86821 GAGATCGAGA CCATCTTGGC TAACACGGTG AAACCCCGTT TCTACTAAAA ATACAAAAAA  
86881 TTAGCCGGGC GTGTTGGCGG GCGCCTGTAG TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG  
86941 AATGGCATGA ACCTGGGAGG CGGAGCTTGC AGTGAGCCGA GATTGCGCCA CTGCACTCCA  
87001 ACCTGGGAGA CACAGCGAGA CTCCGTCTCA AAAAAAAAAA AAAAAGAATG GCTTCAAGGA  
87061 ATGTTCCCTAC TGCTCACTGG AATAACTCAC CTAAATTCCT GGCAAGATGC AGGTCTAGAT  
87121 AAAATGTTAT GACATCTAAG TATTCAAAAC ACATTCCCAG CACTGAGAGT GAGTGTCTAG  
87181 TGGAGAGTAG AAACGTATAG AGCCAGAAGC TAGTCTGGAA AGAATTCCTA CAAAGTTTAC  
87241 AACTTACATG TGAAAGGAGC TTAACAGAGG ATTTTCCAAA TTTGAAAACA ATCCTAAAAA  
87301 CTTACTTGAC ATTACCAATA ATGTGTTTTG AAAGTGAATG ACTTCTAAGT TATGAAGAAA  
87361 ACATATTATC ATCAGCCACC CTGGAGGAAA GATTGAATTC TATTTCCATT ACCTATAGAC  
87421 AACATTACAA AATAATTTTC ATCTGAAGAT GGAATCAGAG TATTCAGTCA AAACACAGG

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87481 AAAATATACT TGGTAGTGTC ATATTCAGAA GTTAATAAAA TATGCTATTT TCTGAATTTT  
87541 GTGATGGCTG TTGTTTTGTC AGCTTTTATA AAATTGGAAT TTGATTTTAT TTTCCCATTA  
87601 TAAATTTATA TTTACAGTCT GCAGTACTTT TGCATTTTAT ATTTTACATT ATAGTTTTTA  
87661 ATAGTTAACA AGTTGTAAAA GGTTTGATCC CCAGAAAACC TTGATCTACC CCATCAGTTA  
87721 AGTATACTAA TATATTTAGA AAATGGATGA AATCAGCATT TGAATATTTT TAAATATTTA  
87781 TTAAGAGAGG ACATGGGTAA AAGAGCTTTG CAGTTGCCAC CCTTCATTCT CAATTTCCCT  
87841 GGATAAGGAT GACCGCATAA TCTTTGGATG GTCATACGCA AGTCTTGTGT ACTTGTTACA  
87901 TAAATCTATT TAGTGGACTT TTGGCAGTGT GTACTGAGGC CAGTTTCTTC CACCTGAGCT  
87961 CTGACTCCAC CTCCAGCAGC CCAAAACCAA TACTGAATTT TGGGGTCAGC TATTGTTTTT  
88021 GTGGACTTAG GTAACCTACAC ACACATTGTC TTTATGATAG CTTTAATAAT ACTGCCATCA  
88081 GAACTAAAAT TGTCACGTGG ATTAAGGA GTGACGGTGG TGTCGCCAGG AGCCTTTCAA  
88141 TATGTAAGTA TTTACACATA TACATGCTAA AAAGACCCCT AGGAATTTTT TAACAAGGGC  
88201 AAAACAGTAA CTCAGCTTGT TTTCTCGCAG TAAAACCGGT TGAAAAGGCC TGATAGACTT  
88261 GTCTGCAGTT ACAAACCTTG TGTGTAGTTA TCACCTTTAT ATCTCCTGGA AACTAACATA  
88321 GACAACCGAA TGGGTTACAA CTGTTTTTAA GTGAAATTGT GAGTGGCTCT GAAAAGAGCC  
88381 TTTTCAATGA GGAAGAAACG GGCAGACTTA TGCCCTTTCC CCACGGATGC GACGTGCCAG  
88441 CTGGATATCT TTGGGCATGA TGGTGACGCG TTTAGCGTGA ATAGCGCACA GATTGGTGTC  
88501 TTCGAAGAGT CCCACCAGGT AGGCCTCACA AGCCTCCTGC AGCGCCATCA CCGCAGAGCT  
88561 CTGGAACGCG AGGTCGGTTT TGAAGTCCTG GCGGATTCT CGCACCAGGC GCTGGAACGG  
88621 CAGCTTCCGG ATCAGCAGCT CGGTGGACTT CTGGTAGCGA CGGATTTCCG GCAAGGCCAC  
88681 GGTGCCCCGG CGGTAGCGAT GAGGTTTCTT CACGCCACCG GTGGCCGGAG CGCTCTTACG  
88741 GGCTGCTTTA GTAGCAAGCT GCTTGCGCG AGCTTTGCCG CCGGTAGACT TGCGAGCTGT  
88801 TTGCTTCGTA CGAGCCATTT GCAATGAGG CACACACAAA AGTGTAGTGA ACTGAGAGCA  
88861 AGTGGCCTTT AAATATAGTG AGAAACATTC TGATTGGTCC TGTAATATT CAAAAGTCCC  
88921 GCGCGATAAA ATCATTGGCT GAAGAGTGAC CAGACTGATT GGTTCAATAC TAGACAATCT  
88981 TATTGGATGA GTTGCCCCAC CGCCCATCCT GTCCTTTTCG TTTCAGTTAT CTGCAGCGAC  
89041 AAATTGTCTA AAATTCTAGT TCATCCAGTC CCAAAGAACA GAGTGTATA CAAGGTATCT  
89101 AAGGATTTTT AAAATGTAAA TTCCGATTCA GTAAGTTTGA GTGGGACTTG AAATCTGCA  
89161 TTCCTGACAG TCTCGCAAGT TATCAATGCT GGTGAACACT CACTAAACCA CCAGAAACGT  
89221 TCAGACTCAT GTCGGGAAAT AACGCTTATA TTCAGAGAAT GAGATTCCAT GCTATTTTGT  
89281 TACTGGCGAA CAGCAAGTTT CCTTGCCCTT TGTTTTCTAA GTCCAAGTCA CATTCCCACC  
89341 CTGCCTGTTT TCAAAATGTC TTATTTTGGT TGGCCTTAAG TTTCACTTG TATACTCTAA  
89401 AATGTACTTT CTAAAGGAAG GTGTTATTTT CTCGAAACTT AACTTTTTAA CACCATTAGG  
89461 CTAGGGGGGC GGTGGCTCAC GCCTGTAATC CCAGCATTTT GGGAGGGCGA GATGGGACGA  
89521 TCACTAGAGG CCAGGAGTTC AAGACAACCC TGGCTAAAAT GGTGAAACCC CGTCTCGCAT  
89581 AAAAATACAA AAACCTAGCTG GCGCGGGTAG CAGACGCTG TAATCCCAAG TACACAGGAG  
89641 GCTGAGGCAT GAGAACCGCG TGAAGCGGCG GGGTGGAGGT TGCAGTAAGC CGATATCGCG  
89701 CCGCTGCACT CCAGCCTGGG TGACAGAACT AGACTGTCTC AAAACAAACC AATCCAAACG  
89761 AAAAGCAAAA AATACCCTAA CAGAAGCAAG TTATCATCCT TTCTTGTGTA ACTATGGACG  
89821 GCTCTGAAAA ATGCCGTTT AAGTGTAAGC TACGTTTTCT GATTTGAGTG TTTACTTGAC  
89881 CTTGGCCTTA TCGTGGCTCT GTTATTTTGG CAACAGGACG GCCTGAATAT TGGACAGGAC  
89941 GCCTCCCTGA GCAATAGTGA CGTTGCCAG CTGCTTGTG ACCTCCTCGT CGTTTCGGAT  
90001 GGCCAGCTGC AGGTGGCGGG GGATGATGCT GCGGGTCTTG TCACGTATGG CGCTGCCAC  
90061 CAGTTCTAAG ATCTCGGCGG CCAGGTATTG TAAGTACACT GGCGCACCG CTCCGACCGG  
90121 CTCAAAATAA TTGCCCTTTC GAAAAAGATG ACGGACTCTG CCCTATTGGG AACTGCAAGC  
90181 CCGGTAGCGA CGAACAAGTT TTTGCTTTAG CTCCATTTTC CACGTCCGCA AATAGCGACC  
90241 TATGAAAGCA GCGGAAACT GTGAAAGACA AGCAAGCTGG AATGGCGCCT GAACAAATCC  
90301 TTTTATACAA ACTGCAAGGC TGCAATAGGA AGCTATCCTA TTGGTCAATT ATGTTTGGTG  
90361 CTTTATCCAA TAGAAAAAGA TAACATAAAT TCCATATTG CATAAACCC ACCCCTCAGT  
90421 GAAACCGTGT TTCTTTTGTC CAATCAGAAG TGAGGAATCT TAAACCGTCA TTTGAATCTC  
90481 AGGACTATAA ATACATGGGC TCTGAAGTGT TCTCTGTACT ACTCTGTAGT GGAGAGTGTT  
90541 AGTAGCTTTT CTATTCTGTT TAGGAATAGC AATGCCTGAA CCCTCTAAGT CTGCTCCAGC  
90601 CCCTAAAAAG GGTTCCTAAGA AGGCTATCAC TAAGGCGCAG AAGAAGGATG GTAAGAAGCG  
90661 TAAGCGCAGC CGCAAGGAGA GCTATTCTAT CTATGTGTAC AAGGTTCTGA AGCAGGTCCA

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90721 CCCCACACCC GGCATCTCAT CCAAGGCCAT GGGGATCATG AATTCCTTCG TCAACGACAT
90781 CTTCGAGCGC ATCGCGGGCG AGGCTTCTCG CCTGGCTCAC TACAATAAGC GCTCGACCAT
90841 CACCTCCAGG GAGATTGAGA CGGCTGTGCG CCTGCTGCTG CCTGGGGAGC TGGCTAAGCA
90901 TGCTGTGTCC GAGGGCACTA AGGCAGTTAC CAAGTACACT AGCTCTAAAT AAGTGCTTAT
90961 GTAAGCACTT CCAAACCCAA AGGCTCTTTT CAGAGCCACC TACTTTGTCA CAAGGAGAGC
91021 TATAACCACA ATTTCTTAAG GTGGTGCTGC TGCTATTCTG TTTCAGTTCT AGAGGATCAA
91081 CTGGAATGTT AGCGAAGACA AGTTTTAGAG CCAAGGTAA CTTGGACGGG GCCGTGCGCG
91141 GTGCCTCTTG CCTTTAATCC CGGCAATTG GGAGGCCGAG GCGGGCGGAT CACGAGGTCA
91201 GGAGATGGAG ACCATCCTGC TTAACACGAT GAAACCCCGT CTCTACTAAA AATACAAAAT
91261 AATTAGCTGG GCGTGATGGT GGGCGCCTGT AGTCCCAGCT ACTCGGGAGG CTGAGGCAGG
91321 AGAATGGCGT GAACGCGGGA GGCGGAGCTT GCAGTGAGCC GAGATCGCGC CATGGCACTC
91381 CAGCCTGGGT GACAGAGCGA GACTCCGTCT CAAAAAATAA AAAAAAATAA AATTAAAAAA
91441 ATATGAAGTT TTGAAGCAGA AATTATTTTG TCGTATGTTC TTTCATAAAT TTTTGCCTG
91501 CCTGCCTTCT TCCTTTGTGA CAGAACTCCA AACTTACCC AAAGGTAGCT GTTGGGTCAG
91561 GGTTCCTGTA CTATAGTCCC TTCTGTGGT GCCAGAAATA TGTTACAGGA AAGAGGTCCC
91621 CATCCAGACC CCAAGAGAGG GTTCTTGGAT CCCGCGCAAG AAAGAGTTCA GGGTGAGTCC
91681 GCAGTGCAAA GTAAATGCAA GTTTACTAAG AAAGTAAAGT GGTGAAACGA CAACTACTCC
91741 ATAGACGGAG CAGGACATTC CCGAAAGTAA GAGGAGGAAG GCATCCACCC TAGGTACAAT
91801 ACTGTATAT ATGGGGAGAT GTGCTCTGCT ACAAGTTTGT GATAAAGGAT TAATTTTCTT
91861 AGTTACTATA TTTTGCAAGA ATCAACATTA TTATCTTTAA ACAAATTA GAATGCCTTT
91921 GTTCTCCAGA TATAGGGATA TCTGGACACT CCTAAGTCTG AGTCTGTTTA GTAAACATTA
91981 TTTATTTGTT CCCTTAACCG TAAACATCTA GAAGCTAGGA ATGACTGACT TTCTGGGAAT
92041 GCAGCCCAGA AAGTCTCAGC CTCATTTTCC TAGCCCTCAC TCAAATGGA GTTACTCTGG
92101 TTCAAGTAAC TCTGACACTT TTCTTCTCTT TTTTCTTCT TTTTCTCTT CTTTATTTT
92161 TATTTTTTAT TTTTGAAATA AGAAATCAAG AATACTTGAT GTTTCATCTA AAACAATACC
92221 CATAATTGAT AAGCCAAAAC AAAACCTAG GTCTTCTAAC TCAAACCTAG GATGTTTTGC
92281 TGTCTCTGCT GATACTCGGC TGATCGTTAA TAGGTAATTA ACAAACAAGC CTTGCTATGT
92341 CCCCCTCAGT TTATTACCAT TAGATCATAT GCCTACTGTC AATCATATTA ATCCACAAC
92401 ATGCATTTCA CAAAACCTGC CATAAAAT CACAGGTTTC CCGCTTCCCT CGAGTTTTCA
92461 TTTCCGAAGG GTCCCATGTA ATATAAACT TATATTAAAT ACATTTGTAT GCTTTTCTCT
92521 TGCTAATCTT TTTTTTTGTT TTTTGAGACT GAGCCTTGCT CTGTCAACCA GGCTGGAGTG
92581 CAATGGGCGG ATCTCGGCTC ACTGCAACCT CCGCTTCCCA GGTTCAAGCG ATTCTACTGC
92641 CTCGCCCTCC CGAGTAGCTG GGACCACAGA TACGTGCCAC CATGCCCCGC TAATTTTTGT
92701 ATTTTTAGTA GAGACAGGGT TTCACCGTGT TGGCCAGGAT GTTCTCAATC TCCTGACCTC
92761 GTGATCCGCC CGCCTCGTCC TGCCAAAGTG CTCGGATTAC AGACGTGAGC CACTGCACCC
92821 GACCAATCTG TCTTTTGTA GAGGGGCCCTC AAGCATGAAC TTAGTGATGG GTGAGAAAAA
92881 CAGAATTTTC TTTTCCCTA CAATATAAAC ATTAATTGTA ATGTTATCAT TCAGGACATT
92941 TTGGTGACCA ATCTTACAGA AATTTATCT TGTGCAAGTC TATGCAACC AATATGTAAA
93001 TCTTCTATAA GTGAGATTGT ATTTCACTTT TCTAGTATCC TTTTAAATTA ATAAAAGAGA
93061 TTCTAATGAT TATTTTCATT ACTGCATTTT ATTGTAGGGA AGTAGATAAT TGCCCTTTAT
93121 TCACTGACCT TCGCTTTTAA AAAATTTAAA CCATGTTACC ATGAAAATGC TTTTCAGTAT
93181 TTCTCTACAC ACAAGATTGC TGTAAGGGCA AAAATAGAGA TAGGAATCAT GCATCCATTG
93241 ATATACATAT TTTGATTTTT AATACATGTT ACCAAGTTGC CTCCTGAAGG TCTGTTTACA
93301 CTCTACCAA CAGGGTGT TTCTCTGACT TCCACAAATG CTCTGAACA GTGGGTGTGT
93361 TAGTCTGTTC AAATGCCGA CATGAACAAT TAAATCTCAT TGTGTTTTT ATTTTTAAGA
93421 CAATTATTGT TTGAGACTGC ACATTTTGAT AATAACATTT CTCTATTAT GGTGTTGATTA
93481 CTCATGATTC TTGCCCATTT TCTTTTGGGA TGTGCTTGA TGTACATTAT TTTAAATAGA
93541 TAGCTCCATG TATTAAGAA TTATTAAGTT TGAGGGCTTA TGATATGTCA GTTACATTTT
93601 TAAGATTTTT TTTTTTTTTT TTTTGGAGAC GGAGTTTTC ACTTGTTGCC CAGGCTGGAG
93661 TGCAATGGTG CGATCTCGGC TCACCGCAAC CTCGCTCCAG AGGGTCCAAG CAATTCCTCT
93721 GCCTCAGCCT CCCCAGTAAT TGGACTACT GGCAAGCGCC ACCACGCTG GCTAATTTTG
93781 TATTTTTTATT AGAGATGAGG TTTCTCCATG TTGGTCAGAC TGGTCTCGAA CTGCCGACCT
93841 CAGGTGATCC ACCCGCCTCG GCCTCCCAA GTGCTGGGAT TACAGGTATG AGCCACTGGG
93901 CCCGCCACA TTTCTAAATT CTTTATAAGT ATAAATTCAT TCAATCTTCA CCAAACCTCA

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93961 ATGAAGTGTG AGTACTATTA TTATCATTGT TTTACAGATC AAAACAAGTA ATACAGTCAC  
94021 TTAGTGTGTT CTATACACCT GGTAATTTTT TTGTTTCGTT GTTCTATCAA TTATTGGGGA  
94081 AGGGGTGTG AAATCTCTAC CTTTAAATCA TGTATGTGTC TATTTCTCCT TTCGGTCTTA  
94141 TCAGGTTTTG CTACACATAT TTTGCAGTTC TGTATTGTTG TGCATATACA TTTAGAATTG  
94201 CTTGTTTTTC GTATTGGATT GACCCTGTTA TCATTATGTA ATATCCCTGT CTGTTCCCTAG  
94261 TAATTTTCTT TGCTCTGAAA TATACTTATC TGATATATCA TCCAAAAGAC CACCAAGGATG  
94321 GCTAAAGAGT AGAAAGGAGA GATTTACTGG CAATACTAAT TTGCAAGCCA GGAAGAGATG  
94381 GTCCCAAGAC CTGCCAAAAT TACTCTCTCT TTGGGGAGAA GGAGCAGGTT GGTTATTTTT  
94441 ATGCCTCATA GGCTATATAT TACACAATAG AGTCATACAT ATTTAGCACG TTTGGGGGGA  
94501 CAGCTATATA TATTATGAGG GGTGCCAAGT GCATTCACAA TGGATAAACA CGTGTAATAT  
94561 ACCTCCCATG TTCACTTCGA GGTTAAATTT TGGTTAAAAT GAGGTAGAAT TTAGGTCTTT  
94621 ACATCACAAG GTGAACTATA GGAACAAAGT TTACGTGCTG CCTCTAGCAG CTGGCTGAAA  
94681 ATGGCTTAAG GTCTACAATT ACGTGTAAGA ATAGAATGTG TGTCAAGGCG GTCCTCTGTC  
94741 CAAACAGAGT TGTAGTGGAC TGGACTGTAA ATCAGAGTTA GGAGGGCTTC TGATAGCTCC  
94801 TATAGTTAAG GAATTTAGCA AGTGTGAGTT TTTGGTAGT CTTTGAATT TAGGAATTTG  
94861 CCATGCCAGC CAAGCCATGA ATGCTCTACC AGTAGGTAAC TTTGTTGCT TAATCTTAGA  
94921 GTCTGTCTTA GTTGGTATAG GGGCATCTAT TTTGGTCTTT CAGATCCCAG ATATTATTAA  
94981 TACAGATACT CTTGCAGTTT TGGGCTGATG TTTATATGGC TTATCTTTTT TGCAGCCTTT  
95041 AATTCAACC TGCGTTATGT TTATATTTGA AGTGAGATTC TTGCAGACAG TGTACAGTTG  
95101 TTGTTTTTTT TTTTGTGAGA TGGAAATTTCA CTCTGTGTTG CCAGGCTGGG GTGCAGTGGC  
95161 ACAGTCTCAG CTCACTGCAA CCTCCGCTC CTGGGTTCAG GGGATTCTCC TGCCTCAGCC  
95221 TCTTGAGCAG CTGGGATTGC AGCCATGCGC CACCACACCC GGCTAATTTT TGTATTTTTA  
95281 GTAGAGACAG GATTCACCAT GTTGCCAGG CTGGTCTCGA ACTCCTGACC TCAAGTGATC  
95341 CGCCAGCCTC GGCCTACCAA AGTCTGGGA TTACAGGTGT GAGACCTCGC GCCCAGCCAA  
95401 ACTGTTTTTT TATGGGTGTA TTTATACCAC ACACATTTAA TGCAATTATT GATATCTTAG  
95461 GGCTTAAGTT CATGAAGGGT AGTGTGGGAA CCATAGTCTC TTGGCCCACT AAATGTTTGC  
95521 CAGAAATCAC TGACAAGGCA GATTGATTAA TAGGTGAAAA GGCATTTTAC CTATTGTTTA  
95581 ACGTGTCTAT GTGGGAGCAT TCAGAATTAA TTACCTAACT TCCCAATGAG TTATAGATGC  
95641 TTATATACCA TTTTATGATC ACAGAAAGAA TTGGGGCTTA GATCTGGTA AAACAGGTTA  
95701 TGGGAGGCAA AAGAGGTTTG GCTTGCAAAG GTGGCCTTGT TAGGTAGGTG AAGCCTCCCT  
95761 CAGAAAGAAC AGATGGTAAA TGTTCTTTT ATGATTTTTA AGTGTGAGAC TCTCAGTCTC  
95821 TCCTGGATCT GGGGAAAGGT ATAGAAAGGT GAGGAGGCT GGCTGCATTA ATGGAGATTC  
95881 TCTACAGATG TAAAATTTTT CCCATTTAAG GCAGCTTTGC AAGCCCCATT CTGCCTGCTG  
95941 GCCAAGCAGC AGCCATTTCA AAATATGTCA AAGAAATATA TTTTGGGGTA AAATATTTTG  
96001 ATTTCTTTTA GACTGGTGGC CTTATAAGAA AAGGAAGAGA CACCTGAGCT GACACACATA  
96061 CCCTTGCTCT CTCAACATGT TATGATGCAG TAAGAAGGCC CTCACCAGAT ACTAATTCCA  
96121 TGCCCTTAGC TCCCAGGTT CTAGAACAGT AGGAAATAAA TTTCTTTTCT TTTAAAGTTA  
96181 GCCAGTCTGT GGTATTCTGT TATAGTATCA CAAAATGGAC TAAGTAACATA TATTATGATC  
96241 ATCTTACATG ACTGATCCCT CCTACATCAT ACACATACAC AGGCCACATT TGGAACATTG  
96301 TTAGAGGTTT CTCTGCCCAG TACAAATGTA CTACAAATTA TATATGTATT TTTAAATTTT  
96361 TGAGTATCTT CAATAGTATA TTTTCGTTAA CTTTGTAGT CAAAATGTCA TTATAACATG  
96421 TATTCAATAT GCATAATTAT TAGTCAGATG TTTTACATTC TTTCTTCATA CTAAGTGATA  
96481 TGGTTTGGAT ATTTGTCCCC TCTAAATCTC ATGTTGAAAT GTAATCTCCA ATGTTGGAAG  
96541 TGAAGCCTGG TGAAAGGTTT TTGGATCGTG AGGGTGAACC CCTCATGAAG CGCACTCTTC  
96601 AGGGTAATCA ATGGGTTCTC ACTTTGAGTT CACAAGAGAT CTGGTCTTTT AAAAGAGTGT  
96661 GACACCTCCC CCATCTCTCT CGCTCAGCTC TCACCATATG ATATGCCTAC TCCCTCTTCA  
96721 CCTTCCACCA TGATTGGAAG TTTCTGAGG ACTTGCCAGT AGCAGATGCC TGCACCACAC  
96781 CTCTGTACA GCCTGCACAA CCGTGAGCCA AAAAAAATTA CTTTTCTTTA TAAATTAGTC  
96841 AGTTTCAGGG ATTCCCTTAT AGTAATGCAA GAACGAACATA ACACACTAAG TCTATTTTAT  
96901 ATTTACAGAA TAGCTCAATC TGAAGTACCC TTTTCAACT TCACAGTAGC TACTTGTAGC  
96961 TAGTGGGCAC TGATTGAGG CGTGTTCGAG GGTGAATTGT ATTATGCAAT TAACAGATTT  
97021 TTTTATATTG TTTGCGAAAC CACGAGGCAT AGATTGTCTT ACTTTCTCTG CTCCTGGTGT  
97081 TGGAGTTGTT ATTGGGAAAC AACTTATTTT CCTCTTATAT TTATATGGAA TAAATAACCC  
97141 CCAATATTTT CCTCCCAAT ATCTGCCTTT TGTATGTTTT TTGAAGGCAA GTGCCTAGAA

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97201 TTTACTGTTT TTGAAGCACT TACTGAAAGG ATTGCCATCA AGTTGTTTTG CTAATAGTAC  
97261 ATGCCAGGCG CTTGTTGGTT TGCTTAATTC AAGGTAACCT GGATGAGAAG AAGAGTTTTT  
97321 CTCATCCATG GCTCAGTGGA GTATAGATTA CTGATATTGT GACTGGATGT ACTCCTGCTT  
97381 TCTAGTCTGA GTTTTTGAAG CTACCCTTAA TCTTGGTTTC AATTTTATCT AGCCCTGTAC  
97441 ATATCCAAGG CTCTTTCCAA AATGGTCTAC GATTTGTTTA GGAAGTTAGA ATAGCTGTAC  
97501 TTTCTGAACC ACGGTTCCCTG ACATTTTCTG GACTTCAAAC ACATCCAGCA TTTTATCGAA  
97561 GTATTTATCC TTCCTACTTG GCTGGCTTCT TCCTTGCCCT CAGGTCTGAA TTCAAATGAC  
97621 ATTCTCCTGA TGAAACTTTC CATCCTTATT TCTATTCTTT TTTCTTATCC CCTTCTTTA  
97681 TTTTCTCCCA CAGCACTCAT CACTTATCTC TACATTTTCA TTATGTATTT ACCTTATTGT  
97741 GCACCTCCCA CTACAAGACA AGTAGCACCG TAAGGAAACA GGTTGTCTGC TTTTCACTG  
97801 CTATGCTCCC TGCACCTAGA ACACCTCTCG GCACCTAGCA GGTTTTCACT AAATATATGC  
97861 TGAACATAATA ATGCTGGATA TACATCTCCC TCATGAACTC TCTAAATCCT TCTAATTTAC  
97921 ATTGATCAAT CTTCTTTTCC ATGTGCTTTT GTATGATTTA TTGCTCAAAA TCTTTATTTT  
97981 ATATGCAGAA CGTGCACCTGC TATTTAATCT TCATGTACGT AAGTCCTCCC TTCTCTGAGT  
98041 ATAATCTCTT CAGGGCACTA TCTGAGATAA CTTTTTAACA TCTCCATCAT GAATCTTGTA  
98101 CCTTTTCAAA GAAAATGAGC CAGTGATTAC TGATGTTTAC GGCTATTGTT GAGGGTGAAG  
98161 ATCATTATAA TTTTGAAGG GGAAGTTGAA TATTGTGAAG GGAAAGATAA CACTAGAGTC  
98221 AGAAGACTTG GGAGAAGGCA AAAAACAAAC TAAAAATGAG CACTTTTAGT CTCCTGACAG  
98281 TTTCTCTGAA TCAAATCCAT AGTTCGTGTA CAGCGTTGGC TTAGAAGCAG ATTTTTTTTT  
98341 TTTTTTTTTT TGAAATGGAG TTTCGCTCTT GCCCAGGCTG GAGTGCAGTG GCACGATCTC  
98401 GGCTCACTGC AACCTCTGTC TCCAGGGTTC AAGCGATTCT CCTGCTTCAG CCTATGGAGT  
98461 AGCTGGGATT ACAGGCTCCC ACAACCACGC CCAGCTAATT TTTTGTATTT TTAGTGAAGA  
98521 CTGGGGTTTC ACCATGTTGG CCAGGCTGGT TACGAACCTC TGTTCTCAAG TGATCTGCCC  
98581 GCCTTGGCCT CCCAAAGTGT TGGGATTACA GGCATCAGCC ACCGTGCCCC GCCAGGAGCA  
98641 GATTTTTTTA CACTCATGTT TCTTTTCTCT TCTGTCATCT TGTTCAGTA TAAGCAGACC  
98701 ACAGATAGAA GTAGTAGATA CCTCAGAAAT TCCTGGAATA ATTAATCCAC GTTCATCTGT  
98761 ACTCCATCTG CTCCTATCTC ATGGAATATA AAAGGAAAAA CACCAAGATT TCCCTAGGCA  
98821 ATCTGTCTTG ATTTTAGGTT CCTCAACAGG AGAGCCAGAC AATGGCTGTA ATAATATTGT  
98881 CCCGGCCAAG GAAAACTTC CCCTTTGCCC TCCCAAGGTT TATGGAAAAT TACTGGCAAA  
98941 ACACAGATTA ACTGGAGAAA AGGCATATAT ATTTATTTCA TCACAATTTT ACAGGAGATT  
99001 TTAGAATTAA GACTGAAAGA TACAGGGGAA ATTGCCCAT TTTATGCTTA GTTTCAACAA  
99061 GATAAACAGC TGTATAGGGT ACGATCTAAT GCTAACAGAC TGAGTGGGGA AGCCCCGCAA  
99121 GGCTTGTCTG TCAAGATTCT TCTTGACCTC TCAGTGCAGC ATTTCTTCCT TCTGGTTATA  
99181 GGACAAGACT CTCTTTTAGA ATGGGGGGTC TTATGACCTA CAGGCAACA AGGTAGTTA  
99241 GAGTAATACT TTTAGGTTTT ATGGCTGGTT CTAGGGAAAA GGAGTTCTGG TTGTATGGC  
99301 CTACCTTGAG GAGGAATTCT GGTTTCTATG GCTAGACTTT GGGGAGAATG GGAATTACAG  
99361 ACAGGAAGGC AGAAGGTGGT CAGTGAACA CTTTTATAAT CATAATCCCA TTTTGAGTAT  
99421 TTCTGTGTTA TGGAATGTTT GTTCTCTCAT TTCCTGAAAG ATTCCAGAGA CTCCTCATT  
99481 AGTGTGTGTA AAAAGTTCAG GAAATGCAAC TCAAAAATGT GCCACTTTGT TACGCTGATT  
99541 TCTTTGAACT GAGGGCACCT AGGAAACAGT AAATTCAGG AAGGGCTTTC GCTGAACTCT  
99601 AATCAAAAAT TTGAAAATTA AAAAAAATT CAAAAAGGAA TTTAGTTGTT AAGATTCACT  
99661 TCCCTGGGGA ATCTCATCAA CCAGAGAAGA TTAAGTGTAT CACAGGAGAG GAGACTGGTG  
99721 GTTAACACCA TCTAAACAGA CTTTGTACCA GCTGTCACCT ATTCTTTGAA ACACCCATTT  
99781 ATTTTCTCC AAAATCATAT ACTCTCCCT AAGTTGCCTA CATCCCCCTT CTTTCTCCCT  
99841 TATGAATCAA GAGAGCTTAT AAGCTTCTAC AGTTCACTGG GATTTGGGGT ATTCGCTTTT  
99901 CTTCCCTCCC ACTCCCCCTC CCCTTTTTTT GTCTTTGAGA CACAGTCTTC TGGCTCTGTC  
99961 GCCCACGCTG GAGTGTGGTG GCTCTATGTG AACTCACTGC AACCTCCTCC TCTCGGGTTC  
100021 AAGCGATCCT CCCACCTCAG CTTCTCGAGT AACTGGAACT ACAGGCGTGC ACTACCAAGC  
100081 CCGGCTTTTT TTTTCTTTTT TCTCCCCCGT TTCTTTTTTG GTTATTTTAC TGGAGACAGG  
100141 GTTCTCCATG GTTGTCCACG CTGGTCTCGA ACGCCTGACC CGCCGTCCTC GGCCCTCCAA  
100201 AGTGCTGGTA TTACGGGCAT GAGCCACTTG GCCCGATTG AAGGACCTCT TAAATATCTA  
100261 TTTAGAAATT GGTCGGAGTC CACTCCCTTC CAAAAACATG AGTCACAATC CGGGAAAAGC  
100321 ACGAGCGGCT GAAAGTCAAA ATAACCAGAA CAAAACCTCC ACTCATGCTT AAAAAAGGTA  
100381 TTTTGACAAA ATCCTAATTC GGCCAATTAT TATTAGTATT CAAGTCGAAG GCTCGTCAAG

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100441 CCAGACTGGG GATTGGGTCA AACATAAACC TTACACCAGA CGGAAGGATT ACATGCAAAT  
100501 GAAGGATGCA GATTCTGATT TCCCATTGGG TATTTGACAT TAGCCAATGG GAGAATTCCT  
100561 CACAGCCTAC CTCCAGTCAG TATAAATACT TCTCTGCCTT GCGTTCTAAT GTAGTTTCAT  
100621 TACATTTTCT TGTGGCGATT TTCCCTTATC AGAAGTAGTT ATGTCTGGTC GCGGCAAACA  
100681 AGGCGGTAAA GCTCGCGCCA AGGCTAAGAC TCGGTCTTCT CGTGCAGGTT TGCAGTTTCC  
100741 TGTGGGCCGA GTGCACCGCC TGCTCCGCAA AGGCAACTAC TCCGAGCGCG TCGGGGCTGG  
100801 CGCGCCGGTG TATCTCGCGG CGGTGCTTGA GTACCTGACC GCCGAGATCC TGGAGCTGGC  
100861 GGGCAATGCG GCGCGCGACA ACAAGAAGAC CCGCATCATC CCGCGCCACC TGCATTGGC  
100921 CATCCGCAAT GACGAGGAGC TTAATAAACT CTTGGGGCGT GTGACCATCG CGCAGGGTGG  
100981 CGTTTTGCCT AATATTCAGG CGGTGCTGCT GCCTAAGAAA ACTGAGAGCC ATCATAAGGC  
101041 CAAGGGAAAG TGAAGAGTTA ACGCTTCATG CACTGCTGTT TTTCTGTCTAG CAGACAAAAT  
101101 CAGCCTAACA GCAAAGGCTC TTTTCAGAGC CACCTACGAC TTCCATTAAA TGAGCTGTTG  
101161 TGCTTTGGAT TATGCCGCCC ATAAAGATGT TTTTGAGGTG TTTTAAATGG CTTTGAGTGT  
101221 GGCACCTTTA GTAATTTGTC CTGCAGAAAT TAGATCCATA GAAACCTCAG GAATTCTAGG  
101281 TATGTGGGAG AAGTGCCATG CAGCACAAAA CATGTTTACA GGGGTGATTG GCGTTAAGTT  
101341 TCACACACAG CAGTTACTAC ATTTTAGAGG AAGGAAATTA TACCCATGAG TGCATTCTTA  
101401 ACTATCTTGA ATGGAAGTGT TAAAACCCGC ATGCCCCACA CAAGTTTGAA TATGTCATAC  
101461 CATTTGCTGT AGCAATTAAT GGCATACACA ATTGAGAGCA CACACATTAC CACTGAACAT  
101521 TTGAGTATGT ATTTCCCAA ATGAGCTTTT TTCCAGTTTG GGGATGTTTT GCTTTGTTTT  
101581 GGGGTGGAGT CTCCCTCTCG CCCAAGCTGC AGTGCAGCGG CGTGATAACA GCTCACTGTA  
101641 ACCTCGAACT CGGGCTCAAG CGATCTCTT GACAGCCTTC TGAGTAGCTG GGATTACAGG  
101701 CGAGAGCCGC CACGCCCGGC TAAGAGCATT TTTCTAATTG CCCACACTTC TTATGCGACA  
101761 CCCAGAAAAA TACAATTTA AATAAAGCGC ATATGCAAAT TTCCCTAATC GTCTCCAATA  
101821 TCTCTGATT TCTTTTTTAT ATTTTAACTA GAAACAATTG GAGGTTTCCG CGTTGCTTTG  
101881 TGTGTTGTA AATTTTAAGA CTTTCAGAAA CTTTCCAGT ACAAGACTTG TCCACAGTGG  
101941 ATATAGCAGC TAAGGGGTGA ACAAATGAC GTCAGAGTAG CTACGGTAAT GGGCAGGAGC  
102001 CTCTCTTAAT CTGCAACCAG GCACAGAGAT GGACCAATCC AAGAAGGGCG CGGGGATTTT  
102061 TGAATTTTCT TGGGTCCAAT AGTTGGTGGT CTGACTCTAT AAAAGAAGAG TAGCTCTTTC  
102121 CTTTCTCCA CAGACGTCTC TGCAGGCAAG CTTTCTGTG GTTTTGCCAT GGCTCGTACT  
102181 AAACAGACAG CTCGGAAATC CACCGCGCGT AAAGCGCCAC GCAAGCAGCT GGCTACCAAG  
102241 GCTGCTCGCA AGAGCGCGCC GGCTACCGGC GCGGTGAAAA AGCCTCACCG TTACCGCCCCG  
102301 GGCACGTGTTG CTCTGCGCGA GATCCGCGCC TACCAAAAGT CGACCGAGTT GCTGATTCGG  
102361 AAGCTGCCGT TCCAGCGCCT GGTGCGAGAA ATCGCCCAAG ACTTCAAGAC CGATCTTCGC  
102421 TTCCAGAGCT CTGCGGTGAT GGCGCTGCAG GAGGCTTGTC AGGCTACTT GGTAGGGCTC  
102481 TTTGAGGACA CAAACCTTTG CGCCATCCAT GCTAAGCGAG TGACTATTAT GCCCCAAGAC  
102541 ATCCAGCTCG CTCGCGCAT TCGCGGAGAA AGAGCGTAAA TGTAAGTCA CTTTTTCATC  
102601 AGTCTTAAA CCCAAAGGCT CTTTTCAGAG CCACCCACTT ATTCCAACGA AAGTAGCTGT  
102661 GATAATTTTT TGTGTCTTA ACAGAACAAA TTTCTAAGGA CCCCCCGGA AAGCATTAGA  
102721 CTATGGTCTT AAGTTGATT AACAGAAATA ACGGTTTGGT CAGTCTTGCA GTGTAGGTTA  
102781 TTTCTGACCT TATTAAGGTG CTATTTGGAG AGAAGCTGTG TAAGTCCACT ATCATTACAGG  
102841 CCTCTAGCTT GCTATGATTA GCATTGTGTT AAACAACCTT GTAAGAGTAA GGGAAAAATC  
102901 TGGTAAGTAG TTAAGTGGCG CTTACTAGGC ATTTTGTCAA AGCTTTGAAA AGATTAGAAA  
102961 ATTGTGTCTT GCGAGTTCCA GTGCTTCTT CAAAATGCTT AGGAAGATTT TCTCAGCTCA  
103021 ATACATAGTC CCCTAGGTTT TCTCATATAT TATATATATA TATATATATA TATATACTGT  
103081 TAAATTCATT TGGCTGTAA CATTAACTG AAATTTATTC TGGTGCAAAA TGTGAGGCAG  
103141 GGATCTAACT GGCTCTCATT TTATCCATAG CTAGCTACCC ACTTTAAATC TGTCACTCTG  
103201 TCGACCAAGC ATAATTTAAT CCCTTATATA TGAATTTTTA TATGTGTGGC TTTGCTTGTA  
103261 AATAGTCTAT CTGGTTGCAT TGCTTTGTCT CCTCTAGGAC TATGCACCAT GACATGCCAC  
103321 ATTCTTTTTT TCACTACTTC TTGCCTGTAG TTATTAATTA CTAGAATTTA CAAGTTTTAA  
103381 CCATTTTCTT TCTGTTGATC TTGCTTTTCG GTTTTGAGG TTGGGGATTG AGTACTGGAA  
103441 GAAAATTTAG AGGGATGGGA ATACTGTACG CAAACAAAAG TAATATTTAT TTTAAATTTT  
103501 TTATATTTTG TATTTTTTTA TCATATAGCT TTTACATCAC ATTTTACAGA CTAACCTTAG  
103561 AACAACCACA GAATGTCCAA CATTAAACT ACTAATTCCA AAGACCTTGC CTCACATTCT  
103621 TTTTTACAAT AAATATTTTT TACACCTAAC ATCTTTCTT GGCCTACATC TAGAATGTAA

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103681 ACTGATGTAC CATACTAAAA TCGCCTGACC AACTGTCAAC AACAACAAAT CACACACACA  
103741 AAAGATTAAA TTTGAATTGC ATCGTTTACT TAAATTCATT TGTGTTCCAG CTTTTAATAA  
103801 GGCAGTTTTT GGTTTATAAA GTAATATTG CATTTTAAAA ATTATGAAAA TGAATATGTC  
103861 AGTTTGTGTT ATGATTCGTT TTTCTTGACT CTTATACAAG CGACTCTAAC TGGCATAGAC  
103921 ATTTGTTATC CACAGACAGT ATAGATATGT TAGAGATGCC AATGGACTTG GTCTATGCCA  
103981 AGGTGACTAC TCACAAGCTC TGGGCCGAGC TGAAGGTCAA GTATTTTTTT TCCAGTTATA  
104041 GATGTGCTGG ATCTGATGTA TAGCGCTTGA CTTTTTATAT TTTCTTTATC TGTAGGAAAC  
104101 AAATGTGTTG GAGGTACTGG GTCTGACGAA TAGCATAAAA GAATAAAGTT ACATTACTGT  
104161 CTGAGGATCA GATGGACAGG GGGTGGTAGC TCAGTCCAGC TATTTTCCAC TCCCTCACTT  
104221 ACATTCTTTG CCCCCTCCTC AACAGAACAA GGATTCTGCT GTAACCTCTC ATTGACAGTT  
104281 GATATTTAAA AATTAACGAA TGGATGAAAT TCTCATTTGT GAAAGAAAAT TTATTGAGCA  
104341 TTTTGTTATG GTGAGTAGTG CAAACATTTT AATATTATAT TAAGAATCTA TTGTTTTGTA  
104401 TTAGAGGAGT AATTAAGGAG AGATTGGAGA CAAAAAGGGG GTGTTGTTTG CAGAATATAC  
104461 CATCCAAAAA TAGACCACTG TGGGATCAGG ATTCTTTTGA GCTAAAAGCA CTTCAAAAAAC  
104521 AGCATTCAAG AAGGGAATTC TTCTAAACTT TTCTTTCTGA AAACAGGAGA TAAAAGTTCC  
104581 AATGTGAAAA ATGCTCTGCT TGTACCAGGT GAAAAGACAT ATTCTTCAGC CCAGAGGCAT  
104641 AGATGAGATA ATTCTGCACA AACACAGCAG GGAGTCATAG CCGAGAGACT TCTATACACA  
104701 AACAAACCTT GTTAAATAAA TCATATATTC CTTTAACTC CTCATATGGT TTACTTTCCC  
104761 ACAATTGCCT CTCTTAACT TAATGTGAAA GCATTTAGCT TTTGCCATTT CTTTGGGGCT  
104821 TCACTTTTTT ATGAGGGTTC TCCTGTCCCA TAAAATTTAC ATTAATACA TTTGTATGCT  
104881 TTCATTCTGC TAATCTGTTT TATGGCAAAT GAATTATCAG GTCCAGCTGG AGACCCTAAC  
104941 AGAGTAGAGG TAAAAATTTG CCTCCCTACA AGATAGAGAT TGTGTGCATT AAATTTGTT  
105001 TGTTCCAGT TGTTCACTT GTCAGCCTC TGAGCCGAAG CTAAGCCATC ATATCCCCTG  
105061 TGAAGTGCAC GTATGCCTCT AGATGGCCTG AAGTAACTGA AGAAACACAA AAGAAGTGAA  
105121 AATGCCCTGT TCCTGCCTTA ACTGATGACA TTACCTTGTG AAATCCCTC TCCTGGCTCA  
105181 TCCTGACTCA AAAGCTCCCC CACTGAGCAC CTTGTGACCC CCACCCCTGC CAGCCAGAGA  
105241 ACAACCCCTT TTGACTGTAA TTTTCCACTA TCTACCCAAA TCTTATAAAA CGGACCCACC  
105301 CCATCTCCCT TCGCTGACTC TTTTCGGACT CAGCCCGCCT GCACCCAGGT AGAATAAACA  
105361 GCCTTGTGTC TCACACAAAC CCTGTTTGAT GGTCTCTTCA CACGGACGCG CCTGAAACAG  
105421 TTTAACAGGG TTTTTCCTGC CCAGTCACAA CAAAGTGATG TTATGCTGCA GGCTGAAGTT  
105481 TACAGCTAAT GCTGTTGAAG TCTAAATCA GTTTTGGTTT GTTAGATTG GGTGAGATGG  
105541 CTAAGATTCT CAGAGAAAAG AGTCAAGTTT GGGGTGCATT TTTCAAGCTT AAAAAATTTAG  
105601 CAGTAGCCCT TGCAGTTTTT CCAATAGAAG TGATTTAAGA ATGTTTTAG GAAATTTAAA  
105661 ACAACAGTGA GAAGCGTGTA TGGAGAGTTG AACTACACTC CAGACTTGGC TATAGGAAAG  
105721 CACGAATGCT GCTATTGTAT TGCACCTTGG AAAAGAGAAC AAAGGAATAT TTTCCGACAA  
105781 TTTTAAACATG TCACATATGA AAAGCTAAAC GGAATCTGTC AACACCTTGT ACGTTATTAC  
105841 AGGCTGTGAT TTTAAAAAAA CAATCCTTAC TAATACATAC ATAGTTGCTG CTAGCAATAT  
105901 AGTGTGTTGGA GTAAAAACAC GAAAATGAGA GTTCAGGACA ATATCCCAAC TCTGAGCAGA  
105961 TTTTTTTAAG TAGTAACATC TAAAAATTA CCATATTATG TAATATTTAT TTCTTTTCCA  
106021 CAGTCTCTTC TCATGCCTCG TTCACATTAG CTAATTAATA GTCCCTGAG TATCATCATA  
106081 ACCCGATTTA CAGATGAAGG CACGGTTGCA ATGAGCTATC ACCCTCTTCT GAATGAGACA  
106141 GTACAGTGTG AAGGATAGCA AAATCCACT CCCATCCTCT TAGGGCTCTG GCTGGACCAG  
106201 CAAATTAAAT TAATGTAAAA TGGATTAACA GGAGAAAGGT ATATGCATTT ATTTAACACA  
106261 GGTTTACGT GACACAGGTG CTCTCATAAG GTAATGAAAG CCAAAAAA GCAGTTAGCT  
106321 ACTTATATAA TGAATTGGAC AATTAGTAAA ATGTAAAAAT GCGCTAAAGC AAAGGGATT  
106381 AGGCTAGAAT ATATAACTGT GTAGAGAAGC GCCCAGCAAG GGCTAGTGCA AGGTTTGTAC  
106441 AGAATTCTCT TGGCCTCAGC CTCCTATCCT TGAGAAGAAT GTTGCTTTT TTAACCTACA  
106501 GTGAGAACAT CTTTCATATG AGAATTTTAC CTACTGCTTC TAAGAAACAG GTCAGCTTTC  
106561 AAGAAAAACAT AAGGCCAGAG TGATCTTTTC ACGCCTGCTC TTTTAAGTAC CTTTGAATAG  
106621 TCAATATGTC TTCAAGCACT TGAAGACTT AAAAAAGTTA CCACTCCGGC ATATTAGTGA  
106681 AAGCCCTTAA TATAAGCCCT TATTAATAAT CTCAGTCGAG GGTATAAAT CAGATTCAAA  
106741 TAGTAGTGTC GTAAACGGGA GGGAAAAACT AAAGGGATTA AAAAGTGAAT CTATTGTGTT  
106801 CTCCTCGCA GTCCTTAGGT CACTGCCCC CTGAGGGGCGG AGCAAAAAGT GAGGCAGCAA  
106861 CGCCTCCTTA TCCTCGCTCC CGCTTCAGT TCTCAATAAG GTCCGATGTT CGTGTATAAA

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106921 TGCTCGTGGC TTGCTTTCTT TTCGCGTACC TGGTTTTTGT TGTCAGCTGG TTAGACATGT  
106981 CTGGTCGCGG CAAAGGCGGT AAAGGTTTGG GTAAGGGAGG TGCCAGCGT CACCGAAAAG  
107041 TGCTGCGGGA TAACATCCAA GGCATCACCA AACCGGCCAT TCGGCGCCTT GCTAGGCGTG  
107101 GTGGGGTTAA GCGAATTTCC GGTTTGATTT ATGAGGAGAC TCGTGGCGTT CTCAAGGTGT  
107161 TTCTGGAGAA CGTGATCCGG GACGCCGTGA CCTACACGGA GCACGCCAAG CGCAAGACTG  
107221 TCAGTGCCAT GGATGTGGTT TACGCGTCA AGCGTCAAGG ACGCACTCTG TACGGCTTCG  
107281 GCGGTTAATC TTTTCGTCAG TTTTCTTCCA ATGGCCCTTT TCAGGCGCGC CCACCTCCCTC  
107341 TCAGAAAGAG CTGTGATTGT ATTCTTTCGG ATGGTAACAT CTCAATGGCT TTAGCTCGGT  
107401 ATTCTGCCAT GTATGTAGAA CTATTATAAA CCAGTTGGGA GAGACCAGGT TGTTTGGTCT  
107461 GAGTGGCTGC TAAAGCAGAA ATCAGCTAAG TAAACGAGGT CTCCGAGATA AGTGAGCTAT  
107521 AAACCTCAAT GCTATAGTTT TGACATGTCA AGCAACTTAA CGTGACGCGC GAGTCCGATA  
107581 AATGAGTAGC TCAGCTTTT AGTTTTAAAA ACGAGTTGTG CGTTATTTGT ACGAGAGCCT  
107641 AAGATGCTAG CTGCCTGGAA CTGAGTAGGT GGATTAAAAAT GGGTGTGAGG TCTGTTTTCC  
107701 CAGGCGTATC TGAATTAACG TCAGCAAAAG CTGTACTTTT AGCTTCCCTG GTAACACCTG  
107761 CCGTCCCTAA CCGCCCCCTG CCGGTAGCGC CAGAAGCCTT TACTTCCATT TACGGTTGAG  
107821 CTTGGCGTCC TGCTGAGTGA CGTCACCTCC CCCTTCTCTG GAGTAGGACT GCGGGTTAAA  
107881 GCTGCTTTGC TATTTTCAGT CCTCAGGCTG GAGGCTCCCC TAAGCAGGCT GCCTACGCAG  
107941 TTCGTAAATT CCCACTTAGT AGACTAAGGG AGTCTGTTTT ATAAATAAGG ACTCAAATTT  
108001 CTTCTGACTC CGAGGTCCGT GGCAGCAGCT ATAAGATGGA AGCCCCCTCT GATGTAAGAT  
108061 TCTCAGATGA CTTGCATCTT CACTGTACCT GTCAACCCAA TAGTCTTCTA TTCCTGCCTT  
108121 AAATTGTAAG TTCCAAAAC GATTTAATTG TGAAAGTTTC AAACGTACG ACCTAGGAAG  
108181 TGTCAAAGTT AGGTGACCAG ATTTTGTAGAA GTCAGCCAAA TATTCAGCAT CTTTGATTTA  
108241 GTAACAAATA TATTGATGGC TACTTCAGCA AAAAAATCA ACTTTGTTTT CTGGTTACTT  
108301 TGCTAACAG CTTCTCCTGA CAGGAGGATA TAGTGAATAG GCAGTTGAAT AAGTAGGTTT  
108361 GGGTGAGAGG TCTGAGCTGG AGATAAAAAAT GTGTGAGTCA TCAGCAGATA AATAAATGCT  
108421 GAGACCAGAT GAGATGGCTA AAAACTGAAA CATAATGTAG TGCAGCATTG TTTGTAATAG  
108481 TAAATGAGTG GCAACTGTAA AGTTTTATC AGAAAGGACT AGAGTGATCT ATACATCCAT  
108541 AAAATAGAGT ATTTCTCTAC ACAGCCCTAC TAAAGAATGA GAAAGCTGTA CTCCACTACA  
108601 TACTCTGGTG TACTCTGGCT CAGTCTTGG ACTCCTCTTT TCTTGGCTAA CTCAACTGGC  
108661 CTCACCACTT ACATGCTCTG TGCTCTGTCA AATAGTTTGT TCAACAGAAC ACCACGGCCT  
108721 AGCTGTAAGT GCCACGTAA CTTCTAGCAA TGCCAAAGCC TGTGATAGTG GCAGCTTCGG  
108781 GCTGTTTCTC ATTCCCGGGA TGCCTAACCA CCTCTCCAAA TTCTATCAGT TTGCTTCCAC  
108841 CCACTTCAAG CTTCAAGACG AAACATAGAG CTTAAGAAAT ATAGGCCCGG CAAGGTGGCT

108901 CACGCTGTGA ATCCCGGCAC TTTGGAAAGC TGAGCCTGGT GGATCACCTG GGGTCAGGGG  
108961 TTCGAGACCA GCCTGGCCAA TATTGTGAAA CCGCTCTCT ACTAAAAAA AAAAAAAT  
109021 TAGCTGGGCA TGGTTGCGG CGACTGTAAT CCAAGCTACT CCGGAGGGTG AGACAGGAGA  
109081 ATAGCTTGAA CTCGGGAGGC AGAAGTTGCA GTGAGTTGAG ATCGCGCTAT TACACTTAGG  
109141 CCTGGGAGAC AAGAGTGAAA CTGTCTCTCT AAATAAGTGT TTGCAATTAT AAACCATCTC  
109201 CCTGACCTTA AATCTCTAGA CTCATATACA ACTGCATATT TGATGTATCT AATTGAATAA  
109261 TGGGCATCTC GAACTGTGCC AAAATATGTT TATACGTAAA CACCAAGTCT GTTCTTCCTC  
109321 TGATATTTGT CATGTCAATC AATAGAATC CATTCTTCAA GCAGCTTGGG CCAGGAATTG  
109381 TGCAATATTG TTTGTCCTGA GCTTCTTACA ACTTTCACCC AATGCAGTCA GCTCTGTTGA  
109441 AAATCAATCA GAATACCTTT CATTGTTTTT TTTGCTGCTT CTCTAGGAGC AAGCTGCCAT  
109501 GGCGGTTTGT CTGAATGACC ACAGTGACCC CAACTGGTC TTTGTTTTCA CTTTAAATCC

109561 CCCTGTCATA CAGTTTTTTC TCTATCCAGC ATCAACAGTG ATCCTTTTTG AAGGTATTAT  
109621 GTCCACTGTC TGCTGAAAAG ATTCCACTGG CTTTCCATCA CCTTCATAAT AAAAACCAGC  
109681 ATCTTATCA TAGCTACAA GTAAGATGAC CAACCATAC AGTTGCGCTG ACTCTCAGGG  
109741 GTTCTCAGG GTGTAAGACT TACAGTGCTG AAACCTAGAA AGTTCCAAGC AAACCTAGGAT  
109801 GAGCTGCTCA ACCTACTAGA TCTGTACTCT GGCTACCTC TGACCTCATT CTCTTCGAG  
109861 TTCTTTCTCT TCACTGACCT TGCTGTTTCT GGAATGGACC AAGCATTTCC AGCATCAGCA  
109921 CCTTATATC TATCTTTCT CCTAGAAGG GTCTGTCTT GGATATCTAG ATGGCTCTAG  
109981 ATCTCATTTT ATTCAAGCCT CTCCTCAAAT ACCAACCCTA CGAAAGAGAC CTCCTATAAT  
110041 CATCCCTTGT AAAATAAGCT TTTCTGCTCA TTTAGCATAT ATATATATAG TTGACTATCC  
110101 TCAATAGCAT ATATATATAA CATTTCCTCA CCTAGAATTA TATATGTAAT AATATATTTA

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110161 ACAAAAAATA CATATAACTA GATATATTTT ATTTTGTGTT TGTCTCTCTT CCCCCAACTG  
110221 GAATATATTT TTTGAAGGTA GGGACTTTGT TTTGTCCCAG AAGTATCCCT AGCACCTTGA  
110281 ACAGGGCTGA CGTTTAAACAG GTAGTTTATG GAGGTTTGT GAATGAAAGG ATGTGTGAAT  
110341 TTTCTATGTA AGTCTCCAGG CTCTCCACTA AGCCCACCAG AATGCTAACA CAATCAATTC  
110401 CCCATCTCAT TCCTTGACCT GCCACTGCCT GAAGCAATCA GCGTGCACTT TCTCTTTAGA  
110461 AAATCTGGGG GATAGTCTAG GGGTTGCAAA TTAAGCAACA TTATCTTTGT TCTGAACAAG  
110521 GACTGCATGA GTGTTAGGAC TGAAGAAGGC CCAAGGTGGT GGTGGGTATG CCTAAGATGA  
110581 GTATGACATA TCAGCAATGC TATGAACATA GCAATGCTAT GAAAGGCCAG GCAAAAACGTA  
110641 ACAGGAGCTA GTCGTGGCTT ATTGTTACAA CGACTATACC TCCCATATGG GTAATCGATA  
110701 TCCACACACC CCTCTACATT GACTCTGGAA TTCAGGAAAG GGAATTAAAA TTTTCTAACT  
110761 TATGTACCCC AATGATTTCA ACAATATCTG GCATATGAGA TCAATAAATA TCTTTAAAT  
110821 ACCAACTAAG AAAGACATAA AATGACCCAC CCTCCATACC AGGCTCATTT TTGCTCCTCT  
110881 GATTCTGAA ACTATCCAGA ATGCAGCTAT GAATCTCTC CATTTGTCAGT TTTAAATTAA  
110941 GCCAAGCTGG GTACTTGTGT AATTCCTCAA GAAATCCTGG ATGAAAACCTG TCAGGTGGAA  
111001 AACAGGACCT CAAAATAAAG AGACATCCAT CACTGAAGCT AACATCGTGA GGCTGAAATC  
111061 AGTCTTATAA CAATGGTACC AAAAAAGACA CAATGAGAGG CATTTGTGAA TATTTACTCA  
111121 GATGAGAGTA AGATATTTCC CTATCAGCTA ACCTGAAGTT CACATCCCTT TTCCAGCTGA  
111181 GTTCTGAAGC TAGATGTACT TAACTGGAAC ACATAACTGC ATCAGGAACA TCCTTTAAAA  
111241 CTATGGCTAC CATGGCTTGA CTGGACAAAC CCCAGGCTTC CAGGTTTAGC ACAGGTGGCC  
111301 CTTACAGAC CAACATTGCC TATGTACCA ACCTCATGTC CTACCACCTT GCTTGCATCA  
111361 TTTCTCTCTC TGCATATATA AAAATATATG TGTATGTATA TAATCAGCTT TATTGATATT  
111421 TAATGTACCA CAAAATTTGC CCACCTTAGG TACAGTTCAA TGAATTTTAC CGTGTTTTCT  
111481 TAGTTGTACA ACCATCATCA CAATTTAATT TCGGAATATT TCTATCACCC AAATTTCCAT  
111541 TTCTGCGTAA AGGGGGAAAA AAAAAAGTTA ACTGCTGAAG GCCGCGGTAA CACTGAAAAA  
111601 GGTGCCTTTT CTCTCTAAAA CAGATTTTAA TCTCCCTGA ATTTAGTGTC CTGGGTATTC  
111661 CAGGAGTCTG AATAGGGTTT CAATTTTCAG GGTCTTTTAA ATAGAGTAAA ACTGTATTGG  
111721 TGGCGATAAA TTTAGTATTG CTCTCAGTAC ATGATTGAGG GATACTTAAA TGTCTCTGTG  
111781 ATTTTATTTT ATAATCGCTA AAAGATGGTT TTTTTTTTTC CTAAAACAGG GTTTTTGTIT  
111841 TTTCTCAATA AGCTTCTTAG CTTCCTCTCC GGCTCCCTGG CTTGCCTCAG GAAATATTAG  
111901 CTCATCAGTT CTGATTGGTT GACAGCTACG AATGGCCCTC ATTGATTGGG CAGCGCTTCT  
111961 TTGTCCCTTG GAAACTAATA CAAATTTTAA ACACACTTTT TTTTCCACTC TTTCTTCAGA  
112021 GTTGAATAT CGTTGCTCCC CTACCCATAT GTAGTGAGTG GAGGGCAAAC TTGGAGTTCC  
112081 CCTAATCTTT CCTTTTAGG ATCTCAGCTC AGTATCATT ATCTTAATTA CACATTGAGC  
112141 TTCTTGACTT AATGATACA GCTCTTCTTT TGTTTAGTTG GGCGGCCCTG AAAAGGGCCT  
112201 TTGGTTTCAA AATGCAAGCT GTGGAGAAAT CAGCAACCTT AACCGCCAAA GCCATAAAGG  
112261 GTGCGTCCCT GGCGCTTAAG CGCGTAGACC ACGTCCATGG CAGTGACTGT CTTGCGCTTG  
112321 GCGTGCTCCG TATAGGTGAC AGCGTCACGG ATCACGTTCT CCAAAAACAC CTTGAGCACC  
112381 CCGCGAGTCT CCTCGTAGAT CAGACCAGAG ATCCGCTTCA CACCGCCACG CCGGGCCAGA  
112441 CGCCGGATGG CCGGCTTGGT GATGCCCTGG ATGTTGTAC GCAACACCTT GCGGTGGCGC  
112501 TTGGCACCCC CCTTACCAA ACCCTTCCCG CCCTTACCAC GTCCAGACAT GACTTCCCAA  
112561 GAAGTGAACC AAGAGCAAGT GAGAGAATAG GAAACCGATC TTTATATATC TACGTTACCC  
112621 CTGCCCCCAC CTCCAGCGGA CACTGAGACT GAAAAGCGCG CAGGCGGGAA ATGTGACGCC  
112681 TACAGTCCGC TCCTTTAAACC CCTCTCCAA GCCCAGGAA ATGGCGGGAG CAGCGATTGG  
112741 GGGAGGGTGG GGAGATGAGG GTGGGACCAA GCAGGCTTGA CCAATGGCCT TTATTTTCTT  
112801 AACAGAGCTA CAGGCTTTGA GGAACCTGGT TAAGAATTAA ATGTAAACCC ATTCTGACTC  
112861 CAGAATTATT TTAAGTCGAA CTTTTTTTTT AACCGAATCT CTCTGTGCGC CAGACTGGAG  
112921 TACATTAGAG CCATCTCGAT TCACTGAAAC CTCTGCCTCT CAGGTTCAAG TGTTTCTCCT  
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113161 GCGACCGGCC GAAATCGATT GGTTTTGAAG CCTTCAGTAG CATTAACACG AAAAGTGTCTC  
113221 CCAATGCATT CCCTTTTGTG TTAATTTGGT TTCTTACAGC TACTTTACTT GAAAAGGTGG  
113281 TGGCTCTGAA AAGAGCCTTT GCTTGGACCG TCAGAGAGAC CACAGTAATC ACGCCCTCTC  
113341 TCCGCGGATG CGGCGGGCGA GCTGGATGTC CTTGGGCATG ATAGTGACGC GCTTGGCGTG

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113401 GATGGCGCAC AGGTTAGTGT CCTCAAATAG CCCTACCAAG TAGGCCTCGC ACGCCTCCTG  
113461 CAGAGCCATC ACAGCGGAGC TCTGGAAACG CAGGTCTGTT TTAAAGTCCT GCGCAATCTC  
113521 GCGCACCAGG CGCTGGAAG GTAGTTTACG AATAAGCAGT TCAGTGGACT TCTGATAACG  
113581 GCGGATCTCG CGCAGAGCCA CGGTGCCCGG CCGGTAGCGG TGGGGCTTTT TCACGCCGCC  
113641 GGTGGCCGGA GCGCTTTTGC GGGCTGCCTT AGTGGCCAAC TGTTTGCCTG GCGCCTTGCC  
113701 ACCAGTAGAC TTCCGAGCAG TTTGCTTAGT GCGAGCCATG ACGGAAAAAC AGCACAGCGG  
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113881 AAGCCAGCAA CAATCGTGCA GTTTCACCGG CTACTATATT CTATTCCAAC TCTACAGATG  
113941 ATTATTTAAG TGGTATTTTA TTACTACTAT TATTTTATTT TACTTTTGCT TTGTTCCCCA  
114001 AGCTGGTCTT AAACCTGGGC TCAAAGGATC TTCCCGCCTC AGCATCCAGA GTAGCTGGGA  
114061 TTACAGGGGA GCCCCACTGC GCCGGCTTGG ACTTTAATTT TTAAACTTG TCCTCTTCTA  
114121 CATCTGGTTT TCATAACCTG AAGGCTGTGT TTATTTTCCA TAAAACAAGG CATTGATTCC  
114181 AAAGGTATTA TAATCCCCA ATTCCGTATA ACCTTCAGCT CTTTAGGAAA AAAAAAAAAA  
114241 AAAAAAAAAA GAGGGAATAC TGCTCACCTC CTCTCCGGAA ATGTACCCTT TACGGGAATT  
114301 TCTGAAACCT TTCACAAGAA TTGGATTCCCT TTGTAATGCT TTAATTGACT TAGGAGTGTT  
114361 ATTGAAATCT ACAAAGCATC TCAAACATAG TAGGATTACA CTATTACTCA GAAACATTTT  
114421 CTATGAGACG TCTTTCTCTT GATTATGCTC TTTGAATCCT AAACCTGTCAG CGTTCTGCAG  
114481 CTTTTGTTTT CTAAAGCCTA GGTGTACTCT GCCAGTCACA AAATGGCGTT TCTCCAGCAC  
114541 TGCCGCCAGG TACCACCAGC TGGGAGTTGT TCCTCTTGC GAGCAGGAGG TGGACTTGGC  
114601 CCAAGAGAAA CTGGATAGTG GTTCGCAAGG AACATAATT AGCATTGCCA AGAGCTAATG  
114661 CAATCATTTT GAAAATCTCA AAACACTGAA AAGTGGATTG TGACCTTTTT AAATTCACAA  
114721 GAGACAGGCC ACATTCTATC TTTTGATTGG TTTAGGCTAT TTTCTTGAAC AGCCATTGAG  
114781 AAAGCAGATC TATCATCCTT CATTTCATG GAGCGTCCC ATTTTATTTG AAACAGTTT  
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114961 AAGAAAGGTT TATATCTTTC ACAAAGGTT TACTTACAAA AATCTTCCAA TTTTGTATAC  
115021 CTGTGTTTCA TAACTGACTA GCCGTCAAAC CAAGATGTAG AGTTTCCAAC CGTTATTTTC  
115081 CAAATTTTTA GAAATTACGT GAAATATTTG AATGCATGCC TTCTCAATAA AATGGGACGT  
115141 AGGAAGCACT GGTGCAGAAG ATGGGTACAA TACTTATCTG GGACCACTCC ATTATTTGGT  
115201 TGGCACGTTG TTTGAACAAA AAGGGGAAAA GCTCAGGTTA CTTAGCATGG TTCGGACTTA  
115261 TTTGAAAACT ACCACAGCAG GAGCGGAAAT AAGACCGCAT TACCTCACTC TCTGCTGTGC  
115321 TGTGCTAGGG GGTATCCAG AATAGGATTG TAGAAGTGGA TGTCGATTTA ATAGTTTTTT  
115381 ATTCTCCCAT TAGCTGAGTC TCTGATTGGC AATGTGAGAT CGTTTAGCT TATTGATACT  
115441 TTGAAATGCA CTTAACAGCC ACAAACAAGT TAAAGGGTTG TTACCATAAA ATCTTATCCC  
115501 CAGGGTGTGC TTGCATTTAT CACCCGTGTT TGCTTTCACA CTAAGTGGAC TTAACCCCC  
115561 AGCAGAATGC CTGTCAGGGA ACCGTTTCG TGGACCCAGC ATTTAACGCC TTTTCGAGGC  
115621 TTGTGAGGCC CATAAATATT TGTGAATAA AAGAATGAGT TGACCATGTC ATGGTGCCT  
115681 GATTGCGTGT GCTGACATGG AACACAGGTT GTAAACCTTA ATACCAATTT GGGGCATGTT  
115741 GTATGGATGA AAAGGGCATT GGAAATTCCT GAAGTGCATC CCACATTGGA CTGTGGAAAT  
115801 AAGTTGCAAG TGCAGAAACG TTCCACACT TGCAGTTGA GTATTAATTG CAGCGTTTGT  
115861 GAATTCTGGT GTTGTCTACG ATTCATTCTT GTTTGACGTG AAAGGTATTG GCGAGACACA  
115921 TCGCTCTAAA ACATTGCCAG AAAATGTAAT AGAGTTGATG ACAACTGGCC CTAACACGGC  
115981 CTAAAACTCG CACTTTTCTC TCCCTCCGCA ACTATTCAA ACACTGTATT TTACATTTCT  
116041 TGCAAATTAA AAATAACAT CTCTGGCAAC GGACCTCTAA AAATTTCTAA TAAAACTCCT  
116101 CGGATGCTTG TGGCACTGCA TTGTAAACC GCCCCCTCTC AACCTACTCC CTAATAAAGA  
116161 GCTGCTTTTT GAGAGAGAAG CCGTACCCTC TGATGTTACT GGGCGGCAGT CTGCCTACAA  
116221 TTTCTTTCAC AATGAGGCAA CCAGAGCGGC TTTTCTGTG TGTTTGCTTG CGTTGAGGGG  
116281 AGCAGGACCA TAGGCCCTAG AGGCCCCAG CTGCCTTCTG AGACTGGGCG AAACCTCGG  
116341 CAGCGCGCAG GGGGCGCTAG GGGCGGAGG GCGGGCACTG ACGGGCACA ATCAGCGGCT  
116401 AGTCCCACCC TATAAATAGG CTGCGTTGGG GCCTTTTTTT CGCATCCTGC TTCCTCAGGT  
116461 TTATACCACT TTATTTGGTG TGCTGTGTTA GTCACCATGT CTGAAACAGT GCCTCCCGCC  
116521 CCCGCCGCTT CTGCTGCTCC TGAGAAACCT TTAGCTGGCA AGAAGGCAAA GAAACCTGCT  
116581 AAGGCTGCAG CAGCCTCCAA GAAAAACCC GCTGGCCCTT CCGTGTGAGA GCTGATCGTG

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116641 CAGGCTGCTT CCTCCTCTAA GGAGCGTGGT GGTGTGTCGT TGGCAGCTCT TAAAAAGGCG  
116701 CTGGCGGCCG CAGGCTACGA CGTGGAGAAG AACACAGCC GCATTAAGCT GGGCATTAAG  
116761 AGCCTGGTAA GCAAGGGAAC GTTGGTGCAG ACAAAGGGTA CCGGAGCCTC GGGTTCCTTC  
116821 AAGCTCAACA AGAAGGCGTC CTCCGTGGAA ACCAAGCCCG GCGCCTCAAA GGTGGCTACA  
116881 AAAACTAAGG CAACGGGTGC ATCTAAAAAG CTCAAAAAGG CCACGGGGGC TAGCAAAAAG  
116941 AGCGTCAAGA CTCCGAAAAA GGCTAAAAAG CCTGCGGCAA CAAGGAAATC CTCCAAGAAT  
117001 CCAAAAAAAC CCAAACTGT AAAGCCCAAG AAAGTAGCTA AAAGCCCTGC TAAAGCTAAG  
117061 GCTGTAAAAC CCAAGGCGGC CAAGGCTAGG GTGACGAAGC CAAAGACTGC CAAACCCAAG  
117121 AAAGCGGCAC CCAAGAAAAA GTAAATTCAG TTAGAAGTTT CTTCTAGTAA CCCAACGGCT  
117181 CTTTAAAGAG CCACCTACGC ATTTACAGAA AAGAGCTGTA GTACACAGAT GAAATCCCCC  
117241 AAGCAAATGC AACACGCCCT CAATTATATT AGAATCACTT GGAGAGTCGA TAGAATTTTA  
117301 ACATAGCCTC ATCTAGTAAG AATTTACTAC TCAATCTATC AAAGATAGCA AGGTGAATTC  
117361 AAATGCACCG AGTTAAAAATC GAGTTTTAAA GTCACCTGGG TTTCGGTAGC CGGAAGTCCC  
117421 GCGTCTCAGC ACTCCAAGCT AATTAGTCAT AACCGTATTG AACCAAGGTT GATATTGCGT TTTGGGGTCA  
117481 CCCAGGCTTG AGGCTTTTTA TTATACAAGG TTAAAGTGGG GATATTGCGT TTTGGGGTCA  
117541 ATATTGCTAA AGTAGCATTT TCCGAAATTG GGTGGTCTTA AGAAATGCTT CTGGGATAGT  
117601 TGGCAAAATA TATGGCTTAA CCACGCCCTC TCCACAGGAG TGGCTAGCGA GCTGTCTGTC  
117661 CTTGGGAAGG ACGGTGACCC TGCTGGCGTG GCTGGCGCCC ACGTTGGCGT CCTCTGAAAG  
117721 CCCCCCAGG TAGGCCTAGC TCGCTTGCTT TCTGCAGCGC CATCATGACA AAGCTTTGAA  
117781 ACGCAAAATG CTTTCTTTGT GCAGCGCCTT ACCATGGGTG CACTTACGGG CTGTGCACTT  
117841 GGTTTAGGCC CTTGTCAGGA CAAAGGAGCT TAGTTTGTG GAGTTTGTAG GCTGCAACCC  
117901 AAAATCCCTT GCTCGGTTTC TCTGTTTTTA GAAACGGAAG CGCCCTGATT GGATATTTGA  
117961 AAATTAATGT GCTTAACTGG ATCGTGTTC ATCAGTCGTG CAGGATTTTC AACCCCTGTG  
118021 GAGCCACAC ATTCAAACT GAAGATCCTT TTCTCAGAAC TGCCCCTTTA AGCTTTTGCA  
118081 ATTTAAATTC TGGGGGTCAG ATTTTAATAA TTGGACTTTT TTGTTTACAT CTGACAAGAG  
118141 TATATGATGA GCCAAGTTTA CTCACCTTTA CTTAGTGCAG TTCAATTCTA AAAGTTTATT  
118201 TTTGCGTGTG TGCATATGAG TTAATAATCA GTTGTATTTT TCAAACGGTC TTTTTCAT  
118261 TGTTTTGCTT AGCTCCTTCC ATCGTCTAAA GTCAGGGATA CAGGCACATC ACATCCCTGT  
118321 TCCCCCTTCC TCAAATAAT ATGTAGCTAC CTAGGTTTAT CCTTTAAAAC AAAAATTCTC  
118381 ACCTATTTTT GTGAGAAATA TACATGTTTT TCTTTGAACT AAGTATTTTA CATAACCTA  
118441 TCTATATACA TGCATACTTG TGGTTTTGTT TTTTAAAAA AAAAAAAAAA AAAACACGTT  
118501 ATCTTTTGAG ACTGGGTCTC AGTCTGTTGC CCAGACTGGA CTGCACTGGC ATAATCACAG  
118561 CACACTGTAA CCTCCAATC CTGGGCTCAG GCTATCCTGC AGCCTCAGCA TCCGGAGTAG  
118621 CTGGGATTGC ATGCACGCAC CACCAAGCCG GGCTTTTGT TTTTATTTT TGTGGAGACA  
118681 GTCACACCAT GTTGTCGAAG CTGGTCTAGA AATGGCCTCA AGTGATCATC GACCTCCCAA  
118741 AGTGTGGGA TTACGGTCAC TGTGCTGGC CTTGTATGCA TAATTGTTTT GTCTTTTGAT  
118801 TAGGGTTATT AATTTAAAAA ACAAAGCCTG GACGCAGTGG CTCACATCTG TAATCCCAGC  
118861 ACTTTAGGAA GCCAGATGGG CAGATTACTT GAGCTCAGGA GTTCAAGACC AGCCTGGGCA  
118921 ACATGGTGAA ATCCCATCTT GACAAAAAAT ACAAATAATT AGCAAGGCCC AGTGGCACGC  
118981 ACTTATAGTC CCAGTACTT GGGAGGCTGG GGTGGGAAGA TGAAGGGAAC CTGGGAGGTA  
119041 GAGGCTGCAG TGAGCAGAGA TCGTGCCACT GCACTCAAGC CTAGGTGACA GAATGAGACC  
119101 CAGTCTCAAA ACAAATAA TAAAAATTTT TTACAACGAT GTTATATACA CTTCTGCATG  
119161 TTGCTTTTCT CTTAACCAAA CTTTCTAAA ACCCTGTCAT GAAAAAGAA ATCCTTCACA  
119221 TGGAATAGCA TAAGTTATTC ATCCATTTCT TATTGATAAG CATTGATGTT TCCAGTTACC  
119281 ACTGCTGAAC ATGGTGCAAT TGAATAGAAT TCCAGGGCTG AGATTGCTAG GTTTTAGGTT  
119341 GTATTTTATT ATTTTATTTA TTTATTTATT TATTTAGACA GAGTCTTACT CTGTCACCCA  
119401 TGGTGGAGTA CAGTGCCATG ACCTCAGTTG CAACCTTTGC CTCCTGAGTT CAAGCGATTG  
119461 TCATGCCTCT GGTCTCCCGA GTAGCTGGGA TTACAGGCAC CTGCCACCAG GCCTGGCTAA  
119521 TTTTGTATT TTTAGGAGAG ATGGGTTTTC ACCATGTTGG CCAGACTGGT CTCAAACCTC  
119581 TGGCCTCAAG TGATCTGGCC ACCTCGGCCT CCCGAAGTGC TGGGATTACA GGTGTGAGCC  
119641 ATGGCGCCAG ACCTGGACTT TGTCTTCTGT TTCATCAGTC CTTCTGTTGG TTCAAGCACA  
119701 GTATCACACT GAAGACTGAT GATTCTATAT AAATATGGTA AAGACTGTAC ACCCTAAGTG  
119761 TTCTTATTTT TTAATTTTAA GGCAATTTTA GATTCCAGCT TTCAAAGAA TTGTGGAATG  
119821 CTTAGAGCTA GAGAAGCCTT GGAAGTCATT TAGTTTTTGT TTTGTCAGAG AAAATTCTGT

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119881	AGAGACTCTG	TCCTGCTCTC	ACTGAATACC	ATCCCATAGT	ACCCCCCAAC	AGCTTTAAAG
119941	GGCAATAATA	CCTTATGGAC	AGTATGCTTT	TCCTCAAATA	TATTCTAAGC	CATGGTCAAT
120001	GCAAAAGAGT	GAGAAGGAAA	GTAAGAATAAG	TTATCTAAGA	ATCAGTGGGT	GCTCTCTTTA
120061	AACTGATTTA	TCACTCCCCC	TTCCAAACTC	TCTTGAAGGT	CACTCTGCCT	CCCTTTCTAC
120121	ATAAGAACTC	CTAACTCCAA	GGGAGGAAGG	TAAGTTATTC	TTATTCCTTG	CTTAGAAAAA
120181	GAGAAAAATAG	GTTTGGTAAG	CATCCGCTTT	CTGCTACCAT	TCTCTGTGTT	TCTGTGTTTT
120241	TTATAGGATC	ATTCAATTAT	TGGTTGGCTC	TTGAGAGGGA	ATGCAAGGTT	CAAGGACACA
120301	AGCCTAGATC	TTGCCTGTAT	AGAACCCTCAT	GATGTTATGC	TTCTCTAAAA	TGAGGCCTGG
120361	AGGAGACATG	TTGAAAGTGA	CCCATAAATC	TGCAGTATCT	CATGTCTCTC	AATGGGGACA
120421	AGGAGTACCA	TGGGAAATAG	CATTAGGTCA	ATGACAGTAA	CAACTCCCAG	GTGAGTTGAT
120481	TTATTCTTTT	ATTTATAAAG	TTGTTAATAT	GCTACATAGT	CCCTAATTTT	GCCACAAATA
120541	GTCATTATTT	TAATTTTCATA	TTTCACTATT	GATAAATGAA	GGAAAAAATG	AGTAGCAGTT
120601	AAGCAGTCCA	TAAACCTACA	TATAAAGCAA	ATTGGAGATT	TTAAAATTGA	TTCTGGATGC
120661	TTAAAATCCT	TCTCATTGAA	AAAAAATTTT	GTATTAGAAG	ATTTCAACAT	TCTTTAAACT
120721	GAGAAGCATA	ACATATAAAC	AGAAAACCAC	AGCAAAACAA	AAATGCAAGG	CTCAATAAAT
120781	GAACACAAAG	TGAACACCAT	AATAATTGCC	ACACAAGTAA	AAAAACAGAA	AATCAGCCAA
120841	CCCTCCCGAG	GCCGCCTGAT	GCTTGCTTCC	AGTCACATTA	TCACTCCATC	TGCCCTAAAC
120901	ATAACCCCTA	TTTTTGATTTC	CAATGCTGTA	ATTTAGTATG	CCTGTTTTTG	AAACATATAA
120961	AATGGAAATA	AAACAAATGT	AATCCTATGT	ACCTGACATA	TTTCACTCCA	GAACATTAGG
121021	TTTGAATAGA	TTTCATCTGTG	TTGCTGTGTA	TAACTTTAAT	TCATTTTTAT	TGTTATGTAA
121081	TATTCATGT	TATGAGTGCA	ACAATTTAGG	TGTCTACTGT	TGATGCATAT	TTGCTTCCCT
121141	TTTTTCAGCTA	ATATAAACAA	TACCGTGAAT	ATTCCTGTGT	ATGTGTCTTG	GTATATATAG
121201	GAATACATAT	TTTGTGTTGTA	TACCTAGGAG	AGGAATTGTT	GGGTCAAATG	CTAAACTCTT
121261	TTTGAAAGTG	GTGATATTAG	GTTTACATGC	GATGAAATGA	AAATTAAAAA	CACAGTTATA
121321	AACAGCATGG	ATGAACCTCA	CAAACCTAAT	GTTGATGGAA	TCTAGCTGGG	AATTCCTGTT
121381	CTTCCATATA	CTTCCCAATA	TTTTTTTCCA	ATTAAAATTG	TTAATCTTTT	GAAGATGTTA
121441	TCCATTGTGG	CAGATGTGCA	GTATTATCTC	ATTATGGTTT	TATTTTACAT	CTTTTGCCCA
121501	TTTTTTCTTA	ATTGGATTGT	ATATCAGTCG	ACTTGGGCTG	CCATAACAAA	AATACTAGAC
121561	TAGGTAGCTT	GAACAAAAGG	AGTTTATTAC	CTCACAGTTC	TAAAGGCCAG	GCCAGAAATC
121621	CTAAATTGAG	GTGCCAAGAG	ATTCAAGTTT	TAGTGAGGGC	TCTCTTATTG	ACCTGAAGAT
121681	AGTTGCTGTC	TTAGATTGTT	TGGTGCTGAA	CAGAATACCA	GAGACCAAAT	AATTTATAAA
121741	GAATACAGAT	TTATTTCTTA	CAATTCCTGGT	GGCTATAAAG	CCTATGGTCG	AGGGGCCAC
121801	CTCTGGCAAG	GGCCTTCTTA	GCTGTATGTC	AGATGTGAGA	TGTCATCTCA	TATTTCAAAC
121861	ACAGCAGTCG	CCTTTTGTGT	CCTCATGTGG	CCTCTTCATA	TGCCCATAAA	ATGACCTCAT
121921	GTCTCTTCCT	TTTCTTATAA	GGACACCAGA	TCTATCAGAC	TACTGGCCTA	CTCTTATGAC
121981	CTCATTTAAC	CTTAAATATC	TCCATAAAGT	CCCAAAATCC	CTATCTCCAA	ATATAGGCAC
122041	ATTGGGTGTT	AGAGTTTCAA	CATCAATTTT	GGGGGAACAC	AATTTAGGCC	AAAAAGATTG
122101	TGTTTTTTCT	TGTTGGTTTA	AGATAGCTGT	CTTTTTGTCC	TTTTTGTCC	TTCTTTTTTT
122161	TTGAGGTGGA	CTCTTGCTGT	GTCACCCGGG	TTGGAGTGCA	GTGGCGCTGT	CTCAGCTCAC
122221	TGCAACCTCC	ACCTCCTGGG	TTCAAGAAAT	TCTCCTCCTC	CCAAGTAGCT	GGGACTACAG
122281	GTGCATACCA	CCGCGCCCTG	CTAATTTTTG	TATTTTTGAT	AGAGACGGGG	TTTCACCATG
122341	TTGGCCAGGC	TGGTCTCAAA	CTCCTGACCT	CAGGTGATCC	ACCTGCCTCG	GCCTCCCAAA
122401	ATGCTGAGAT	TACAGGTGTG	AGCCACCAAA	CCTGGCCTGT	CTTTTCTGTT	TTAAGTTTTT
122461	AAATTTTGCT	CACGAACCCT	TTATCCATTT	TATGTGTTGC	AGGTATTTC	TCTGTAACTT
122521	GTCTTCACTC	TGTCAGAGGC	TGGAGTGCA	TGGCACAATC	ACAGCTCACT	GCAGCTCCA
122581	CCTCCCAGGA	TCAAGCGATC	CTCCCATCTT	ATCCTCCTTA	GTAGGTGGGA	CTACATGTGC
122641	AGGCCACCAT	GCCCAGCTAA	TCCTTGATAT	TTTTTGTAGA	GATGGTGCTG	TTGCCCAAGT
122701	TGGTCTCAAA	CTCCTGAGCT	CAAGCAATCC	ATCAACCTTG	GCCTCCCAAA	GTGTTGGGAC
122761	TAGAGGTGTG	AGCCACCACT	GCACCCAGCC	AATGATATCT	CATGATGCAT	TAAAGTCATT
122821	AAATTTAGTGT	ACTCAAATTA	AGCAACATGC	CCTTTTATGC	ACAACCTTTT	TTGTATCTTA
122881	TTTAAAAAAT	CATTTTCTAT	TTCAAGGTCA	TGAAGATCTT	ATTTTATAAT	ACCTTCTTGT
122941	GAAATTAGTT	CTCAAGACTA	CCCTCACTTC	TAACACCAAT	TATAAGTTGG	GAGGTCTGTG
123001	GTTCCCAATC	AACCTTAGGT	TAGTAATTTG	CTAAAAGGAC	TCACAGAACT	TGCTGAAGCT
123061	GTTAGCCTCA	TGGTTACAAT	TTATTATAGG	ATATATAGCT	TATTATGTCA	TTCCAATGCA

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123121	ATGTAAAATT	ATACAACTAC	TTTTAAAAAG	ATTTTAGCAT	TTGACCCAAC	AATTTCACTC
123181	TGAGGTATAC	AAACAGCAGA	TATGTGTGCA	CATATATACC	AAGACACATA	CACAGCAAAA
123241	TTCATTGTTT	GTAATAGTTG	AAAAGGGGAA	ACAACTCAAG	GAATAAAGAT	TAAAAATCAGC
123301	TGAGAAAAGA	AACACACAAG	GCAGTATTAT	GGATCGAATT	GTATGCAGAT	CTCCCTTGCC
123361	CCCAGAAGAT	ATGTTTAAAG	TCCCAACTCC	CAGTACCTCA	GAATTGTGGC	CTTATTTGGA
123421	AATAGGATAG	TTGCAGATAT	AATTAGTTAA	GATGAGGTTA	TAGTACAGTA	TGATGGGCTG
123481	GTGACTTAGA	AGAAGTAGTA	TATATATATT	TTTAAATAGA	ACTAGTATTC	TTCTAAGGTG
123541	GTCACGTGAA	GACAGACACA	CACAGGCAGA	GACTGAGGTT	ATGCAGCTGC	AGGTCAAGGA
123601	ATGTCAAAGG	TTGCCAGCAA	GTACGAGAAG	CTAGGAAGAG	TCAAGGAAGG	ATTTTCTTAC
123661	AGGCTTCAGT	GGAAGCATAG	ATCTAATGAT	ACCTTCATGT	CAGATTTCTA	GCTTCCAGAA
123721	CTACAAGAGA	ATATATTTGT	TGTTTTAAGC	CACCCTAGCT	TCTAGCTCTT	TGTTACAGCA
123781	GCCCTAGGAA	ACTAATATAG	GCACAATCCA	GGCAAGTTCC	AAATATGAGC	TTCCAGTTGT
123841	CCTCTCCAG	TAATATGAAC	AGTATTACTT	TCCCAGCATT	AATGTGTGAC	AATACACATG
123901	ACGTACAGAG	CAGTCCCCAC	TTATGCACAA	AACATATGTT	CCAGGACCTC	CAGTGGATGT
123961	CTGAAACCAT	GGATAGTACT	GAACTCTATA	TAGCTGTTTT	TTCTTATACA	GACACAGCTA
124021	TGATAAGGCT	TAATTTATAA	ATTAGGCACA	GTAAGAGATT	AATAACAATA	AATTAGAATA
124081	ATTGTTAAGA	ATATACTGTA	TAAAAGTTAG	GTGAATGTTT	ATTTCTGAAA	TTTACCGTTT
124141	ATTATTTTTG	GACTGCAGTA	GACCACAGGA	ACTAAAACCA	TGTAGAAACC	GTATACAAGA
124201	GAACTGTATT	TCACCCGAGC	CTCAGTGTGC	AGTTTTAATG	GCCTGCCATG	GTTGACTGCT
124261	CACATGGCCG	ATCTTTTAGT	CTACCTCCAC	AGGTAGAGCT	GATACTGTGT	GGCTCAAAGT
124321	TCCTATTATA	AATCACATTG	TTGACTGTGT	GGTGGTCAA	ACCTCCAGGT	AAACAAAGAC
124381	ACACTTATCA	GTGAGAACAT	TTCAAGGGTC	TAAAATTTCAT	CTCCAGTAG	CTGAGGGCAA
124441	AGGCTAGACC	TCTTTTGGG	TAAAGATAAT	TTTTTACCAT	ATACTTTATT	TTGCTTTTCA
124501	TGTTTAACTT	TATTTTGCTT	TTTCATGTTAG	TTCCCCTGGA	ATTGTTTTTT	GTGTATAGTG
124561	TGAAGTAGGG	GGTCAAGTTT	CTTTTTTTTT	CCTTTTGTGTT	CTTTTCTGTG	TTAAAAGGCT
124621	ATACAATTGT	CCCATGCCAT	TTATTTACAA	GAGTCCTTTC	ACCATGTTTG	TATGGTGCCA
124681	CTTTAGATGT	AAATCAATGT	CCATATTTGT	TTGAGCCTGT	TCCATTGCTT	TGTCTATTTT
124741	TGGACAACAC	TGCCCTGATT	ATTGTCATTT	TATCAGTTTT	GATATTTAAT	AAAGCAACAG
124801	ATTTGTTTAT	TTTGGGCCCT	TGGATTTGTG	TATTAAATTT	GAACCCTGTT	TGTCAATTTT
124861	TATAATAAAG	CTTATTGGGA	ATCTGATTAG	GATTACAATG	GTTTGTGAGA	TCAGTTTGGG
124921	GACAATTAAT	ACCTTTAAAA	TATTGACCGC	TTCAACTGTA	AATATACTCC	TCCATTATTT
124981	AGTTTTCTCT	TTTAATTTAT	CTGAGTAATA	CATTATAGTT	TTCTTCGTAG	AAGTCAGATA
125041	CGTAGAAAAT	TCAAAGCCCC	AGTGCAATAG	CTCATGTCTG	TAATACCAGC	ACTTTGGGAG
125101	GCCGATGTGG	GTGGATCACC	TGAGGTCAGG	AGTTTGAGAC	CAGACTGGCC	AACATGGTGA
125161	AACCTCATCT	CTAGTAAAAA	TACAAAAAAT	AGCTGGGTGT	GGTGGCGGGC	ACCTGTAATC
125221	CCAGCTAATC	AGGAGACTGA	GCGAGGAGAA	TCGCTTGAAC	CCAGGAGGCA	GAGGTTGCAG
125281	TGAGCCAAGT	TCCTGTCACT	GCACCCACC	CTGGGCGACA	GAGCGAGACT	TCGTCTCAAA
125341	AAAACAAAAA	AAAGAACATT	CAAATAATCA	ATGTAGATAA	TTCAAATAAC	TAAAAATGA
125401	ACAGTTATTA	AAATATCAGG	ATATAAAAGC	AAAAAAATCA	ATAACCTCCA	TATATACAAA
125461	ATGGCCAGTT	AGAGAAAAAA	AAAAGAATAG	GCGAGACTTA	AAAAGGCTGG	GAATCTCCCT
125521	GAAAATCTTT	GAGAGCCTTG	GCCCTGCCCT	CAGGGATTTC	TCTGGCTTCA	TGCCCAGATA
125581	CGGGTACAGT	TCCTTGTTTA	AAAAAATTTT	GCTCCATCAA	TCAACAAGGG	GCTCCTTCCT
125641	CAGAGCACAA	GGACCTCCAT	AACACCGGAC	ACTAGATGTC	TAAGGGACAC	CTCTTAAGGA
125701	AGTTAGACTT	CCAAAGAATG	GTGTTTCCTC	TGTCCCCAAA	CTCTGGAAC	CACAGCACAA
125761	CTGCTCCTTG	GAGTTCGGTT	TCAAATCTAC	AAGGCTGTCA	TGGAGGTTGC	AGACCAAGTC
125821	CGTGGCCTCA	GTGTCCGGAT	GTACGGTGGC	CTTGGCACCT	GAATGTGAGA	ACATGACCTC
125881	CCTGAAACCA	CCACAAGTAT	TGTTTCATGT	TATGTATGTT	TTTTCTTATC	TGAAATTCCT
125941	TTTCTTTAAA	AATTCAAATT	ACATATTTTG	CAAGCCCCTG	AACAAGCTTC	ATGAGCATTT
126001	ATTGAACCCA	CAGCTTTTAA	AACCTACTGA	ACACTTTGCT	CTATGTTGTC	ATTCACTATC
126061	CACCAATTAT	TTAATTATTG	ATCAATATTG	TTTCCTTAGT	GTTGGGATCA	TTTATGCATG
126121	TATTTCTTTT	ATATTGCATA	TTTATATTTT	CTGCATTACA	GTTATTACAT	ATTACTTTTG
126181	CTACAGTAAT	AGTTCAAAAA	TGTACATCCA	AAATTTAGCT	GTGAAGTGGA	TGGACTGAGG
126241	CAGAACTGGA	GGCAAGAAAA	TGTCACAGTA	ATTCTAAAAA	AGATGATGTA	CAATTAGAGC
126301	AAGAGAGTAG	CACTGAAATT	GAAGAAAAAT	AGATGCGTTT	GAGAGAAAAA	TAGGAGGTAG

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126361	AATCAACAGA	TTAGATGTAG	GGATGAGAAG	GGTCAAAGAT	GACACTAGGG	TTTTTAACTG
126421	GAGCAAGTAG	GTAACAGAG	CATTTCTTCC	TGAAAGGGCA	GGTCAGATCA	TGTGTTGTCT
126481	CAAAGGGCAT	GAAGAGTAGA	AAGCCTGGGA	CAGATCCTGA	GATGACCAAT	ACCCATGGTG
126541	CAGGGAGAGG	GAGGGAGATC	TGCTAAAAAG	ACTGCAAATG	TCAGGATAGT	AGAAAATCAT
126601	GAGTGTGTGA	TGTCCTGGAA	GTTGAGACAG	TATCACATTT	GAGAACATTT	AAATTGGTAA
126661	CTCTGACAAA	AAGCTGGAGG	CCAACGTGTA	ATGCCCATGA	GAGTGAGAG	CTCCACACT
126721	TTTGTGGGCA	TCAGAAAGCC	CACCAGGTTT	CTGCAGTGAA	GATCTGAGAA	GGATCCTCTT
126781	GTGGCTTTGG	CAGGGAGAGA	AGAATTATTA	TGAAATACAC	CCCAGAACCT	TCTTCAAAAC
126841	AAAGGCCTAC	TCTCAAGGGG	AAAACATTTT	GCCAGAGTCT	TATCCCAGCT	GGGAGAAGGT
126901	AATTCTTCCC	ACTGCAGCCT	CATCTAGGCT	TTCTGTCTCA	CTTAAGGGAA	GAAAATTAGT
126961	CAACAGGGAT	CAGAGCTTCA	TGAAAATAAA	TTGGAAATGG	TGCAGCCAGG	AAAGGAGCAA
127021	AGGTCTGAGG	AGGAGGAGAA	GGAGGAAGAG	GAGTTGTATC	ATTATAAATA	CTTGAGGAAG
127081	AGGAGGAGAA	GGAGGAGGAG	GAGGAGTTGT	ATCATTATAA	ACACTTGAGG	AAGAGGAGGA
127141	GGAGAAGGAG	GAGGAGGAGT	TGTATCATT	TAAACACTTG	AGGAAGAGGA	GGAGGAGAAG
127201	GAGGAGGAGG	AGGAGTTGTA	TCATTATAAA	CACCTGTGAC	GGTCCCAGCC	CCAAGATATA
127261	GGCATGCTAA	TAAACTGAGG	CTTAACACTT	TGACTACAGA	ATGCTGCTTC	TCCCTAACAC
127321	CATCAAGGCT	CCAACCTGAAT	AACAATGAAT	TATGAATGAA	AGAGCTGTAA	GGAGAGACAA
127381	AAGTTAGAAT	GAGACAAGTA	TTGTTATCTA	GAGATGCCAA	GAAGGCAAGG	AAGATAACTA
127441	AAAAGGCACT	CTGGATTTAG	AAATAGGAAG	TCATTAGTGA	CCTTGTAAT	AATGGAGCCA
127501	GAGGAATACC	AAGGGCAGAA	GCCTCACTAT	AGTGTGTTGC	ACCTGTCAGA	GGTCAGGAGG
127561	TGTAAC TGAC	TCTCCACAG	TGTGGCTTTG	GAAGAGAGAA	GTCAGCAGCT	GCATGGAGAT
127621	TTGGGAGAGG	GAAAGCTTTT	TTTTTTTTTT	TTTAATTGGA	AAAGACTGAG	CTATGTGTAA
127681	ATAGAATAAG	ACAGGAAGAG	TGTAGACACA	GGAAAGAGGG	CAGACAAAAA	CAAGTGCACA
127741	GTTATCTAAG	GGAAACAATG	GGATCAAGCT	GCAAGTATAT	AAACTTGTCT	TGATAGTACT
127801	ATCCTTGATC	TGGTTTATTC	AGTGTGTTGT	CCAAACCCAC	ATCCCTGTTC	TGCCTGTCTC
127861	TGACTTGCTC	TGTGCCCCAG	AAGCCCAGCT	TCTACAGATA	GCATTAGCTG	GGCAGCCCTG
127921	CCCTCTTGCA	ACAGCTGGAT	TTGGCCAGTG	ATCAGCCCAG	CAGGAATGTA	GATGGCAAAG
127981	GAGAGAGAGG	TTAGTGTACT	TATTCCTGCT	ATCACCCCCC	TGCTTGGTGG	GCAGCTCTTC
128041	CTCCACAGTC	CCAGCTCTGG	CCTAGCTCTG	GTTACAGGTT	CCCTCCCAT	GCCTCTTCAG
128101	ATTTAAAGGT	GTGTCTGTCA	GGGTATAACT	GGGAGCTAGA	AATTGCACTG	AAATTGAACA
128161	AAGAATTTTA	TGGGAATGGT	TGTTAACTAG	TTATAAGAGG	ACTGAAAATG	GAAAAGTGGA
128221	CAAACGTATC	AGAGATAGTA	ATGACAGAAA	GCAACTACCA	CCTCCAGGTT	TAGGAGAACA
128281	AGGAAAGAT	TCTTTGAAGA	GATCCCCAGA	ACTGGGACCT	CTGAGGAGTG	TATGCTGGAC
128341	CACTGATGAT	GATATGTCTG	TAGATAGAGG	CATGATGAGG	CTGATTTTAG	GAGCATGGAA
128401	GATCTCCAAA	CTGAAGCCAA	CTGCTGTTAC	TGGATTCAAC	TGCCACTGCC	AGGTTGAAGA
128461	ACCCATTCTG	TGAGGATGTC	AACAAACAAA	GTGGGAAATC	TTTTTCACATC	CTTCCAGCCC
128521	TCTAGTCTTC	CTCCAGTGCT	TTCTATTGGT	AGGGTTTGGG	GAGGTGGCTA	GCAAAGCGGT
128581	ATTGGAAAAG	ATAGAAGAGA	CTAAATCTTC	ATAACCAGCA	CAGGGTGACA	CTGGATCACT
128641	ACTGTTGCTG	ATCTTGGGCT	GCCTCATATC	CCCTGTTCTT	CCCATTAGCC	CTGTCAACAAC
128701	TTTGTAGATA	TCCCTTCATT	ATATGCCCTT	CATATATTCT	TTTGGTTTAA	CTTTTCTGT
128761	TGGAATCCTA	ATATGGCACT	CCTCCATTTT	TCAGGACCAA	AAGAGTATAA	AAGATTATCT
128821	TTTACCAAAA	AAAAGACAAA	AAACTGATCT	AATTCCTGAT	TTGATCATT	CACAATCTAT
128881	ACATGTATCA	AAATATCACA	TAGTACCCCA	TAAATATATA	CAACTGTGTC	CATTAAAAAT
128941	AAAAATTAAA	GAAAAGATGG	TAAATATAGC	TCTGTCAGGC	AGTGGAGGTT	TTACCACGAT
129001	GGCTGTATT	TCCCCCATGA	AGGGGGGAGT	GAGGGAGCAG	CTGAAAGTAG	GTGCTTATAG
129061	GGGTATAGAG	GGGCTCAAAG	CTTTGAGAGA	GGAGAATGTC	TGAAAGAGCT	GCCAAATAGC
129121	ATGCAGGTCC	CATGGGGGCA	GAGCCTCTGC	TCATTACCA	GTGCCTCTTC	AATATCTACA
129181	CTTAAGCCTA	ACACAAAGTG	TGTGCTTAAT	AAGTATTTGC	TGAGTATGTA	AAGTGGAAC
129241	AGAACCAATC	TGGCAAACCT	TGTAGGACTG	GTGGGCAATG	AAGATCAGTC	AGGTAATATC
129301	TGTGATATA	AATTTATATT	GATCAAAAAA	TTCAAGGTTA	GGTGTTTTTT	TTCACTCATG
129361	CTCAACGATG	CTTCAGCCAT	GCTCAACTCT	TCTGTAGCCA	CAGAAAAAAG	TTTACCCATA
129421	ATCGAGCTGT	GTCTGTGTCT	GAATAATGAA	AAGACCATGA	TGCAAGGGAG	TTGGAGACAC
129481	AGAAACAGTG	TTTGAAGTAA	TGGGTAATGG	AAGCATGCTA	CCAGGGAAAG	GAAAGAAGTG
129541	GCAATAGGAA	GGAACAGAGA	TCTGTGTCTC	TATGTCCCTT	GAGCATATTC	ACATGTTAAA

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129601 GCTAATTCAG TTTTCAATCA TCATTAAAAAT TTTGTTCCCTA AATATATGGC CATTATTTTC
129661 CACAACCACA CTAAACTTTT ATTACCTCTG GCAAGTGACT ATGCAAGTAA CTAAGAGCAA
129721 AAATATCCAC AACTACCATT TGAGCTATCA ATTTAGGGAA AGTCATCTGG CTATAATCTA
129781 AGTGACCCCTC CACTGAATGT CAGTATCTTT GCATATGTGA TTTAAATCTG GGCCTTCGCA
129841 ACACCATGAA CTGTTCTTGT CTTGAATATC CAGATTGAAG GAAATAATCT GAGTAGTTAC
129901 GAGTCTTGAA GCTAGAAAGA TGGAAACCCC ATTTGCTCAT CAGAAAGCCT TAGAGCTTGG
129961 GCGCTGGCGG GTCCTGTCTC ACCGGGACAG AGGGGCTCTT TCCTCCCCAT CTGATAGTCT
130021 GATAACTAGA GAAGCCGGCC AACTTATTCT CCAAGAAGGA GCCATCTTAG TTCCTCCTGA
130081 AATGTTTATA TTTAGAAATT ATTGTTTGTC AGTAATTTAA CCCCTTAATG GGCTTGCCCTT
130141 GTGGTCCATA CCACTGAGTG CAGAGCTTGC CTGGAAGAAT TGTGAGGGCC ATTCCATCTT
130201 CCAGGCAGTA GAGTTCAGTA CTTCTTTAAA ATTGCTGCTG AACTCTGTAT TTGAAAAGAA
130261 AGAATCATTT GGGTGTGGTA GCTCACACCT GTAATCCTAG CGCTTTGGGA GGCTGAGGTG
130321 GGAGGATCAT TTGATGCCAG GAGGACCACT TGAGACCACC CTGGGTAACA TAGCAAGACC
130381 CTGTCTTTAG AAAAAAAAAA TACAATAAAA TAAATACAAAT AAAAATAAAA GCAAAAAGAA
130441 AGAGTCCATC TTAGGGACAG ACTGTAACTA CTCACTGGAG CTTACCTTTA CATAGTTTCA
130501 GATCAATTAT AATAAAACAC TTTTGTGCAG ATTCAATAGG ATTATTTTAA TCCCCATCAT
130561 CTCTCTGAGT TTCCAGTCAG TTTCTCTGCA TGTAGACACC CTTCTCCAGC CCACCATTGT
130621 CTCTCCTCCT ATAGCTCCAC CAACAAATCA GAACTTTTTC TAACTGCACC TAGTGCACCT
130681 AGAGTCTACT CCAGAATGCT CATGGAGAAA GTTCTTGAAA GGTAAACTC TGAATGATAT
130741 TTGTAGCTAA AGGGAGACTT GCTAGAGACA ATAAGCTAAT AGTTGTAGAC TTCAGTAGAA
130801 GAGGAATGAC ACTGCAATGT CAGGGTGCAG GACTTCAAGA GGGCAGAGTA TGGAAACCCA
130861 ATGGGAAAAA TGCTCACCAG GAACATGAAG AGAAGGAATT ACGTGTAAGG ATTTCTCAAT
130921 GTGTTCCCAA ATTTGCCCAG CAGAGGGAGG CCTCGGGTTG ATGGCAGGCT GACCACACAA
130981 TTAAGAAGG CTGAACCTGG GGGCTTTTAA CAACCATCGT GGGCTCTACT GTAAGCATTT
131041 AGAAAAAGAA AGTTATCCAT TCAAAAATAT ATATATTTT AAACCTCAGA ACAAATTAT
131101 GAAGAGCTAT ATTTACTTTT CTACATTTCTA ATTTTATAA ATCTGAGTAT ATTTTGCTA
131161 TATTGTTATA GTACATATTC AATTTTGTAT TTTGCTGTTT TCACTTAACC ATTTTACTA
131221 GATTACTCTG TGTTTATAAT AATCACTTTT TTAACACTTT TATTTTATT TATTTATTTT
131281 TTTTTTGAGT CAGAGTCACA CTCTGTCGCC CAGGCTGGAG TGCAGTGGCG TGATCTTGGC
131341 TTAAGTCAAC TTCCACCTCC TGGATTCAAG CAGTTCTCCT GCCTTAGCCT CCTGAGCAGC
131401 TGGGATTACA GGTGTGCACC ACCAAGCCCG GCTAATTTT GTATTTTATG TAAAGACGGG
131461 GTTTCACCAT GTTGGTCAGG CTGGTCTCCA ACTCCTGACC TCATGATCTG CCCACCTTGG
131521 CCTCCCAAAG TGCTGGGATA ATCACTTTT ATGCTGCATA ATTCTTCAGA TTTGTGCTA
131581 CGACTGTATT TACACTCAT TGTTTTATTA GAAAGAAATC CAGAATATT TGGCTGCCCT
131641 AATTAATTTT ACAATTAATA TGATTTTGAA ATTGGGTATT GGCTCCTTCT GAATTGGTTT
131701 ATTAAATAT ATTCTAATGT AATTTATGAC ATTTTCATCA TATTAGCATA TTTATTCTGT
131761 TAGAATTTCA TAATTTATAA AGCTACAAAC TGTATGTGAT ATAGCTTGTA ACTTTATCTC
131821 ATAACCTTAT GCAGTTACAA GTAGAAATAA AATGTTCCCC TCAAGATTGC TTAATAATTT
131881 ATTATAAACA AGTGTAACAA ACAAAATCAC TAAAACACTC CCTCTTTTTT CCCCCAAAT
131941 GCATGTTTCC ATTTTAACAG AACCCGTATT TAATCAGCAG ATTTCTATGG TGGCTAGATT
132001 TGTAAGCTAA ATATTAAGG TCCCAAAGCA AATGCATTTT TCTCTTAAAT TTTACTGACT
132061 TTTTTTTTTT TTCTTTTCT GAGACGGAGT CTGCTCTGT CGCCAGGCT GGAATGCAGT
132121 GGCACAACTC CGGCTCACTG CAACCTCCGC CTCCCGATT CACGCCATTC TCCTGCCTCA
132181 ACCTCCCGAG TAGCTGGGAC CACAGGCGCC CGCCACCAG CCCAGCTAAT TTTTGTATT
132241 TTTAGTAGAG ACAGGGTTTC ACCGTGTTAG CCGGGATGGT CTCGATCTCC TGACCTCATG
132301 ATCTGCCAC CTCAGCCTCC CAAAGTGCTA GGATCACAGG CATGAGCCAC CGCGCCCCGC
132361 CTACTGACTT TTATCCAAAG AAAATATAAG AGCTCTTCAT CATAACGTAT GTTCTTGTCT
132421 CTTGTTATTA AATATGACAC ATTTAGACTT AAAGTATTT GAAGGTTTAT GACATTGTTT
132481 AAGTTATTAC ATAATTAATT CATAAGATA ATGACTAGTT TGAAGTCTG ACAGCTCACA
132541 CATCATCAGT TGAACAGCAG AAAGCTTACT AAGCTACTTT CTTATGTTTC TGTCTCCCAG
132601 CTACTAAAAG AAACGAAACC CTTCCAGGTG TTAAGGCAAA ACTTTCCTCC CCCTTCTTCT
132661 TATAAATCTG ATTCCATGTT AGTGAAATTT CTACTGATGG CTTTGGTTTC CTCTATAGTA
132721 GAATAGAGAT CCTATGGCAA AAGTCATGTC TGACATGGTA GCAAATAGAA ATGGGGAAAA
132781 GGAAGGTCTG CAAGAGCCAA TGTGGGAAAT GGGGAGAGGA CTGACTACAA AAACCCAGCA

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132841 GGAATTCCAG AAGAAAACCTC CTCAGGACGG GCACATTGGC TCATGCCTGT AATCCCAGTA  
132901 CTTTGGGAGG CCGAGGTGGG CAGATCACTT GAGTCCAGGA GTTTGAGACC AGCCTGGTCA  
132961 ACATGGCGAA ACCTCATCTC TACAAAAAAT AAAAAAATTT GTCAGGCGTG GTGGCATGCA  
133021 CCTGTAGTCC CAGCTACTCA AGAGACTTAA GTGGGAGAAT CACTCGAGCC TTGGAGGTGG  
133081 AGGTTGGTGA GCCGAGATCA CGCCACTGCA TTCCAGCCTG GCGGACAAAG TGAGACGCCA  
133141 TCTCAATCAA TCAGTCTCCT CGAAAAGCAA CATTATGGAG AGACAGGATT CCGTCAAGGC  
133201 CTGGGGCACA CAGGAAAATA TTAAGGCAGA AGAGAGTTTC CTCCCCACAC CACACCGTAT  
133261 CCCACAGGCA CTGCGGATGT GCATATGCAA GAGGGGTTGA TCCTAAGAAT TTAGAGTCAC  
133321 AGAGGAGGAG GCACCAAGCA GACTGTGGAG AAAGTCATGA CCAGAAAGGG ACAGAATGTA  
133381 AAGCTTCAGC TGATTATCTG GCCTCAGGGA TTCCAGAGGA ACTGGTCCCA ATGGTCTCCT  
133441 GGTGATGTAG GTTCTTAGGT TTCTTTTACA GGGGTTTTCT GGGAGATCGT TGACCCAGTT  
133501 AGCATTCAAG CAACTTCCAC CCTGCACTTT TATTCTTTCC CTTTCACCTG CTTAGGTTTT  
133561 ATCTGTCCAG GAAATAATAA TAAAATTATT GAGCCCTGGA CATGTACCTG TAAAGCTCCT  
133621 TAAAGATGAT GCCTTCTAAC TCCTCATTCA ACAGATACAA AAACATTACA ATAAAATGAC  
133681 TCATGCAAGA CACCCAGGTA GTTTATAGCA GCTAATAAAA ACAGAATAAC TATAAAATAT  
133741 GGTAAGTTTA TAAAAGTTAC ATTGAGTATA CTTTATAAGA ACTGCTTATT GAGTTTGCCT  
133801 AATAACCACA CAGCACAATA ATAATATGTA TATATTTTTA AATATGTGTA AATATGTGTA  
133861 ACACAACTT GTAGAAGGTA TATCTGAGTA CAACCCTATT CTGTTTGGTT ACCTTTTCTA  
133921 GTTCATTATG TAAGTGGCAT AGCTACCTAA GGACTTATGC TTATAAATGT TACTCAAAAA  
133981 AATACAGAGG ACATATGTGG ATAGATAATG GAAGAGATAA GATAGGTAGG TTGAAGGGTT  
134041 GGGCTGCCCC TCCACACCTG TGGTTGTTTC TCGTTAGGTG GAATGAGAGA CTTGGAAAAG  
134101 AAAGAGACAC AGAGACAAAG TATAGAGAAA GAAAAAAGG GGTCCAGGGG ACCGGTGTTC  
134161 AACATACGGA GGATCCACAC GGCCTCTGAG TTCCCTTAGT ATTTATTGAT CATTATTGGG  
134221 TGTTTCTCGG AGAGGGGGAT GTGGCAGGTT CAAAGGATAA TAGTGGAGAG AAGGTCAAGCA  
134281 GGTAAACACG TGAACAAAGG TCTCTGCATC ATAAACAAGG TAAAGAATTA AGTGCTGTGC  
134341 TTTAGATATG CATAACATA AACATCTCAA TGACTTGAAG AGCAGTATTG CTGCCAGCAT  
134401 GTCCACCTC CAGCCCTAAG GCAGTTTTCC CCTATCTCAG TAGATGGAAT ATACAATCGG  
134461 GTTTTACACT GAGACATTCC ATTGCCCAGG GACGAGCAGG AGACAGATGC CTTCTCTTG  
134521 TCTCAACTGC AAAGAGGCGT TCCTTCCTCT TTTACTAATC CTCCTCAGCA CAGACCCTTT  
134581 ACGGGTGTCG GGCTGGGGGA CGGTCAGGTC TTTCCCTTCC CACGAGGCCA CATTTTCAGAC  
134641 TATCAGATGG GGAGAAACCT TGGACAATAC CTGGCTTTCC TAGGCAGAGG TCCCTGTGGC  
134701 CTTCTCAGT GTTTTGTGTC CCTGAGTACT TGAGATTAGG GAGTGGAGAT GACTCTTAAC  
134761 GAGCATGCTG CCTTCAAGCA TTTCTTTAAC AAAGCACATC TTGCACAGCC CTTAATCCAT  
134821 TTAACCTGA GTTGACACAG CATATGTCTC AGGGAGCACA GGGTTGGGGC TAGGGTTAGA  
134881 TTAACAGCAT CTCAAGGCAG AAGAATTTTT CTTAGTACAG AACAAAATGG AGTCTCCTAT  
134941 GTCTACTTCT TTCTACACAG ACACAGTAAC AATGTGATCT CTCTCTCTTT TCCCCACAGG  
135001 AGGTGATGGC CGGAAGAACA TGGCAGAGGG CAAAACAAA CAGCATTGGG AACAAAGCTCT  
135061 GTTTAAAAGG AGACTTGTGA ACAGCAAAGA GTAGAAAGGG TTCTCTTACA ACTGAAGCCC  
135121 ATGGAAGACA AATGTGTACT GCGTGAGTTT TAAGGCAATA GGAGTAGTGG GACCTAGGGC  
135181 ACACCAGAGA GCATATTAAC TCTCAAACCT TTAACAAACAT TATATCTGCT GGACACAGTG  
135241 GCTCACACCT TAATCCTACA ACTTTGGGAG GCCGAGGCGG GCGGGTGTAG CTTGAGCCCA  
135301 GGAGTTCGAG ACCAACCCTG GCAACATGGC AAAATCCCGT CCCTACAAA CAAACAAACA  
135361 AAAACAAAAA TTAGCCAGGC ACGGTGATGC GTACCTGTGG TCCCAGCTAC TCAGAGGCTG  
135421 AGGTGGGAGG ATCGCTTGAG CCCCAGGAGG TTAAGGCTGC AGTGAGCCAT GATAATGCCA  
135481 CTGCATCTCA GCCTGGGCAA CAGAGGGAGA ACCTGTCTCA AAACAAAAAC AAAACACAC  
135541 CATACCCAAC CACAATGCAT CTGTCTTAAG TACCAGTACC ACACCCCTCT ACTCACTACT  
135601 AAATAGGTGA GTTCCCAATC CCTGGTAGCA GGTTTAAGCA TGTTATATTA AAGGTCTTAG  
135661 GCTAGTGACT CATTCCTCA TTAACAAAT ACTTATTGTG CATCTACTAT AAACAAAGTA  
135721 CTGTGCTAGG TACAAAAGCA AATAATCTAA GCTCTATAAA CTTTACTTTT TTCATCAACA  
135781 AAATGGAGAT GTTTTAGGCA TCTACTCATC ATTCTGAGCT CCATCTTTTG TGACTGTAGT  
135841 TGGCAGAGCT TTTTATCAGT TTCTCTAAAT AGCTCTACCA GTCCCTGGTG GATGCTGGCA  
135901 TGCCCAAAGG ATCCATCCTG ATGGCCCTGT CTGCTTACCT TACCTGCCTG CCTTTGCAGC  
135961 ACCGCTCTGC TCTTCTGCAG GACTTCCCTT ATCCTTTGGG GTCTTGCTGC TCTTAGGCTG  
136021 CTCTGCTTGT TTTGATCTGC TTTGCATCAC ATGTATGTAA AGGTCCTTTC CTTATTTACC

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136081 CATGACCAAG GTATTATGAG ATTCTGGAAT TTCCCCAAAC CACATTGATT GCTGGGAGAA  
 136141 TAGAAGAAGT GGATTACAAG TGGAACTTAG AAGGGGAGTA TTCGAGAAGA CGTCTCTGCA  
 136201 AATCCATTTA GAGAGACCTT TCTCCAGTGG TGACTCAAAG ATGCAGCTCC TTTCATCCTG  
 136261 TGGCTTGGCC ATCTTCAGCA CATGGCTCCC AAGGATGTCC TCAGGATGGT CTCTAATCCA  
 136321 AGGAGCCTGA AGAGAAAAAA AGGCATGGAG TATTGTGAGT GGTAGGTGGT TATGGACCAG  
 136381 TTATGGAAGA ATACACATCA CTTTTGCCCA CCTTCTACTA ACCAGAAGTC ACACAGCCAT  
 136441 AGACACTGAC AAGTAGGACT TAACAAGAAT CTAATTTTGA GTCTAGGAAT ACGACTGTAG  
 136501 CAAATATTTA ACAGCTTCAA ACACAGGTGC ATTGCTATCA CTATGCTTGG CCCAGGCCTG  
 136561 TCTCCCTTTC CTGCCATGTC ACAGGGGCCA GCATTTATGT CTAGATTGGG TTGGTTGGGA  
 136621 TATTAAGACA ATAATGAACC AATACAACAT CTTGAGCATA AAACCAACTG ATACAATGAT  
 136681 GTACAAGTCA GATGATTCTG ATGATTATGA ATTATGTCAA TAAAAGAAAT GTGATAACTA  
 136741 AGGTAATTTT TGTTTTGGCA AATTTTTGTT TGTTTCATGAC AGGATGAAAT CCTGTCATTT  
 136801 GTAGCAACAT GGATGGAATT GCAGGATATC ACATTAAGTG AAATAAGCCA GAAACAGAAA  
 136861 GTTAAACACC ACATGTTCTC ACTTATATGC AGAAGCTAGC TAATAAGTA AATAAGTTTA  
 136921 TCTCATTGAA GTAAAAAGTA CAACAGAGAT TACTAGAGGC TGGGAATGGT AGGGGAAAGA  
 136981 GATGATAAAG AGAGATTCGT TAAAATAAGT TACAGCTAGA TAAGAGCAAT CAGTTCTAGT  
 137041 GTTCTATTTG TACTACAGAA TGGCAATAGT TAACAGTAAT AAATAATTTT AAAGAGCTAG  
 137101 AAAAGAGGAC ATTGAATGTT TCCAACACAA AGAAATGAGA AATGCTTGAA ATAATGGATA  
 137161 TTCTAATTAA TTACCCTGAT CTGATCACTA TACACAGTAT GTATAAAAAAT AACACTATGG  
 137221 GCTGGGCGCA GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCAAG GTAAGCAGAT  
 137281 CACTTGAGGT CAGGAGTTAG AGACCAGTCT GGCCAACATA GTGAACTCC ATCCCTACTA  
 137341 AAAATACAAA AATCAGCCAG GCGTGGTGGC ATGTGCCTGT AATCCCAGCT ACTCAGGAGG  
 137401 CTGAGGCAAG AGAATTGCTT GAACCCAGGA GCGGAGGTT GCAGTGAGC GAAATCGCGC  
 137461 CACTGCACTC CAGCCTGGGT AACAGAGCAA GGCTCTGTTT CAAAAATAAA TAAATACATA  
 137521 AATAAATATT TTTTAAAAAA AGAACATCAC TATGCACCCC ATATATACAT ATAATTATTA  
 137581 TGTCAATTG AAACATAATT TTGAAAAATG AAAAAATGAA ACACAAATAT GAATCAATCC  
 137641 TCTCCAAGTT GATATACTTA AAAGGAAAAA AGTCCGAGGG CTAAACTAT TCAATCAAAA  
 137701 TTTTATTAAA ATGCTATAGT AATCTGAAA GTATTTTACA ATGAATTGGT ATAAGGTTAG  
 137761 ACACAAAGAT CAGTGAAACA AAACAGAGAA CCCAGAAATA GATTCACACA TCTATGGACA  
 137821 ACTGTTTGTG ACAAAGGTGT CAAGGCTATT TAATAAGTAA AAAAATCGTC TTTTCAGTAA  
 137881 ATGTTTCTTG AACAAGTAGA CATCCGTTGT GGGGAGAGG AGCAGGAGCC TTACCTCAAA  
 137941 CTTTATGCAA AAATTAAGTC AAAATAGACC ATAGACTTAA ATGTAAAAGC TAAAAATATA  
 138001 AAACCTCTTT AAAAAATAGG AGAAAATCAT CAACACCCTA GGATTAGCAA AGATTTCTTT  
 138061 AAAACAAAAC AACAGGTTTA TAGTTTATAA AACATAAATA ACAAATGAT AAATTTCTATC  
 138121 AAAAGTGAAA ATTTGCTTTT CAAAAACAT TATAAAATGA AAAGCAGGAG GCTGAGGCAT  
 138181 GAGAATCACT GGAACCCGGG AGCTACAGGT TGCAATGAGC CAAGATGGTG CCACTGCACT  
 138241 CCAGCCTGGG TGACAAAGTG AGACTCTTCC TAAAAAATAA ATAAATAAAT AAATAAATAG  
 138301 AAAAGAAAAA GAAAAATCAC AGGCTGAGAG AAAATATTTA TAATACATGT ATCTGACAAA  
 138361 GGACTCGCAC CTGGAAAATA TAAGGAACCT TATACTTAG TAAGATGACA AGCCAAAACA  
 138421 AAGAGTAAAA GTTTTCAACA GACATTTTAC AAAAGAAAAC ATACAAATGG CCAGTATGCA  
 138481 CATGAAAAGA TTTTAAACAT CATTAGTTAC TAGGGAAATG CAAGTCAAAA CCACAATGAG  
 138541 ATACTTCACA TTCAACAGAA TAGCTAATGT TAAAAGGACT GACAATCCCC AGGGTGAGCA  
 138601 AGGGTGTGGA GGAAACTACT CTCATATATT GTGAATGTAA GAGGACAATG TTACAATAC  
 138661 TTTGAAAAAA GTTTGGCTGT TTCTAACATA AAATTAAACA CTTATACAGC CCAGCAATAT  
 138721 TTCTGGGTCA TTTCTCCAG ATAAATGAAC ACATGTCCAT ACTATGACAT GTACAAATGT  
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 138841 GTGAATGGGT AAATAAATTG TAATATATCG GCCAGACGCA GTGGTTCATG CCTGTAATCC  
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 139081 GTTGCACTGA GCCAAGACCA TGCCATTGCA CTTCAAGCTG GGCAACAAGA TGGAACTCC  
 139141 ATCTCAAAAA AAAAAAAAT TGCAATATAT CTATATCTTG GAATATTATA AAGCAATAAA  
 139201 AGGGAATAAA CTAATGATAT ATACACAAAA TGGATGAATC TCAAAAATGT GAAGGAAAAAT  
 139261 AAAAAATACA TATGATATAA ATTCCATTCA TATGAAATTT TAGGAATGGG AAAACTAAGC

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139321 TGTAATTATG GAAAGTACAT CAGTGGCTGC CTGGGGCCAA GAGGATGGAA GAGGCGGCAC
139381 AGGTGATACT ACAAATGGAA ACTATCTAGG TTGACGGAAG TGTTCTGTAA CTTGATTACA
139441 GTAGTAACTG TTTGGGTATA TAAAACGCAT CAAATTGTAT AATTAATACA GGTGTATTTT
139501 ACTGTGTATA AATTATTCCT CAATAAAGTT GATTTTTCAT TAAATATATT ATTTGCTAAA
139561 ATGAGGAGAG ACAACTATTA TCTTAAATA GTTAAGCACA ATAAAAATAC TACAATCAAC
139621 TCATTATATA TGGAAATTAA AGGAGAAAAA TAGTGGTATG ATTAATTAAA ATAAAAAGAA
139681 AACCTTCTAA ATTTTATCTT AGCTCATAGT TGTAAGAGCT GCCATCCCTA ACCAAGGCCA
139741 CCCTTGACCC TTTCTCATGT TCCATCTTTC TGTTTGTTTC ATAGTTTATG TCTCACAAA
139801 ATCTATCAGA TAAACGTATT CATATGAAGA TTAAATATA TTACATGTTA AGCCTTAGCG
139861 AATACTTCAA TATCTAAAGA AGGTACAAAC AAAACAAAAA TCAACACTTA GTTATAAGAG
139921 ATTACATACT CTCCAGGGAA GACCTGAAGA CTAGCCCTT TCTGGATCCC ACTAGCCCTT
139981 CATCCCACTC CAAGCCCTCC CCTCCAATCC CATATGCACT GGGCATTTCAT ACAAATAAGA
140041 CCATCAGCTC TGGATATCTG TACTGATTGA TGCTCCTGCT AACTACCTGA ATGATTGCGA
140101 TGTAAGGACA GCACTGCCTG AATCCTATTT ATCTCTCGCT ATGCCATAGC GGCCTTCCAT
140161 GCTGATGGCG TGTTTGAGGA TCCAGAGGGG TCTTTGGTTG GCAGGATTGT TTTATTTCCC
140221 CAAGAGGAGA GCCTTGATGC AAAAATAGGT GAAGAAATCA GTACAACAAA ACAGAAAGCC
140281 TAGAACTAC TATGAACACA ATAGAGCAGA AGTAGCCTTA AGAGTTGGTG GAGAAAGGAT
140341 GGTCTATTCA ATTACCTGGG CTGAGAAACT GGCTTTCATA TGGAATAAAA ATAAAATTAT
140401 AGCTATACCC CATATCATA ACAAAAGTTT CTACATCTAA CAAAGACACA GATAGAAAAT
140461 GTTTTAAAT TTTAGAAGAA AATAGTGACG AATTTTAGTG CAGAATTTCT TAGACTAGAT
140521 GCAAAAACAA AAATGATTAA AGTGGCCAGG CACGGTGGCT TATGCCTGTA ATCTCAGCAC
140581 TCTGGGAGGC CGAGGTAGGT GGATTAGTGG AGGTCATGAT TTCGAGACCA GCCTGGACAA
140641 CATAGTGAAA CCCCATCTCT ACTAAATAC AAAAATTGGT AGGGTGTGGT GGCTCACGCT
140701 TTTAATCCA GCTACTTGGG AGTCTGAGGC AGGAGAATCA CTTGAACCTG GGAGGCAGAG
140761 GTTGCACTGA GGGGAGATGG GCCACTGCA CTCAGCCTG AGCAACACAG CGAGACTCTG
140821 TCTCAAAAAA ATCTAAAAAT AAAAAGATTA TTTTAAAAAG ACTATTTTAA ACAAAAAAAA
140881 TCGTTTAAAT GATATGACAC ACTACATCTA ATATTGGAA AAGTACTTCT TAATACTTTT
140941 AATAAAAAGA GCGCTGAGA GCATACAACC TATCCTCAGA AGAGTGTGTT ACCTCTAGGA
141001 GGGACGCAAG CGCGTTCTT CTTCATTTTA ACTGGTCATT TTCATTTATT TCAGGAACAT
141061 CTGAAGTAAA CACAGTCACA CGTTAACCTT TAAAAATCTA GGAGGTGCGT ACGCATAGTT
141121 CCATTACTTC AATTTTGTGA CTTTTCATT TTAATATATC ACAGGGAAGC TCGGTACAGC
141181 TTCAAGGCTA GGAGGGGTGG CTCTCTCTTA AGCCCTGTCC CCGCCAGCCC CAGACCTCTC
141241 GTCCCGCCCC CATTGCCAG TCCCACCCT CACTTCCCCA TTTCCCCCT CCCGCGTCT
141301 CTTAACGCAC CTCGTTTTTC GTCCAGTGA CTCAGACCTG TAGTCTTCCA CCAGGATCGG
141361 CTCCTTTCCC GGAGCTCTCG CTCTTAGAGG AAATGAGAG AAGCATCAGC GGAGACCCAT
141421 CTGTGGCTCT CCAGAGGGCG CGGCATTGAG ACCCCAGATC CAGCTGTGAG AACGGACCCC
141481 AGGCTCACAC CAGGCCTGCG GGAGGCGGCC CACCAGAGGC GCTAGAAAAC AAGCCTCGCG
141541 GGGAGGCGCG CAGGGCGACT GCAAGCTGTA GGGGGCGCTG GCGCCCTCAC AGGCCAGGGG
141601 CAGGGCCGCG GCTGCGGGCG GGGCTCTGCG GCGGTGAGGG GCGGCCCCAG GCCAGCAGCT
141661 GCGCCCTGGC TGGGAGCCGG GGAGCATTTG CTGCTCTGCT GGACCCTGAG TCTGGCGGCG
141721 GGCGGCCCTC TCTCCGCTCC CCGCCGCCA TCCCCCACT CCCGATCTCT CTGCTGCGTC
141781 TGGCCTCAGG CTGAGACCCC AACGAATCAT TCCCCGATG GGAACATTTT ATGATATAAC
141841 TGAATTCAGT TTTATGTATA ACTGAATTAC GGATATGAGA ATCTCAAATG AGGACGAATG
141901 GTTTTACGC ACAAACATG AGACACAAAT CTGTAAGAAA TATAAGTCG TGACCACGTC
141961 CTTTCAGAAC TTTAACCTGT TTGCTGAAGT ACGTCAGTAA CAATGGCAGG GAAAGGGTAT
142021 CTTAAATTTT ACCACAGCCT CAAAGAGGCC ATTTCTGTGA TCCGCTGAGG CTTGGAGTCG
142081 GCCTTCTGAC CACGAGTCCT GCGGCTATGA AAGAGGAAGC CGCGGTTGAG GCGCTCTCG
142141 CGAGTCGTGC AGCCCGCCCT GCTCCAGCTG GGGACACCGG TGGTCACGGC GCTTTCCAGC
142201 TGCAGATCCA GCGGCGAGCC CAAGATTTGG TCCAGCCGCC AAGGGGTGGC TCGAGTGACT
142261 GACGGGCCTT GAACGCTCCC AGGACCACCA TCTGGAGAGG GAGGTGGGGG TGGGGTGTCTG
142321 AAGTCATTCT TGGGGCCCTT GGGGCGGGC ATGGACCTGG GTAAGGCCAG AGAAATTTGAC
142381 ACCTCGTGAC ATCCCTGGAA GAGAAGTACG TTCAGTGTCA CTCAGAGCT GAAACCGCCT
142441 TCTGGCTGGT CCTCCTCAC CTACATACTT TTCTAATTTG TCTGGAGCAG GCCGGGCATC
142501 TGTATTATCT GGTATTATA ATATCTGGTT ATTTAAAAGC TCTCCATTAA ATTCACATAC

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142561	ACGAAAATAA	AAATTAAAAA	AAATTTTAAA	AAAAAGAAAC	AAAAGCTCTC	TAATGACCAC
142621	GTCCTACACG	ATAGTGAATA	AAATTTTGTG	TGTGGTCCCT	AAAATTGAGT	TCATGCCTTT
142681	TCTGAAGTAA	TAGACGCCCA	GAGAAGGGAT	CGACTTACCC	ATCATGCCAC	AGAGATTAAAT
142741	TGGCCCCAGA	ATTCTTTAGC	AGACCGTGTA	TATGAACGTC	CTTTGCAATC	ATATAAATTA
142801	ACTGGGAAAA	CCTCATTTAG	TATGTTACAT	GCCTAGCGTT	TTGTGCCTGA	ACACCTTACA
142861	AGAACCAGGG	ACTATTGCCC	CAATATTATA	TTTCAGGAAA	GGAAGGCCCA	GACAAATGGT
142921	GTCACTGGTC	CACTTTCACC	CAGTTGGTAA	ATGAAACCAG	AAATTATAGC	TGTACCACAG
142981	AAAGGTGAAA	ACGTTTCTTT	TATAATTTCA	CATACAATCT	TAAATGGACC	CAGTGTCCAA
143041	CACATTAAAG	CAAGTGCTCA	GGAGTGACAT	CAAGATGTAA	AAAATAGTCC	TGTCCTCAGG
143101	GAGTTTAGGT	CTTGGAGAAA	AGAGACCCAA	GGAGACACAA	GACAAAGGGG	AAAGAGAAGG
143161	AGCGCTGAAG	ACTGAGGACC	CTGCCTGTGG	ACTGAAGTGA	GGATGGGGAC	ACCCGATGCC
143221	CGGAATATGA	CAGTTTGGAG	GGGCCTGAAG	GACTCTTCTA	TTCTCTATCA	GAAAAACAGA
143281	ATTACTCTCC	TAACCAGAAA	AGGTATTTCA	ATTTATATTT	TCCATCACAG	CACTTTCTG
143341	GTGATAATTT	AATGTGTTTT	AAAAATGTGA	TCACAGTGAT	GGCCTGGTGT	GAAATAAATA
143401	ATAAAATTTT	AAGAATTAAA	AAATATAAAA	ATCTTTTATA	TAGACATTAG	GAGTTACAAG
143461	GATAACTGTG	AATTATAATT	AGTAATTAAA	TTGAAATACT	GATTATTTTC	ATTTTATTTT
143521	AATTATTTAA	TAAAACCTAT	TTACATTTA	ATATTTATCA	GTAATTAAT	CTAATTGTTA
143581	ATATTTATTA	TTATAAATTA	TTTTAGAATT	AAAAATAAGT	GTAGAAGCGA	GGCATGGTGG
143641	CTCAAGCCTG	TAATCCCAAC	ACTTTGGGAG	GCTAAGGTGG	GAGGATTGCT	TGAGCCCAGT
143701	AGTTCAAGAC	CAGCCTGGGC	AACATGGAGA	AACCCTGTCT	CAATACAAAA	AAATGAGCCA
143761	TGTGTGGTGG	TGCGTGCCCTG	TAGTCCCGAGC	CATTCTGGAG	GCTGAGGTGG	GAGGATGACT
143821	TGAGCCTAGG	CAGTCAAGGC	TGCACTGAGC	CCTGATCTTG	CCACTGCACT	CCAGTCTGGG
143881	CAACAGAGCA	AGACCCTGTG	TCAATATACA	TATGGACAAA	CTTAAAATTT	AAAATGAAAG
143941	CATACTACTG	ATACAGAATT	GAGTAGAGAT	GCAAAGCTAG	TCCTATAACC	AGACAATAA
144001	AGATAAAAAG	GAGAGTGGAA	GAGGTATGT	CATGAATTTT	ATGATAAATG	GCAATTGCAA
144061	ATATCCTGTA	GCAGAACAAA	ACAACAAAAC	TGTAGATAAA	ACATATCCAA	CCCTTTGGAA
144121	GGCCAAGGAG	GGAGGATTGT	TTGAGCCCAG	AAGTTGGAGA	CCAGCCTGGG	CAACATAGTG
144181	AGACCCTGTA	TCTAAAAAGG	AAGAAAGAAA	AAAAAAAAAA	GGATGATAAA	GTAGACAATA
144241	TTGAAAGCCA	TTTCTGCAA	ATACATAGTG	AATTGTATCA	GTAATTTTCT	TCCAACAGTG
144301	CAAAAATGAA	TAGATATTAG	TTGCCTGAAA	TAAAAATCAA	ATATCCAACA	AAAAATATTG
144361	ACTATCTAAT	AGTATCTAAG	CTAGTAAATT	TGGCCAGTTA	TAAAATGTCT	TAAATTTTTA
144421	TTTAAAAAAA	GAAAACCATA	TTTATAAGAA	GAGGTGATAA	AGAGAAATTA	TTTCAGTTAT
144481	GAAGATTTTG	TTAGAAAAC	ATGAGAAAA	AACATTTTTT	TGTTTTCAAA	AAGTGAAAGA
144541	TTAAGTTACC	AAACAGTTGC	TAAAGAATAC	CAGATGGCTG	AGCGTGGTGA	CTTATGCCTG
144601	TAATCCAGT	ACTTTGGAAG	GCCAAGGCAG	GAGGATCATT	TTAGGCCTGG	AGTTTCGAGC
144661	CAGCCTGGGC	ACTGTAGCAA	GACCCGTCTC	TATTAATAAA	AAAAAAAAAA	AAAAAAAGA
144721	ATACAAGACC	TTGCTAACAA	TAGCAAAGAT	CAATTAATTC	AAAATTTGAA	AAACTGTAAT
144781	TTATTTAGCT	TTAGAGTACT	CTCGTGATAT	GAGATTGCCA	AATTAATACT	TTGGGTGCAT
144841	TTCTTTTCTC	AAAGGACTTG	CAAAATTTACA	AAGAAGTGTT	GAAGAAAAGC	CACACATTGG
144901	CAGGTAATGT	TTGCAAAAGA	CAGATCTGAT	GAAGAACAAT	ATTTTATAGAA	TATACAAAGA
144961	ATACTTAAAA	CTCAACAGTA	AGAAAATAAC	CTGATTTAAA	GCAGGCCAAT	GACCTGAACA
145021	TCTGTTCCACC	AAAGAAGATA	CACAGATGCA	AGTATGCATA	TGAAAAGATG	CTTGACATCA
145081	TGTCATTAGG	GAACTGCAAA	TAAAGACAAG	TAGATAACCAC	TGCATACCTA	GTAGAATGAC
145141	CAAAATTTAG	AACACTGTCA	GCACCAAAGG	TTGCAAAGAT	ATGTAGCAAT	AGTAACCTTG
145201	TCATTACTGG	TGAGAATGCA	AAATGTGCAA	TCACCTTTGGA	AGACAGTTTG	GTGGTTTCTT
145261	ACAAAAGTAA	CCATACTTTT	ACCATAAGAT	TCACCAATCA	CACCTCCTAG	TATTTATCCA
145321	AAGGAATTGA	AAACTTATCT	CCACACAAAA	ACCTGCACAT	AGATGTTTAT	AGCAGCTTTA
145381	TTCATAATTT	ATCCAAAAC	TGGAAACAAG	ATGTCTTTCA	GTAGGTAAGT	GGATAACTGT
145441	GGTACTTCTG	AATAATGGAA	TGTTATTTAG	AGTTAAAAAG	AAATGCATTC	ACTTTGGGAG
145501	GCCGAAGTGG	GTGGATTGCT	TGAGGCCAGG	AGTTTGAGAC	CAGCCTGGTC	AACATGGGAA
145561	AACCCCAATT	AGCCGGGCAT	AGTGGCGTGA	GCCTGTAATC	CCAGCTACTC	GGGAGGCTGA
145621	GATATGAGAA	TCGTTTGAAC	CTGGGAGATG	GAGGTTGCAG	TGAGCCAGTG	CCACTGCACT
145681	TCAGCCTGGG	CAACAGAGCA	AGACTCCTCT	GTCTCAAAAA	AAAAAAAAAA	AAGAAAGAAA
145741	AGAAAAAAGA	AAAAGAAAAA	GAAAAGAAAC	GATCAAGCCA	TGAAAACACA	TGAAGGAAAC

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145801 TTAATGTAT GTTACTAAAA AGCCAACCTG AAAAGACTGC ATACTATATG ACTCCAACCTG
145861 ATGCAGGGCA AGCAAGCCAA AAATTAGGGC TTAGCCCGGG AAGAATTCAA GGGTGAAGTG
145921 GTGGTGTTAG CAACTTTTAC TGAAGCAGCA GTGTACAACA GCAGAACAGG TACTGCTCCT
145981 TGCTGAGCAG GGCTAACCCA TAAGTAATGT GCCCAGAGTA GCAGCTCAGG GGCAGTTCTG
146041 CAGTAATATA CCTGCTTTTA GTTAAGTGCA TGTTAAGGGG GATTATGCAG AAATTTCTAG
146101 AAAAAGAGTG GTAACCTCGG AGTAGGTACA GAGGAAAGAA GTCGATAATG TCCTGTTGTT
146161 GCCATGGCAA CGAAAAACTG ACATGGCGCT GGTGGGCGTG TCTTATGGAG AGGTGCTTTA
146221 ACCTCGTCCC TGTTTCGGCT AGTCTTCAAT CTGGTCCGGA GTAAAGTCCC TGCCTCCGGA
146281 GTTCACTCCT GCTTCCTGCT TCACAACCTG ATGACACTCT AGAAAAGACA GTAACATATG
146341 ACACAGTCAA AAGATTAGTT GATAGAAATT GGGTGACAGG AAGTGTTGAA AAGGCAGAAC
146401 ACAGGATTTT TAGGGCAGTG AAACCTCTGT GATACTATAA TGGTGAATAC ATGACATTAT
146461 ACATTTGTCA AAACCCATAG AAAGCACAAC ACCAAGAATA AACCCATAATG TAAATTACAG
146521 ACTTTCGTTG ATAATGACGT GTCAATGTAA GTTCAATTGT AATAAATGTA CTACTGTGGT
146581 GCTGGATGTC TATGGTGGGG GGACATTTTT GCTTCAATAG TTACAGTTGA AGTAAATGTT
146641 TGTGTTTCCC ACAATGCATA TGTAGAACT CTCACATTCA ATGTGATGGT CTTTGGAGGT
146701 GGGCTCTTTG GGTGATAGTT AGGTTTAGTT GAGATCCTAG CAGATCGAGT CTTTCATGATG
146761 GGCATGATGG GACTGGTCCC TTATAAGAAA AGACCAGAAA GCTAGCTCTC TCTTTGCCAT
146821 GTGAAGACAT AGCAGGAAGG TAGCCATCTG CAAGCTAGGA AAGGGCCTTC ACAAGAATC
146881 AACTCAGACC TCAGAACAGT GAGAGATAAA TTGTCGTTGT TTAAGTCACT CAGGCTGTGG
146941 TATTTTGT TT CAGCAGCCCA ACCTAAGACT GTTAATTGGA TTAGAAATTT CTTTTTGGGG
147001 ATGGTGTGTG GCGGGCGGGG GCGGGGAGT ACCTTTGTTA AGCTTTTATA TCAATGAGTT
147061 TGTAGGCTTT TCTTTTTTGG TCATTGACTA GGACAGTTTA AATAGTATGA GTGTGAAGGA
147121 GATTGTTGGT CATCTATTCG ATGTCCCTTC TCTGTTTTTT AATATGAGAA CTCCTGATTT
147181 TCAGCCAACT ACCCTGGAAG AAAAGCTAAT CTTTCTGACT TCTTAAGTGT GGCCATGTAC
147241 TAAATCTGG CTAATGCAAG GCAAGCCAAA GGTTTTATGA TAGGTTTATG GACACTAGAG
147301 TAAAGAGAG CTGTTGCACA CATGCTCTTC ACCCTACTTT TGTGTCTTT TTTCCATCCT
147361 ACAACTTGGG TTGTGAGTAT GATGGCTGGA ACTTTAGTGG CTCTCTTGGG TCCCAGGGGT
147421 AATTGAGGGG TGGCTGGAAG GAATCTGTGA TTTTCTGGAG TTTCCATACA CAAACAAGAC
147481 CTGGATTTTC TGGGCTTCCC AGACTTCCAC ATCTAGACTT GCTTTAAATG GGAGATAAAT
147541 AAACCTGTTT CAGCCACTGT CATTTTGGGC TATTTTATAG AACTTAATCT AATCTTCAAG
147601 GGTACATGAA TTGCTTTTCC TTAATAAAAA AATCAGCCAT AAAATCATCT TCTTTTTTCT
147661 TTTGTTCCCC ACATTATTTA GTTGGAGCTC TGTAACCTTT TTTTTTTTTT TTTTGGAGAC
147721 AAGGTCTTGC TCTGTCACTT AGGCTGGAAT TCAGTGCCAT GACCATGGCT CACTGCAGCC
147781 TTGCCCTCCT AGGCTCAAGC AATCCTCGTC TCAGCCTCCT GAGTAGCTGA AACTAAGGCA
147841 CATGCCACCA TGCCAGCTA ATTTCTTTTC TTTTAGAGAT GGGAGCCTTG CCCAGGCTAG
147901 TCTCAAACCT CTAGCCTCAA GTGATCCTCC CATCTCAGCC TCCCAAAGTG ACAGGATTAC
147961 AGGTGTGAGC CACCATGCCT GGCTGCTCTG TAAGTGTCTG AATTTTCAAT TGTATTTATC
148021 AGTCTGTTTA GATTTTCTTT CCCTTCTTGG GTCAGTTAGG CCATTGGTPT CTTTTTAAAG
148081 GTTTTCAAAT TTATTTGCAT CTAATCTTTC AAATTACTCT CAAAATTATT CCAGTATATA
148141 TTCTTTTGT CTTATTTTCT TCTGTATTCT TTATTAATAA AGCTAATGAT TTATCTAGCA
148201 GGACTTATAT TCTTTCCATA ACTTTCCTGC ACCCCAATTA ATCTCCAATT TTATATTTCT
148261 TCTGGCCTTC CTTATAGTTT CCACAGGTTT ATTTTATTCA TTTTTTAAAA CTTTTATTTA
148321 ATTGTTTATT TTATTATCAT TCTTTCTTAT TCAGCAATCT AAGTGCTTAG GGATATAGAA
148381 TTTCTCTTAA GCAGCATATG CTAGGCTTTA ACAATGTTAG GGAGGCCTCC CTTTTCTGGG
148441 GAAGACCACA CTTACATTAA CACAGGACTG TGGGATGCCA AGAGGTAGAG AAGAGCTTAT
148501 GAATATCCAG ATTACATCTT CACTGATCCT GCACAAAGGT GGGGTTCCCTC AGTTACCCAC
148561 TGGGTCCTAT TACCCAAGTC TGGGTCAGCA TACCGAGACT ACGGGTATAT AGAACAAGTG
148621 CAACTGGCGA TAATCCTTCT GTTGGGAGGA AAAATCTTTT TTTTCTATTC ATCTTAGGTT
148681 CTCCATCTGT GGCCCTATCA AGTAGACTAA CAAAAGACAG ATTGACAAGA CAGAAACAAA
148741 GCATGTGCAT TGTACAAACA CAGGGGAGTA CTGAGATGAA TACTCAAAG AGGATTTAGA
148801 ACTTGGGCTT ATATAGCATT TTAAGAAAAG AATACATTTT TTAAGTGACA AGGAAGACGA
148861 AAAGGACTTT GAGTTTCTAG TGCAGTAAAT TGTGGGAAGG CAACTTTTTC TTTCCCTTTT
148921 TTTTTTTTTT TTTTTAAAAA AAAAGACTTC TCTGGTGCTA TGTCCAGGCT GATAAGAGTC
148981 TAAAGTCTCT GGTGACTAAC TTTTGTCTCT CCCCAGGTAA GAAGACACCT TCACAATTTT

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149041	ATATCCTGCT	TTTAGGCAAA	TAGGGAGAGG	GCAGAGGTGT	TTGTTTGT	TTAATCTATT
149101	TTTTTCTCA	ATTGTCTTCA	ACTCAAAATA	CTTCTTATGC	CAAAGATGGC	ATATTCTGCT
149161	ACCCTTCACT	TACTACTTAC	AACCCAGCCT	CTATCATCAT	AATTAGAACT	TCTGACCCTG
149221	GGGAACATGG	GCAATAGTTT	GAACCTTTTT	ATATCTCCCT	TAGGCAGAGA	TGGAGGCCCA
149281	GCCATGCCTC	TGACATCTAG	ACACAACTGT	TGCTTCATTT	CTCCTATTCT	CAGAGGTGAT
149341	GTTGTAGGAC	TTCAACAAAT	ATCAGTAAAC	ATTAATTTTT	TTTTTCCTTG	AGGCACAGCA
149401	TGATCTTGGC	TTACTGCAGC	TGCTGCAGGC	TCAAGCAATT	CTCCTGCCTT	GGCCTCACGA
149461	GTAGCTGGGT	TACAGGCCCC	TACCACCATG	CCCGGCTAAT	TTTTGTATTT	TTAGTAGAGA
149521	CAGGGTTTCA	CCATGTTGGC	CAGGCTGGTG	TTGAACTCCT	GACCTCAAGT	GATCCACCTG
149581	CCTCAGCCTC	ACATAGTTCT	GGGATTACAG	GCGTGAGCCA	CCATGCCTGG	CCATCAATTT
149641	TTATGTCAAC	TCTAAATTAT	AACATTAGC	AATTTGTGA	CTTTTTATGG	TCATCAATTA
149701	TGTTGTTTAT	GTTTGTAGTT	TAGTCTGTGC	ATTACTCACT	CGGGTATGGT	AATTTGGTCT
149761	TTTTCAAAAT	GAAGTTAAGG	TCTATTTGCT	CTTCTCTGAA	TCATAATAAG	AACTGCCAAC
149821	AGCCATTTCA	GCAATAACTA	TTTACTGAGA	TTTTAAATA	TTTCAAGGTA	ATTGGTCTTA
149881	GCAGACTGGA	AAATACCAAA	TTCTTTTCCA	GAAGTGAATC	CCCCATCAAA	GTTCAATTTT
149941	ACTCATAATT	CCCTTTTCAT	TTGAAGCATC	TCATTGTAAG	CCAGTCTTAA	CCCTTCTCTC
150001	ACACTTTGCT	TGGCTGTTTC	TCAGGTAGAA	CTCAGTAAGT	CTGGTAGCCT	CCAGGACTGC
150061	CGCTTAGATT	ATTAAACAAC	ATGTCAGTGG	TTGGAAGAGT	CAATGTTATT	TTGATTTTTT
150121	TGTTTGTGTT	TGTTTTAAAT	GCAGTTGGCG	GATAATTGCA	GCTTTCTTTC	ATTCCTTACA
150181	TGAGTTCAAA	TGGCAGCAAA	CAAAGTAGGA	GAACGCAGAC	CTTCTGACTT	GTGGGTACCC
150241	CTACTCATCA	CCTGAAGACC	CTTGGAATC	AAAGCCCTGA	CCCATTAAAG	ACGGATGGAG
150301	ACAGCAACAT	ACGATCATCA	CTATTATCTT	GCTTTGCCCC	AGTCCAGGTT	AACCATCTGT
150361	GGTATTTTTA	GTTGCTAAGT	CCATATATTC	AACATAAATC	AATTATATAT	CCACTAAAT
150421	CTCAGCACTA	GTCTAACTAC	TAAGGAAATG	ACAGCGAAGA	AAACAGACCA	AACGTCTGCC
150481	CTTATGGGAT	TTATATTATT	TTCTCTGTGC	TGGTTAAACC	AAGGAGCTTC	TGCTCTTTTC
150541	CTTAGTCACC	TGGGGGAGGC	AGAAACAAAG	GAGAATATTG	ATAAACCTGG	AAATAGGGCC
150601	GGAGAGTATC	AGAGAAGGAA	GCCTTCGGGA	AAGTAAAGAT	GTGGCAGCCA	GTATTCCTGT
150661	TATAAAAGGA	TACAACTCCG	GCCTCATAGT	CCAGAAAAAT	TCCCACAAGC	AGGGGCTGCT
150721	CATGCAGATG	AAGGGAAGTT	GGGGGAGAAG	TAAGTGCTAC	ATAGCCTTTC	TTTTTGCACA
150781	GCCTGAGGGT	CCAGAATCCA	GACTGAGGCT	CTTGCTTCAT	GCCAGTGCCC	CTCTGCACAT
150841	TTTCCATACA	AACTCCTAAA	TCCCATCCGG	TTCCTTCGCC	AACATCCACT	TCAAAGTAAC
150901	GTCTTCCTGA	GGTGAAGCCT	TCACAACCCA	AGACACAGGG	GAAGGCAGTA	AATCTCCTGG
150961	AAGATGTGTC	CTGATTCTCC	TGGGTGTATC	CACGAGTCAC	TTGTCTCCGA	TCCTCAGAGA
151021	GAATTAGTTC	GTGATGAGCT	GTATCTGGAT	CCAGAGTCAC	ACTAAGTCGA	AAACAAAACA
151081	AAACAAACAA	AAATAATTTT	GTTGCTGTGA	AGAACACAGG	TTATTTTATT	TTATTTTATT
151141	TTGAGATGGA	GTGTTGCTGT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	CAACTCACTG
151201	CAACCTCCAC	CTCCTGGATT	CAGGCAATTC	TCCTGCCTCA	GCCTCCGGAG	TAAGTCCGAC
151261	TACAGGTGCG	CACCACCACA	AGTGGCTAAT	TTTTTTAAAT	TTTCTGTAGA	GATGGGGTTT
151321	CGCCATGTTG	GCCAGGCTGG	TCTCAAATC	CTGACCTGAA	GTGTTCCACC	CACCTCGGCC
151381	TCCCAAAGTG	CTGGATTACA	CAGGTGTGAG	CCACCATGCC	CAGCCACAAG	TTATTTTCAA
151441	TAAAACCAGC	CTGTGTTCAA	ACCCAATAT	TGTTTCTTAT	AACTGGGTG	AGCTTAGGCA
151501	AATCATTTAA	CTTCTGAGC	CTCAGTTTGT	TAAGTATAAA	GTGGAAATTA	CCGTATTTGT
151561	TGCAGAGAAT	GGTGGGTAGG	ATTGAATAAG	CTTATGTTTG	CTTAATGCTT	GGTAAATTC
151621	CTGGTACATG	GTAACCACCT	AATAAGTGGT	AGTTGTTGGG	GTGATCAGGC	CCAACACCAG
151681	GCCGTGGGGG	CTACAAAGTC	CGGCGGGGTC	AAAGGAATGA	GAAAAGACAA	GTTAAGAGTG
151741	CATAAAGTGG	GTCCAGGGTG	CCAGCACTAG	ATTGGAGGCT	GCAAAGGCC	TAAGCTCTGG
151801	GAGCCACAC	TATTTATTGG	TGATCAAAACA	AAGAAGCAGG	TGGTGAGGAC	GTGAGGGTAA
151861	ACAGGTGAGG	GCATGAGGAC	ATGGGGGTAG	AAAGGTAGTG	GTGCATTAAG	CGTAGCTGTG
151921	ACAGTTTAGC	ATTTTCTTTG	ACACATGTAG	AATATACTCT	GCTGCTTGAG	ATAGTAGAGG
151981	ACACGTTTAT	GAGTGAAAAG	CAAGGAACCA	ACAAGTCTGT	GCACTTTCCA	GAGGCTATGA
152041	GGGGTTTTAT	GCCCTGAGCC	CTGGGTCCA	TCCAAGCCAC	AAGGGGTTTT	ATGCCCTAGG
152101	CTTAGATTTG	TGGTGCGGCA	GGGCAGCCTT	CCACCATTTG	GCACAGAGCT	TGGTGTCCA
152161	AAGGCCACGA	GGGGTTTTGG	ACCCTGGACC	CCGGACATCT	TCCAAGACTC	TTTTACATTA
152221	TGACAGACAA	GCCAGTCTCT	CTTCAGCTCT	TCTAACAACA	TGTAGTAATA	ATGATATCAT

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152281 CAACATCATC TTCGTCTTAA TTATTCAAGG ATGCCAAGGT ACAGAACTAA CCTGTTAATA
152341 TGGTTACCAT CCTGTCCAAA GTTCTTCTCC CATGCAGGAC TTCCAGGAAT CATGAGACAG
152401 TTGAGCAGAA AGATACCTTT TCCCTTCTCT ACTGAATAAC CACCAACATT GAGAATCAGA
152461 GAGGGAAAAT GACTCAGCTA ATGTCTTAGC TTGTTATTGG AAGACCCAGG TCTCATGACA
152521 CATGCCTAGT CCCATGACTT TTAATTGTAA GCTCTTCTCT TCCCCCTCAG ATAATGTTCC
152581 ATAAGCATTG GTATGAGATA ATAATACACT GAGGACCAAT ATACATGAAA AATATCAGAC
152641 TAGAATCAAA CAAGACAGAA AAAAGATCTG ATAACCTAAA GTGAGATACT GAACAGTATG
152701 CAGTTTAAAA AATAAAAAAT GGTAATAGGA TGTTCTAACA AGAGAGTTAA GAAACCACTG
152761 TGCTACTGAG TTAAATGTTG ATCAGTTGGT CTGTGACAAT TAAGGAATTC AAGTATTGAG
152821 AAACACTTCC TGTGCTGGAT GCTCTCTGTT TGTTCTTCCA AATAATCCCT CACTTTTCCC
152881 TGTCTTGCTC TGTGCCCAGG AAGGCTGACA TGGACAGATT AACCAGGCTT TCCGCCCTCT
152941 GGCTTGGTTC AGCCAATGGG AAGCACCAGA GGAGACCATA GGGCACAAG AAGCAGCCTT
153001 GGGAGTATTC AGTACCCAG TCCCACGCTA TGATTTGGAG GGTCTGCATT CCTCTGCCTC
153061 TGGGCACACT CTAGTATAGT TACAGCTCCC TACACCTGCC ACTTGAGGCC CAGAGGAGGT
153121 GATGGCTCTC TAACTGTTCC TAGTCTGGG TGCTTCTGT TCCTTGTTGA TTTCCCAACT
153181 CCTCACCTTT GTAAATACCC TCCTTTTCA AACTCTATT AGTTAGCTTT TATCAGCCTG
153241 ACTCAGAGAA GTTTGGGGTT TCAATTCTA TTACCTGAAT GACCCAGGAA AACCCATGTT
153301 GAGAAATTAA AATGTTTACG GGGTGGTAAT ACCACTTAAG AGAAAAATA TCAATTGGAT
153361 TTTTAAAT CCACCTATCT ATTGGTGTGA CACATCAACA AAAACATATA GAAAGATTGG
153421 AAGCTAAAAG ATAGATAATA TAGTCATATA CTGTTATAGT ATTATATCAA AAGATATTAA
153481 GTCAGAGCAT TATTAAGAAT GGAAGAAGGG CCAGGTGTGG TGGCTCATGC CTGTAATCCC
153541 AGCACTTTGG GAGGCCAAGG CAGGCGGATC ACTTGAAGCC AGGAGTTCAA GACCAAGCCTG
153601 CCCAACATGG CAAAACCCTG GCTCTACCAA AAATACAACA ATTAGCTGGG CATTGTGGCA
153661 CATGCCTGTA ATCCCAGCTA CTTGGGAGGC TGAAGCACA GAATCACTTG AACCGGGAG
153721 GCAGAGGTTG CAGTGAGCTG AGATTTCCGC ACTACACTAC AGCCTGGGTG ACAGAGAGAG
153781 ATTCTGTCTC AAAAAAAAAA AAAAAGAAAG AATGAAAGGA GTCACCTAAA AAAGATAACA
153841 CAATTTTAAA CATAAATGTA CTACATTATT AGTGAATTCA TGTTTAGAAT TGTGTTAATA
153901 TACAAAGCAA AAATTGTAGA ATTATGGAG AAATGGACAA ATCTACAATC ATCATGGGAT
153961 GTTTTAAAT TCTTCTTTCC ATAATTGATA GATCAGGCAG ACCAAAAGAA AGAAATAAGG
154021 GAAGATACGG AAGGTCTGAA CAATCTAAGA AGCGCAATCT CATAGTCAAT ACATAAAGCT
154081 CAGCAATTGT TTAATAATAG TAAGCAGAGA ATATGCAGTT TTCTCAGGTA TAGATGGAAC
154141 ATGCACTAAC TGAGTAAATA CTAGGCAGAA AACAGTCTGA ACAAGTTTCA ATAAATCTGT
154201 ATTACACAGA TCATTTTCTC TAGCCTCAAT ATAAGATTAT AAACCAATAA TAAAAAGATG
154261 ACTAAAAAGA TTCTAAATAT TAGGAAATGT AAACACTATA TAAGTCATTA GAAGATGTAT
154321 AGAATGGAAC AATAATAAAA AGTTATTTAT AAAAATATAC AATGAAGCTA AAGCAGAATT
154381 TTAAGGAAAA TTTGTAGGCT TTAATGCTT ATCTTAGAAA AATTAAAAAG CTGAACATTA
154441 ATGAGCCAAG CATCTAATTT AAATTTTAAA AAGAACATAG AAAGCCAAAT ATAATTTTTT
154501 AAAAAGAAAA AATAGATATT AAACAATATA ACAGTGAAGT TAAAGAAAAC AAGAATGCAA
154561 TAAAGAGGAA AAACAACAAA AAAAAAGGT AGCTTCTTTT AAAAGAAATT TAATAAATA
154621 GACATACCTC CAATGAGATT TATCAAAGTA AGACAGAAGG CACAAATGGA ATGAATACAG
154681 AAACTTTTTA AATATTACAG AACTTTTATA TAAATCTTAT GCTACTAATA AAATTGAAAG
154741 TACTGATAAA ATTATTACTT CCTAGAAAAA ATATTCTGTA GTAAACTCA CTCAAAAAAC
154801 AAATAAAGCA TGGGCAGACC TAACATTTAA GAAATGAAAT CACTACTTTA AATTTTACCG
154861 ACAGATAATA AAACGTGCAT CTTTATCAAG CAAAAATGGA ACTTGTCAGT TTTATAGGAA
154921 ATTTAGAAGT CAAGGCATGA GTAATGCCAA TCTCATACCA AATCCTACAA AGAATAGAAA
154981 ATTATGGCTC CCGCTTATAG ACATAGATAT AGAACTCCTG CACAAAATAA TATAAATAAC
155041 AAACCAAATT TTATATTTGC AACTATACAT ATTATATGTG TATGTATTAT ATATGTTAAC
155101 ATATACATAT ATAATATGTA TAGCATATGT TCTACATATT ATATATGTAT AGTGTATGTA
155161 TTTTACAATA TATAAATGAA AACCCAATCT TTAATATATT CATCTAGATT GTCATATATG
155221 ACATATATAA TACATTACAT CAAAATGTG TACAATAATC AGGCCAGGCA CAGTGACTCA
155281 TGCCTGTAAT CCCAGCACGT TGGGAGGCTG AGGCGGGTCA ATCACTTGAG TCCAAGAGTT
155341 TGAGACCAGC CTGGTCAATA TGGCCAAATT CCATCTCTAC AAAAAATATG AAAAAATTATC
155401 CAGGCATTGT GGTGCACACC AATAGTCCCA GCTACTCGGG AAGCTGAGGT GAGAGGATCA
155461 CTTGAGCCTG GGAGGTGGAG ATTGCAGTGA GTCGAGATTG CGCCAGTGCA CTCCAGCCTG

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155521 GGTGGCAAAG GGAGACCCTG TCTCAAAAAA AAATTAAAAA ATTAGCCAGG TATGGTGGCC
155581 TGTTCCCTGTA GTCCCAGCAA CTGGGGAGGC TGAGGTGAGA AGATCACTTT AGCTCAGGTG
155641 GTGGAGCCAT GATCGCACCA CTGTACCACT CGGCTTGGGC AACAGAGTGA GAGCCTGTCT
155701 CGAAAAACA AATATATACA CACAGTAATC AATATATATA TTATATGTAC CAATCAATGC
155761 TTCACTTTTA TATATAATAT AGATTACATC TTATTAGATA TATAGTATTC CTTCTCCATA
155821 GATAGATAGA TACAGATATA GACATAGTAT CCTCTATCCA TATTAGAGAG AGGATACTAT
155881 ATATATCTAT AGCATATAGA GATGCTGTCT CAAAAAAATT TAAACATCAG CCAGATGTGG
155941 TGGCCCCTGC CTGTAGTCCC AGCTACTGGG GAGGCTGAAA TGAGAGGATT GCCATTGATC
156001 CTCTCATTGG TTGAGCCATA ATCGCACTAC TGCACCACTC AGCCTGGGAG ACAGAGGGAG
156061 ACCTGAGGTG GAAGGATATA GATATAGATA TATAAATAAA TATGTATAGA GAGAAATATA
156121 TATATGTGTG TATGTGTATA TATATATATT ATGAAGACAC TGGGAGAGAA TACTATATAT
156181 ATATGTGTGT GTGTATATAT ATATTATGAA GACACTGGTG GGATGGTTTC ATTACCAATT
156241 GGACCAAGAG TCCAGGTATG GAGCCAACAT GCAATGTTGT TGTGACTGA GCTGGCAGAG
156301 CACTGGTCAT AGTTACGGGA AAAGAAGGTC TCCAATGAGA CATACTTAAC AAAATATATG
156361 AACTTGCCAT ATACGTGGAG AGTTCTGGTG TGTATATAGC CTTCTCTCAC CAACCTAGCA
156421 ATTGTCTTCA TCATCATTAT AATGCTATCA GAGCAAAGAT GACAGCTAAA TTTTTTTGTC
156481 CCTTCTTCT TCTTCTCTT CCTTCCCCTC CCCACCTCT TTCTCTTCT CCTCCTCCTT
156541 CATCTCTCTT CTTTTTTTTT TTGAGATGGA GTCTTACTCT GTCGCTCAAG CTGGAGTGCA
156601 GTGGCACAAT CTCAGCTCAC TGCAACCTCT GCCTTCTGGG TTCAAGCAAT TCTGCCTAAG
156661 CCTCCAGAGT AGCTAGGACT GCAAGTGCAC ACCACCACAC CTGGCTAATT TTTGTATTTT
156721 TAGTAGAGAT AGGGTTTCAC AATGCTGGCC AGGCTGGTCT CAAACTCCTG CCCTCAAGTG
156781 ATCCTCCTGC CTCGGCCTCC CAATGTGCTG GGATTACAGG CGTAAGCCAC TGTACCCGGC
156841 CTCCTCCTTT AATAGACAGG GTCTAGCTCT GTTGCCAGG CTGGGTACAG TGGCGTGATC
156901 ATAGCTTACT GCAGCCTCGA ACTCCTGGGC TCAGGAGATC CTCCTGCCCT AGTCTCCCCA
156961 GTAGCTGGAA CTACAGGCAT AGCACACGGG GCTAATAAAA TTAATTAGGT GATAAAATTC
157021 ACTGCCCCCT GATGACTAAG CTCTTTGGAC ATAAAAGACA CAGACCTTGA AGGAAAATGT
157081 GTCTACTTAA TTTTGAAACC CTATTTATCA AAAACAGGA TGAAAATGCA AAATGCCATC
157141 CACATGCCAG AAGATATCAG CTATAATAAG TTCCCATAAA TCAATAAGGA AAAGAACCCA
157201 ATAAAAATTA TTAAACCACA GTAAATCATG GGTAAATCAC AGAGGCCCTGA AGGGCTAATG
157261 GACATACAAA AAGAATCTCA ATCTCACTAG TGAAATCAGA AAAGCACAAA TTAAGTACAC
157321 AATTAGGTAC CATTTTAAAT CTGTAAGACT GTCAAAATCA TAAATTATAT AAGTAAAGAC
157381 TCAGGGAGTT TTGGAGGAGT GAGAGCTCTT ATATTGCTTG TGGGGTAGAA TTGGAACAAT
157441 TTCAAGATCT GTAGTATCTG GTAAAATTAT GATATGCATC CCTCACACCA GCATGTCACT
157501 CCAAGGTATC TCCCTGGAGG GAACATTTAC GGGACACAAG GAAGCATGGA TAAGAATGTT
157561 CACAGTAGTA TTGTCTGCAA CAGCAACAAC AACAAAAAAA CCCAATAACA CACAACCTCA
157621 ATGCCCAGTC CACAAGGCAA TGGATTAAAT AAACCTCAGG CCGGAGATGG TGGTTCATGC
157681 CTGTAATCCC AACACTTTAG AAGGCCGAGG CGAGAGGACT GCTTGAGCCC AGGAGTTCAA
157741 GACCAGCCTG AACAAAATAA AGAGATAGTG TTTCTACAAA AAATTTTAA AAAATTAGCC
157801 AGACGTGGCA GTGCTTGCCT GTGGTCCCAG CTACTGGGGA AGCTGACGTG GGAGGATTGC
157861 TTAAGCCCAG GAATTTAAGG CTGCAGGGAG CCATGATGGG GCCATTGCAC TCCAGCCTGG
157921 GTGACAGAGT GAGACCCTGT CTAAGAGAGA TAAGTAAATA ACAACTTTGC ATTTTCTGCC
157981 ACATTGCAAA ATGGTGAGAG AGTGGTTTCT AGACTCTAGA CTCTTTCTAT GACTACCTTC
158041 TAGTTATGAG ATCCTACAAC ACTCACCTAA CCTCTCTGTG TCATATTTCC TCCTCTATAA
158101 AGCAAAAATG CCCCATATAG AGAGGACTGT GATATAAAAC AAGAACCAAG AAAAGTAAAG
158161 CTTTTCTAAT CTGTCACAGA CTAAAGAGTG CTCAGTATAT GTGAGTCATT ATTCCTGGTG
158221 CTGGTAGGAG TGTATGTTAC AACTTTGAGT CAAGTAATAT GGTACCATAT ATTAAGATTA
158281 ACAACAACCT CGGCAATCCC AGTTTGGGTT ATGTTCCCAA AAGAAATGAA AGCACCAGGA
158341 TATAAGGATG CATGGACTAG AAAGTTATTG TAGCAACATT GTAATACTA AGTTCTAAAA
158401 ACAGCCTGAA GCTCCATCAG TAGGGATATG GTTACATATA TTTATTATAT TCTTATGGAA
158461 TATTAGACAT AAAAAGTAAC GAGTAACATA GAAGAGACAG TGTATATATG TTACGTTTGT
158521 ACAAACCTAG GGAAAGATAT AGATCACCTT ACCTAGAGAA GTCAGATTGG AGACGGGTGG
158581 GAAAAACCTT GAACCTTCTC CTTATATCCT TTATATTGTT TGAAGTATTA AAATGTATTT
158641 GTTGCATCTG CTTGAAGGCA ATGTAAATA AAATAACAT ACATTTAAAA ATAAAAATAA
158701 AATTTATTCC TATCACTTTT GTAATAAAGC TGGGCACAGT GACTAACACT TGTAATCCTA

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